GREAT LAKES
BIOENERGY
RESEARCH CENTER

Department of Energy

Y1-10 FINAL REPORT

Great Lakes Bioenergy Research Center Final Report

TABLE OF CONTENTS

Narratives 2
GLBRC Research Highlights (2007-2017) 2
GLBRC Outreach (2007-2017) 6
GLBRC Personnel Development (2007-2017) 10
GLBRC Research Accomplishments (2007-2017) 13
GLBRC Publications (2007-2019) 58

GLBRC RESEARCH HIGHLIGHTS (2007-2017)

Genomic approaches to engineer plant lignin.

The ability to rationally engineer plant metabolism thereby producing cell walls with modified lignin has the potential to make major contributions to producing fuels and chemicals from biomass. Altering the chemical composition of lignin can increase the feasibility of converting the aromatic building blocks of this polymer into fuels or other valuable products, and make it easier to access the sugars in plant cell walls for conversion to fuels. In a widely publicized 2014 paper, GLBRC researchers reported on deployment of the "Zip-Lignin approach" in which plants are engineered to incorporate monomer-conjugates (named coniferyl- and sinapyl-ferulate into lignin), thereby introducing bonds that are easier to break but retain lignin's structural value to the plant. The Zip-Lignin approach has since been hailed as having "the potential to fundamentally change the economics of lignin degradation" (http://www.sciencemag.org/news/2014/04/cheaper-fuel-self-destructing-trees) and was nominated for Science's 2014 Breakthrough of the Year. Patents have been filed on this approach and agribusiness leaders are interested in licensing this innovation.

More recently we have demonstrated that hybrid poplar trees engineered to contain Zip-Lignin result in enhanced lignin levels via chemical pulping, indicating the utility of Zip-Lignin for poplar processing. Additionally, we have engineered pine tracheary elements to make a monomeric precursor of Zip-Lignin (sinapyl alcohol), indicating the potential for Zip-Lignin production in this species. Surprisingly, a survey of Zip-Lignin content in spermatophytes (seed plants) indicated that many angiosperm species naturally contain low, but detectable, levels of Zip-Lignins, knowledge that may aid in identification of superior sources of biomass that are more easily and economically deconstructed. Finally, we have identified additional genetic engineering approaches for improved processing of plants; for example, augmentation of available pools of soluble sucrose in poplar yields reduced lignin and altered cell wall structure, while mutation of a gene encoding a lignin biosynthetic enzyme increases Zip-Lignin levels in maize. GLBRC continues to evaluate Zip-Lignin performance in bioenergy-relevant crops such as grasses and identify ways to engineer plant lignins for improved processing.

By the end of Year 10, we have analyzed the impact of Zip-Lignin modification in poplar trees on the release of sugars with the use of different deconstruction methods. We have also built upon the Zip-Lignin strategy by genetically altering lignin biosynthesis in poplar and maize, resulting in increased Zip levels and greater sugar release. Field trials of Zip-Lignin poplar began in June 2016, thus we are two growing seasons into testing how translatable the Zip-Lignin approach is from greenhouse-grown material to field-grown trees.

Next-generation plant deconstruction strategies.

The energy and economic costs of deconstructing plant biomass represent a significant barrier to the production of cost-effective lignocellulosic fuels and chemicals. GLBRC developed an innovative, next-generation deconstruction method that is based on using γ-valerolactone (GVL), a "green" solvent that can be produced from plant material, to dissolve biomass followed by acid hydrolysis to release free sugars. The GVL technology is a feedstock agnostic, enzyme-free, and renewable strategy to produce sugar and lignin streams for conversion at lower cost than existing methods. The use of GVL for biomass deconstruction has been hailed by others as "a better way to make biofuels" (http://www.popularmechanics.com/cars/hybrid-electric/a10028/a-better-way-to-make-biofuels-16388312/), with the potential to "save billions on the cost to bring to market new biofuels" (http://www.jsonline.com/business/uw-madison-researchers-are-building-better-biofuels-b99190278z1-241974641.html). In addition to yielding high levels of C5 and C6 sugars from lignocellulosic biomass, the GVL method produces high-quality lignin with a native-like structure. When lignin production is integrated into the sugar platform, the method produces high-value products from each of the major biomass fractions in up to 80% yield. Recently a technoeconomic modeling study indicated that a method utilizing co-solvents to produce sugar and lignin streams and enable GVL recovery appears to be economically feasible, with a predicted modest decrease in minimum selling price per gasoline gallon equivalent as compared to other benchmarked processes.

By the end of Year 10, we have increased GVL hydrolysate production capacity within the Center, providing liter amounts of material to researchers for additional studies. We continue to characterize the chemical composition of hydrolysate to identify major inhibitors and evaluate their effect on microbial fermentation and conversion. A soon-to-be published manuscript describes the effect of GVL on yeast bioconversion and genetic engineering strategies to overcome toxicity, thus furthering the Center's mission to understand and mitigate microbial stress responses to plant hydrolysate. The Center continues research on depolymerization of GVL lignin into aromatic monomers or small oligomers, which may be biologically converted by specialized microbes into fuels and high-value products.

The GVL approach is one of two licensed GLBRC next-generation deconstruction strategies and has the potential to increase the economic viability of producing fuels and chemicals from a wide variety of lignocellulosic plant material, and both are currently being evaluated by industry.

The potential for marginal lands to meet a significant portion of cellulosic biomass needs.

Growing cellulosic biofuel crops on existing farmland conflicts with the necessity to sustainably meet the food needs of a burgeoning global population. Taking land out of food production can raise food prices and motivate continued conversion of non-cropland to agriculture, thereby creating a significant carbon debt. In a landmark paper that was hailed by others as laying the foundation for "biofuel production at the margins" (http://www.npr.org/2013/01/16/169538570/could-some-midwest-land-support-new-biofuel-refineries), GLBRC researchers showed that there is sufficient marginal land in the U.S. Midwest to grow a significant fraction of expected biofuel needs. Michigan field experiments were used to calibrate a cellulosic crop model that was applied to non-forested, non-farmed private land at high resolution across a 13-state region of the central U.S. Forty-five percent of available land fell within 50 miles of a potential biorefinery, and modeling showed that 25 percent of the legislated cellulosic biomass target could be met by productivity on these lands alone, for a substantial net carbon benefit. Biomass production on marginal lands avoids both food-fuel conflict and indirect land use costs. GLBRC continues to extend these analyses to a wider geographic region and incorporate techno-economic modeling to show reasonable potential configurations for future feedstock supplies.

Techniques to valorize lignin.

Lignin is a major component of plant cell walls. The ability to convert this polymer into aromatics and other valuable products has the potential to improve the sustainability and economic viability of lignocellulosic biorefineries. In a study that received a Presidential Green Chemistry Challenge Award in 2014, GLBRC researchers described a process that could "capture the full and unrealized value of biofuels" by converting what is currently burned as fuel into valuable products. At the heart of this process is the ability to convert processed lignin fractions into chemically defined products for conversion into high-value products.

By the end of Year 10, we have made several strides in our efforts to enable lignin valorization. GLBRC has taken several approaches, includin structural and biochemical analyses of bacterial enzymes that cleave lignin bonds; chemical analysis of dimeric degradation products released by lignin depolymerization to verify and quantify components used in lignification; utilization of formaldehyde to facilitate lignin monomer release during biomass depolymerization; identification of valuable extractable "clip-off" bioproducts like the flavonoid, tricin, shown to be involved in lignification in monocots; and identification of new and complex lignin compositions in palm species, including polyphenolic compounds, hydroxystilbenes, incorporated into lignin, and an unprecedented range of monolignol conjugates not previously known to be involved in lignification. All of these approaches help to inform our understanding of lignification and enable lignin valorization, both through extraction of naturally-occurring components and of compounds that have been engineered into bioenergy crops.

Genome- and systems biology-enabled identification of valuable co-products from biomass hydrolysates.

All published methods for processing plant biomass release materials that have a negative impact on the ability of biofuel microbes to produce products. Consequently, GLBRC uses a genome-enabled platform to identify toxic compounds within biomass hydrolysates, determine their mode of action, and develop ways to bypass their negative impact on biofuel microbes. A 2015 paper reported on an unexpected product of this activity, the discovery of a compound (poacic acid) within biomass hydrolysates that is a potent antifungal agent. As a natural plant-derived product, poacic acid has been described as a "valuable new weapon in our armamentarium of antifungals" (http://www.nature.com/nature/journal/v521/n7551/full/521168a.html). As patenting of poacic acid is in progress, an investment from our technology transfer partner has been used to prepare kilogram quantities of this compound for field trials as a natural fungicide against agricultural pests. In the near future poacic acid could be a prime example of how genome- and systems biology-enabled advances can provide fuels and valuable products that can be produced by future lignocellulosic biorefineries.

Feedstock variability and effects on deconstruction and microbial conversion.

Variation in environmental conditions during the growth of bioenergy crops could have significant detrimental effects on microbes during biofuel production. However, the effects of environmental stress on the "field-to-fuel" pipeline have not been well studied. A 2016 GLBRC paper examined the effects of variable precipitation on two bioenergy feedstocks, corn stover and switchgrass, sampling from a major drought year and two years with average precipitation. The study examined effects on hydrolysate chemical composition and the ability of yeast (Saccharomyces cerevisiae) or bacteria (Zymomonas mobilis) to ferment them to ethanol. While most hydrolysates were readily fermented to biofuel, the growth of yeast, but not Z. mobilis, was completely inhibited in hydrolysate generated from drought-stressed switchgrass. Biomass and compositional analysis revealed that drought-year switchgrass accumulated greater concentrations of soluble sugars, likely a stress response to drought, that were degraded to inhibitory compounds during pretreatment. These findings indicate that environmental variation can have significant effects on biomass hydrolysate properties and subsequent fermentation to biofuels. Knowledge of how these factors impact biofuel production can guide pretreatment and biocatalyst choices to mitigate inhibitory effects. GLBRC continues to study the effect of environmental stress on downstream processes, with planned studies on several other variables such as nitrogen fertilizer treatments, exposure to pathogens or pests, and variation in the plant microbiome. Ultimately, we aim to integrate the effects of environmental conditions and microbial molecular signatures into a predictive model that can guide biocatalyst choice or suggest engineering strategies to overcome inhibitory effects.

GLBRC OUTREACH (2007-2017)

Over the past ten years, GLBRC's broad research activities have had significant impact on the research community, industry, and society at large. Through formal educational programming, targeted activities, and informal interactions, innumerable individuals, groups, and organizations have been exposed to the impactful research being performed by the Center. These efforts have increased awareness of bioenergy research and the role it can play in addressing societal problems related to energy usage, supply, and security.

Stakeholder Outreach

GLBRC considers our stakeholders to not only be the taxpayers funding the program and the research community but also local, federal, and foreign government officials including the president, congressional members and staff, U.S. Department of Energy personnel, and other relevant officials.

GLBRC researchers and leadership have impacted the scientific community through research accomplishments and via membership in a diverse, yet relevant, set of advisory boards as well as society/organization officer roles. These include but are not limited to the Army Research Office, American Society of Microbiology, University of North Texas, University of Michigan, and the other BRCs.

In 2016, GLBRC answered the call from the Government Accountability Office (GAO) to represent the BRC program and aid in providing information that generated a report regarding the status of advanced biofuels research and development in the federal government. The two research objectives of the report were: (1) How does the federal government support advanced biofuels research and development, and where are current and planned federal efforts focused; and (2) What are expert and stakeholder views on the commercial viability of advanced biofuels in the short-, medium-, and long-term?

Specific examples of interactions: Over the period of the grant, GLBRC has hosted a wide range of distinguished leaders. Noteworthy are the following events: President Barack Obama and Secretary of Agriculture Tom Vilsack visited GLBRC pretreatment facility at MSU in 2014, prior to the President's signing of the Farm Bill on the MSU campus. In 2012, we proudly hosted DOE Secretary Steven Chu to discuss the research portfolio of the Center. Lastly, in 2015, shortly after congressional confirmation, DOE Undersecretary for Science Franklin Orr visited GLBRC at UW–Madison to see the impact of DOE's significant BRC program investment and to hear about other DOE-funded research on the UW–Madison campus.

Education and Outreach (E&O)

The goal of our E&O efforts has been to broaden the understanding of current issues in bioenergy for the general public, students, and educators at all levels. Bioenergy research and development are extremely important contemporary issues. Therefore, our E&O team used a variety of programs, events, university courses, and even publications (see complete publications list) to present research from GLBRC labs in a way that is accessible and interesting to a broad array of audiences. E&O resources and projects included (1) inquiry-based bioenergy classroom activities, (2) libraries of information on bioenergy, energy, and sustainability, (3) summer undergraduate research programs, (4) public speaking engagements, and (5) collaboration with existing education and outreach programs that address bioenergy and related issues, such as the First-Year Interest Groups (FIGs) program at the UW–Madison and iGEM at Michigan State University (MSU).

Over the past ten years we have directly connected more than 100 GLBRC faculty, students and staff with over 1,000 educators, a significant number of whom were curriculum coordinators or master teachers that went on to introduce our materials to other teachers in their area or school district. We roughly calculate that our E&O activities engaged more than 50,000 students per year through the cumulative work of these teachers and related GLBRC education materials.

Specific examples of impact: Craig Kohn and Lisa Sorlie were participants in both our Research Experience for Teachers (RET) and Bioenergy Institute for Educators (BIE) programs. Kohn participated in the BIE program in 2010 and in the RET program in Cameron Currie's lab in 2011, where he created curriculum materials. A national leader in high school agriculture education, Kohn is currently a graduate student in Joyce Parker's lab at MSU. He has an NSF fellowship for his bioenergy-related graduate studies. In 2013, Kohnworked with TED talks to create a video on biofuels and bioprospecting.

Sorlie is a teacher at Bonduel Middle School in Crawford County, WI. She participated in GLBRC's BIE program as well as the RET program as part of Chris Hittinger's lab. GLBRC wrote a story about her in April 2017 that was distributed broadly by University Communications. This story inspired UW Foundation to choose Sorlie to represent Crawford County for their 72 Counties project, and even put up a billboard in Crawford County with Sorlie on it.

Our summer undergraduate research programs brought over 150 students to GLBRC from an international applicant pool, many of whom were underrepresented minorities in the sciences. These students studied at three different sites (MSU, UW–Madison, and the Kellogg Biological Station) and were involved in bioenergy-related projects ranging from molecular biology to landscape-level ecology. Over 60% of these students went on to pursue post-graduate degrees.

Specific examples of impact: Gina Lewin and Grace Klinger both began with GLBRC as Research Experience for Undergraduates (REU) participants. Lewin was a 2009 participant of the program in Brian Pfleger's lab. Given she attended a small school for her undergraduate degree, the program was Lewin's first opportunity to experience doing research at a world-class research institution. She became a graduate student in Cameron Currie's lab and is now a postdoctoral fellow at Georgia Institute of Technology. The importance of the REU program and E&O activities continued to resonate with Lewin throughout her time with GLBRC that she continued to participate in many E&O activities. A story we wrote on her in March 2015 here.

Klinger started with GLBRC as a UW–Madison REU participant in 2013 while she was an undergraduate student at Wright State University. She is now a PhD student with Eric Hegg at

MSU. Klinger is studying a biomimetic approach to lignin deconstruction, and is a coauthor on a patent application for technology she developed as part of her graduate studies.

Community Outreach

Outreach to the general public was diverse and included participation in science events and festivals, attendance at events where bioenergy was a topic of interest, and working with individuals and groups that visited GLBRC. We also connected with the media via regularly occurring segments on the Larry Meiller Show on Wisconsin Public Radio and active Facebook and Twitter accounts. Such wide reach has allowed GLBRC to not only inform the general public but also attract talented individuals to the Center.

Specific examples of events: GLBRC representatives have been active, invited participants in the French American Science Festival in Chicago, an annual event sponsored by the French Consulate exposing hundreds of individuals to cutting-edge science. GLBRC ambassadors have hosted multiple yearly activities at the Wisconsin Science Festival, a four-day statewide science event connecting people to science, technology, and engineering topics at UW–Madison. Various investigators within GLBRC have been featured presenters for Wednesday Night at the Lab events and other broad outreach activities through the Wisconsin Alumni Association. Many MSU investigators were key speakers and advocates for hosting Fascination of Plants Day in 2017, which has been proposed to be an annual event forthcoming due to its inaugural success.

Specific examples of our wide reach: Jeff Vinokur, a former GLBRC student, has been featured through multiple media (print, television, touring, etc.) for his scientific passion and unique way of reaching many people. Vinokur's entertaining approach has made him quite memorable to all those who have seen or interacted with him.

Jan Hellinger is a high school student from Germany who has come to GLBRC each summer since 2015 and plans to return in 2018. Hellinger's participation in GLBRC was directly a result of our outreach activities and corresponding reputation.

Industry Outreach

Industry Outreach takes many forms at GLBRC, from Scientific Advisory Board (SAB) participation and conference attendance to intellectual property options, licenses and material transfer agreements. The relationship GLBRC has with its SAB members is a strength of the Center. Over the period of the grant there have been numerous, influential members of the bioeconomy involved with the board including venture capitalists, academic researchers, leadership from the other BRCs, as well as executives from the automotive, energy, chemical, and biobased industies. This balanced perspective has had a great influence on the GLBRC portfolio and has pushed knowledge of GLBRC technologies into industry.

Outside of the SAB, industry relations have taken a multipronged approach. Direct industry interactions include representatives from roughly sixty companies relevant to Center research either visiting or hosting GLBRC key personnel. The diversity of industry sectors that have had touch points with GLBRC is representative of the full scope of the research portfolio of the Center. Many of these interactions have resulted in successful technology transfer negotiations or internships for students in the Center with these companies. Additionally, GLBRC has participated in many rounds of the SBIR-STTR program resulting in further relationships being built with corporate partners. Start-up companies resulting from GLBRC intellectual property have strengthened the Center's reputation outside of strictly research-based institutions. Finally, GLBRC strategically utilizes attendance at meetings and conferences to deepen and/or broaden relationships with industry partners.

Importantly, GLBRC partners with the Wisconsin Alumni Research Foundation (WARF) and MSU-Technologies (MSU-T) to identify potential opportunities in all of the interactions described above. Relationships with these technology transfer entities have been critical to the success of our industry outreach.

Specific examples of interactions: Novozymes has been a critical partner with GLBRC. Access to their standardized enzyme cocktails at no cost has allowed Center researchers to develop industry-relevant standard operating procedures that have resulted in strong validation and applicability of Center studies.

GLBRC PERSONNEL DEVELOPMENT (2007-2017)

GLBRC is made of a diverse group of faculty, scientists, technicians, staff, undergraduate and graduate students, and postdocs. These include those funded by the DOE award as well as students or postdocs who have fellowships, other funding, or perform unfunded research in support of the Center.

Personnel Development

GLBRC has employed a wide-range of strategies to develop its personnel for greater impact either within the Center or beyond. Examples of activities that are used to provide either diversification or strengthening of skill-sets beyond that of scientific training include, but are not limited to, planning of the annual science meeting program as well as presenting at the event, sponsoring personnel to attend and present at meetings, workshops and conferences, exposing individuals to impactful outreach opportunities, and providing the opportunity for students to intern at relevant bioindustry companies and organizations.

Featured personnel (in alphabetical order):

Lauren Meyers

Lauren Meyers is the Wisconsin Energy Institute (WEI) and GLBRC Director of Administrative Services at the University of Wisconsin–Madison. Lauren has been with GLBRC since 2008, serving in a variety of administrative roles from being a business operations office employee to pre- and post-award research administrator positions and, finally, director of administrative operations, which affords her a seat on the GLBRC Management Team. She is a shining example of developing talent from within the organization.

Rebecca Garlock Ong

Dr. Ong is an Assistant Professor at Michigan Technological University. Rebecca was with GLBRC from the beginning as a graduate research assistant in Dr. Bruce Dale's Biomass Conversion Research Laboratory at Michigan State University until 2011. After obtaining her Ph.D. in 2012, Dr. Ong continued on as a research technician within the GLBRC at MSU and was then promoted to research assistant professor in 2013. In 2016 she began a faculty position in the Department of Chemical Engineering at Michigan Technological University Dr. Ong has supervised, advised, and taught many students and staff through her career as well as chaired and presented at meeting and conference sessions, become a member of many scientific societies, and is a respected reviewer of publications in her field. Rebecca contributed to GLBRC's recently awarded grant and is listed as key personnel. Dr. Ong went from a graduate assistant to a faculty project lead in her time with GLBRC.

Jennifer (Jennie) Reed

Dr. Reed is the Harvey D. Spangler Faculty Scholar and Associate Professor in the College of Engineering at the University of Wisconsin–Madison. At the time of the initial GLBRC proposal, Jennie was a faculty fellow at the University of California, San Diego. Upon arriving at the University of Wisconsin–Madison, she began to make an immediate impact resulting in numerous awards, recognitions and increased demand to serve on committees and boards. These include but are not limited to: the Presidential Early Career Award for Scientists and Engineers (2013), a DOE Early Career Award (2012), an NSF Career Award (2011), the KBase Scientific Advisory Committee, and the GLBRC Conversion Area Leadership Council. Additionally, Dr. Reed was a major contributor to the recently awarded GLBRC grant and will serve on the new GLBRC Management Team.

Matt Wisniewski

Matt Wisniewski is the WEI and GLBRC Director of Marketing and Communications. Matt has been with GLBRC since 2010, serving in a variety of communication roles from photographer to web-, graphic-, and document designer and, finally director of the entire communications team for the Center. Matt's work has been featured on multiple forms of media from print to web, including DOE materials. From having received his initial job offer from GLBRC on the day he graduated from UW–Madison to becoming the director, Matt is an incredible example of promoting talented individuals.

Center Alumni

Among the alumni of the Center that have been tracked, roughly 60% are in academia (35% of these are in faculty positions), 25% are in industry (including one Vice President, three Founders of business, 3 Directors and 3 CTOs) and 15% are working in non-profit research organizations. These individuals have spread across 28 states and 17 nations, making GLBRC's impact to the scientific community truly global.

Featured alumni (in alphabetical order):

Jeremy Luterbacher

As a Swiss National Science Foundation Postdoctoral Scholar, Dr. Luterbacher joined Great Lakes Bioenergy Research Center via Dr. Jim Dumesic's lab at the University of Wisconsin–Madison. Jeremy's contributions to the Center were numerous and significant during his short, two-year tenure working on solvent-aided chemical biomass depolymerization. He was a pivotal component of many high-profile publications such as the recent Shuai, L. *et al.* (2016) *Science* publication (Formaldehyde stabilization facilitates lignin monomer production during biomass depolymerization. *Science* **354**, 329-333 (2016) [DOI: 10.1126/science.aaf7810]). Dr. Luterbacher is now an Assistant Professor and head of the Laboratory for Sustainable and Catalytic Processing at École Polytechnique Fédérale de Lausanne (EPFL) in Lausanne, Switzerland, where he continues to collaborate with GLBRC researchers.

Maria Sardi

As an NSF Graduate Research Fellow in Microbiology, Maria Sardi joined the Center via Dr.

Audrey Gasch's lab. During her doctoral work, Maria not only published prolifically, but also generated intellectual property on *Saccharomyces cerevisiae* strains relevant to biofuels. Additionally, in 2016 Maria completed a successful summer internship in Cargill's Research and Development Biotechnology team. After completion of a Ph.D. at the University of Wisconsin–Madison, Dr. Sardi returned to Cargill as a Research Biotechnologist. Maria is an outstanding example of a Center alumna that took advantage of the development opportunities afforded to her by being a member of GLBRC.

Karen Stahlheber

Dr. Stahlheber was a post-doctoral researcher in the Sustainability area of GLBRC, studying the stability of perennial grassland communities during the establishment phase. Though Karen was officially assigned to Dr. Kay Gross' lab at the Michigan State University's W. K. Kellogg Biological Station, she worked in close collaboration with Dr. Randy Jackson's lab at the University of Wisconsin–Madison. Dr. Stahlheber was a poster presenter at the 2015 Genomic Sciences Program PI Meeting before moving on to her current position of Assistant Professor at the University of Wisconsin – Green Bay beginning in 2016. Karen shows how leveraging multiple GLBRC partners and field sites can be advantageous for all.

Garret Suen

Dr. Suen was a post-doctoral researcher in Dr. Cameron Currie's lab during the early years of GLBRC. In 2011, Garret became an Assistant Professor at the University of Wisconsin–Madison as part of the Wisconsin Bioenergy Initiative cluster hire. He has since been promoted to Associate Professor studying how symbiotic microbes convert biomass into usable nutrients for their herbivore hosts and how this is applicable to the production of biofuels and bioproducts.

GLBRC RESEARCH ACCOMPLISHMENTS (2007-2017)

Year 1 (Dec. 1, 2007 - Nov. 30, 2008)

- ***Arabidopsis XXT1, XXT2,* and *XXT5* encode xylosyltransferases.** In this first year of funding, we report on two studies of genes involved in xyloglucan biosynthesis in *Arabidopsis*. The first paper demonstrates that *XXT1* and *XXT2* encode xylosyltransferases that are required for xyloglucan biosynthesis; the second paper reports on the identification of a third xylosyltransferase, *XXT5*. These studies further our understanding of the mechanisms of xyloglucan biosynthesis, and offer opportunities for the direct modification of this polysaccharide in order to modify plant cell walls of economically important crop species.
  Cavalier DM, Lerouxel O, Neumetzler L, Yamauchi K, Reinecke A, Freshour G, Zabotina OA, Hahn MG, Burgert I, Pauly M, Raikhel NV, Keegstra K (2008) Disrupting two *Arabidopsis thaliana* xylosyltransferase genes results in plants deficient in xyloglucan, a major primary cell wall component. Plant Cell **20:** 1519-1537.
  http://www.plantcell.org/content/20/6/1519
  Zabotina OA, van de Ven WT, Freshour G, Drakakaki G, Cavalier DM, Mouille G, Hahn MG, Keegstra K, Raikhel NV (2008) Arabidopsis *XXT5* gene encodes a putative α-1,6-xylosyltransferase that is involved in xyloglucan biosynthesis. The Plant Journal **56:** 101-115.
  http://onlinelibrary.wiley.com/doi/10.1111/j.1365-313X.2008.03580.x/abstract
- **The role of native plans in maximizing arthropod-mediated ecosystem services in agricultural landscapes.** We provide a template for the evaluation of local plant genotypes in various areas, and show ways in which arthropod-mediated ecosystem services (AMES), which include crop pollination and pest control, can help maintain agricultural productivity and reduce the need for pesticide inputs. Agricultural producers can benefit from understanding how to best utilize native plants to enhance AMES.
  Isaacs R, Tuell JK, Fiedler A, Gardiner MA, Landis DA (2009) Maximizing arthropod-mediated ecosystem services in agricultural landscapes: The role of native plants. Frontiers in Ecology and the Environment **7:** 196-203.
  http://www.esajournals.org/doi/pdf/10.1890/080035

Year 2 (Dec. 1, 2008 - Nov. 30, 2009)

- **Maize traits relevant to the production of cellulosic ethanol.** In two studies we show that traits used for silage production and also for forage quality are predictors of cellulosic ethanol yield. Our results suggest that utilizing standard genetic variation of maize in breeding programs could substantially increase the amount of biofuels produced from stover per unit area of land.
  Lorenz AJ, Coors JG, de Leon N, Wolfrum EJ, Hames BR, Sluiter AD, Weimer PJ (2009) Characterization, genetic variation, and combining ability of maize traits relevant to the production of cellulosic ethanol. Crop Science **49:** 85-98.
  https://dl.sciencesocieties.org/publications/cs/abstracts/49/1/85
  Lorenz AJ, Anex RP, Isci A, Coors JG, de Leon N, Weimer PJ (2009) Forage quality and composition measurements as predictors of ethanol yield from maize (*Zea mays* L.) stover. Biotechnology for Biofuels **2:** 5.
  https://biotechnologyforbiofuels.biomedcentral.com/articles/10.1186/1754-6834-2-5
- **Radical coupling reactions produce a series of cross-coupled ferulate-coniferyl alcohol dimers.** Radical coupling reactions between ethyl ferulate, a simple model for feruloyl polysaccharides in plants, and coniferyl alcohol, a monolignol, were studied in

order to better understand the polymer cross-coupling interactions among polysaccharides and monolignols or lignin, mediated by ferulate (FA), in plant cell walls. Results from this study showed that ferulate readily cross-couples with coniferyl alcohol through free radical coupling mechanisms producing a series of cross-coupled FA/CA dimers. Thus, these results show that ferulates in plants indeed react with monolignols through free radical mechanisms producing a diverse array of cross-coupled dimers than previously reported.
Zhang A, Lu F, Sun R, Ralph J (2009) Ferulate-coniferyl alcohol cross-coupled products formed by radical coupling reactions. Planta **229:** 1099-1108.
https://link.springer.com/article/10.1007%2Fs00425-009-0894-6

- **High syringyl (S) poplar.** Poplar with exceedingly high syringyl monomer levels was produced by overexpression of the ferulate-5-hydroxylase (F5H) gene driven by a cinnamate-4-hydroxylase (C4H) promoter. The resultant transgenic lignins were more linear and displayed a lower degree of polymerization. The altered structural features of the transgenic lignin polymer, as revealed here, support the contention that there are significant opportunities to improve biomass utilization by exploiting the malleability of plant lignification processes.
  Stewart JJ, Akiyama T, Chapple C, Ralph J, Mansfield SD (2009) The effects on lignin structure of overexpression of ferulate 5-hydroxylase in hybrid poplar. Plant Physiology **150:** 621-635.
  http://www.plantphysiol.org/content/150/2/621
- **A new NMR tool for cell wall research.** We demonstrate how multivariate analysis of 2D NMR spectra can be used to visualize cell wall changes between sample types, where changes in composition and structure for both lignin and polysaccharides can subsequently be interpreted on a molecular level. Different *Populus* wood samples were used and we were able to show that differences in both lignin and polysaccharide composition that are difficult to detect with traditional spectral analysis were revealed by the multivariate approach. 2D NMR of dissolved cell wall samples combined with multivariate analysis constitutes a novel approach in cell wall analysis and provides a new tool that will benefit cell wall research.
  Hedenstrom M, Wiklund-Lindstrom S, Oman T, Lu F, Gerber L, Schatz P, Sundberg B, Ralph J (2009) Identification of lignin and polysaccharide modifications in *Populus* wood by chemometric analysis of 2D NMR spectra from dissolved cell walls. Molecular Plant **2:** 933-942.
  http://www.sciencedirect.com/science/article/pii/S1674205214607097?via%3Dihub
- **Insect symbioses: fungus growing ant research**. Approaches for studying insect-microbe symbioses using the attine ant-microbial symbiosis as a framework draw attention to particular challenges in the field of symbiosis including the establishment of symbiotic associations and symbiont function.
  Caldera EJ, Poulsen M, Suen G, Currie CR (2009) Insect symbioses: a case study of past, present, and future fungus-growing ant research. Environmental Entomology **38:** 78-92.
  https://academic.oup.com/ee/article-lookup/doi/10.1603/022.038.0110
  Pinto-Tomas AA, Anderson MA, Suen G, Stevenson DM, Chu FST, Cleland WW, Weimer PJ, Currie CR (2009) Symbiotic nitrogen fixation in the fungus gardens of leaf-cutter ants. Science **326:** 1120-1123.
  http://www.sciencemag.org/cgi/content/abstract/326/5956/1120
- **Ethanol production from AFEX-CS using *Saccharomyces cerevisiae*.** Enzymatic hydrolysis at high solids loading was identified as the primary bottleneck affecting overall ethanol yield and titer. Nutrients inherently present in corn stover and those resulting in the processed biomass can support microbial growth during fermentation. This process can improve economics of cellulosic ethanol production.

Lau MW, Dale BE (2009) Cellulosic ethanol production from AFEX-treated corn stover using *Saccharomyces cerevisiae* 424A(LNH-ST). Proceedings of the National Academy of Sciences of the United States of America **106:** 1368-1373.
http://www.pnas.org/content/106/5/1368.abstract

- **Chemical transformation of biomass into chemicals without pretreatment or enzymes.** Lignocellulosic biomass is a complex, heterogenous mixture of material that is highly recalcitrant to deconstruction, often requiring harsh chemical treatments and cellulolytic enzymes. This study describes the use of a privileged solvent, *N*,*N*-dimethylacetamide containing lithium chloride, that enables the synthesis of the renewable platform chemical 5-hydroxymethylfurfural in a single step from lignocellulosic biomass. The simplicity of the chemical transformation provides a new paradigm for the use of biomass as a raw material for renewable energy and chemical industries.
Binder JB, Raines RT (2009) Simple chemical transformation of lignocellulosic biomass into furans for fuels and chemicals. Journal of the American Chemical Society **131:** 1979-1985.
http://pubs.acs.org/doi/abs/10.1021/ja808537j
- **Economic and environmental impacts of alternative biofuel crops.** This study describes the initial steps in estimating the cost associated with substantial conversion of land from production of traditional crops to switchgrass and its potential environmental consequences. Initial modeling results indicate that farmers will convert to switchgrass production only with significant subsidies.
Jha M, Babcock BA, Gassman PW, Kling CL (2009) Economic and environmental impacts of alternative energy crops. International Agricultural Engineering Journal **18:** 15-23.
http://www.iaej.cn/EN/abstract/abstract15.shtml
- **Unexplored variables in land change, biofuels, and greenhouse emissions.** Appropriate cropping management strategies significantly reduce the payback period and enhance greenhouse gas benefits associated with the E85 fuel system compared to gasoline.
Kim H, Kim S, Dale BE (2009) Biofuels, land use change, and greenhouse gas emissions: some unexplored variables. Environmental Science & Technology **43:** 961-967.
http://pubs.acs.org/doi/abs/10.1021/es802681k
- **Increasing corn for biofuel production reduces biocontrol services in agricultural landscapes.** This study provides estimates of the value of natural biological control of the soybean aphid, a major pest in agricultural landscapes, and the economic impacts of reduced biocontrol caused by increased corn production in the Midwest. Findings suggest that the value of biocontrol services in the US economy may be underestimated, and furthermore, the development of cellulosic ethanol production processes that use various feedstocks could foster increased diversity in agricultural landscapes.
Landis DA, Gardiner MM, van der Werf W, Swinton SM (2008) Increasing corn for biofuel production reduces biocontrol services in agricultural landscapes. Proceedings of the National Academy of Sciences of the United States of America **105:** 20552-20557.
http://www.pnas.org/content/105/51/20552.long
- **Projected scenarios for conversion of cellulosic biomass to ethanol and environmental impacts of biomass refining.** Seven processes for ethanol and co-products production from switchgrass, as well as 14 mature biomass-refining technologies were evaluated. Results suggest that fossil fuel displacement is decidedly positive and production costs are competitive with gasoline. Furthermore, they offer reduced GHG emissions.
Laser M, Jin H, Jayawardhana K, Dale BE, Lynd LR (2009) Projected mature technology scenarios for conversion of cellulosic biomass to ethanol with coproduction thermo-chemical fuels, power, and/or animal feed protein. Biofuels, Bioproducts and Biorefining **3:** 231-246.
http://onlinelibrary.wiley.com/doi/10.1002/bbb.131/full

Laser M, Larson E, Dale BE, Wang M, Greene N, Lynd LR (2009) Comparative analysis of efficiency, environmental impact, and process economics for mature biomass refining scenarios. Biofuels, Bioproducts and Biorefining **3:** 247-270. http://onlinelibrary.wiley.com/doi/10.1002/bbb.136/full

Year 3 (Dec. 1, 2009 - Nov. 30, 2010)

- **Acyltransferases in triacylglycerol biosynthesis.** We report two significant advances in our understanding of triacylglycerol (TAG) biosynthesis: 1) the first paper establishes *in vivo* involvement of a second confirmed acyltransferase in TAG biosynthesis, and 2) the second paper demonstrates the utility of deep transcriptional profiling with multiple tissues as a gene discovery strategy for low-abundance proteins; we identified the acetyltransferase necessary and sufficient for the production of AcTAGs in *Euonymus* seeds and demonstrate that this activity can be introduced into the seeds of other plants. These advances allow for the evaluation of TAGs for biofuels and other applications.
  Zhang M, Fan J, Taylor DC, Ohlrogge JB (2009) *DGAT1* and *PDAT1* acyltransferases have overlapping functions in *Arabidopsis* triacylglycerol biosynthesis and are essential for normal pollen and seed development. Plant Cell **21:** 3885-3901. http://www.plantcell.org/content/21/12/3885
  Durrett TP, McClosky DD, Tumaney AW, Elzinga DA, Ohlrogge J, Pollard M (2010) A distinct DGAT with *sn*-3 acetyltransferase activity that synthesizes unusual, reduced-viscosity oils in *Euonymus* and transgenic seeds. Proceedings of the National Academy of Sciences of the United States of America **107:** 9464-9469. http://www.pnas.org/content/107/20/9464.abstract
- **A revolutionary method improvement for NMR of plant cell walls.** Here, the NMR fingerprint method to obtain solution-state NMR spectra of the entire array of plant cell wall polymers without the need for component fractionation has been improved by use of a new gel mixture, resulting in considerably elevated intensities and improved resolution of the NMR spectra. This modification therefore provides a more rapid method for comparative structural evaluation of plant cell walls than is currently available. With the new potential for chemometric analysis using the 2D NMR fingerprint, this gel-state method may provide the basis for an attractive approach to providing a secondary screen for selecting biomass lines and for optimizing processing and conversion efficiencies.
  Kim H, Ralph J (2010) Solution-state 2D NMR of ball-milled plant cell wall gels in DMSO-d_6/pyridine-d_5. Organic & Biomolecular Chemistry **8:** 576-591. http://pubs.rsc.org/en/Content/ArticleLanding/2010/OB/B916070A#!divAbstract
- **Natural variation of flowering time and vernalization responsiveness in *Brachypodium*.** Using *Brachypodium* as a model to better understand grass physiology and ecology, we report on the flowering time variability of natural *Brachypodium* accessions in response to temperature and light cues. Changes in both environmental parameters greatly influence when a given accession will flower, and natural *Brachypodium* accessions broadly group into winter and spring annuals. We show that some of the phenotypic variation is associated with changes in expression of orthologs of VRN genes, and thus VRN genes are a possible target for modifying flowering time in grass family bioenergy crops.
  Schwartz CJ, Doyle MR, Manzaneda AJ, Rey PJ, Mitchell-Olds T, Amasino RM (2010) Natural variation of flowering time and vernalization responsiveness in *Brachypodium distachyon*. BioEnergy Research **3:** 38-46. https://link.springer.com/article/10.1007/s12155-009-9069-3
- **Cell wall traits relevant to cellulosic ethanol production.** Maize hybrids with improved stover yield and quality are needed to support the emerging cellulosic biofuels industry, and

knowledge of the genetic variation, covariation, and genetic architecture of agronomic and cell wall traits will help maize breeders improve relevant traits through selective breeding and genetic engineering. We utilized a maize recombinant inbred line (RIL) population to map quantitative trait loci (QTL) and to evaluate the genetic relationships among traits relevant for cellulosic biofuel production, including grain yield, stover yield, neutral detergent fiber digestibility (NDFD), and glucan, xylan, and lignin concentration. This study provides information that will support the development of dual-purpose maize hybrids that are high in grain yield and also high in yield of digestible cellulosic feedstock.
Lorenz AJ, Coors JG, Hansey CN, Kaeppler SM, de Leon N (2010) Genetic analysis of cell wall traits relevant to cellulosic ethanol production in maize (*Zea mays* L.). Crop Science **50:** 842-852.
https://dl.sciencesocieties.org/publications/cs/articles/50/3/842?highlight=&search-result=1

- **Mass spectroscopy sequencing strategy for lignin oligomers.** Current methods to analyze lignin structure focus only on the frequency of the major monomeric units and inter-unit linkage types but do not provide information on the presence of less abundant unknown units and linkage types, nor on how linkages affect the formation of neighboring linkages. Such information can only be obtained using a sequencing approach. Here we describe, to our knowledge for the first time, a sequencing strategy for lignin oligomers using mass spectrometry. This paper launched a large area of study in “lignomics” and became the *de facto* standard for elucidating gene misregulation impacts on plant cell wall development.
  Morreel K, Dima O, Kim H, Lu F, Niculaes C, Vanholme R, Dauwe R, Goeminne G, Inzé D, Messens E, Ralph J, Boerjan W (2010) Mass spectrometry-based sequencing of lignin oligomers. Plant Physiology **153:** 1464-1478.
  http://www.plantphysiol.org/content/153/4/1464
- **Plant cell wall precursors separated and quantified by a liquid chromatography tandem mass spectroscopy method.** The biosynthesis of cell wall polymers involves enormous fluxes through central metabolism that are not fully delineated and whose regulation is poorly understood. We have established and validated a liquid chromatography tandem mass spectrometry method using multiple reaction monitoring mode to separate and quantify the levels of plant cell wall precursors.
  Alonso AP, Piasecki RJ, Wang Y, LaClair RW, Shachar-Hill Y (2010) Quantifying the labeling and the levels of plant cell wall precursors using ion chromatography tandem mass spectrometry. Plant Physiology **153:** 915-924.
  http://www.plantphysiol.org/content/153/3/915.long
- **Evaluation of AFEX pretreatment of switchgrass harvested in different seasons and locations in the production of ethanol.** This paper studied the effect of agronomic factors such as harvest time and location, as well as pretreatment- specific parameters, such as ammonia and water loading, and reaction time and temperature, on downstream production of biofuels. The findings indicate that all of these parameters have significant effects on production, suggesting that an integrative approach is best.
  Bals B, Rogers C, Jin M, Balan V, Dale BE (2010) Evaluation of ammonia fiber expansion (AFEX) pretreatment for enzymatic hydrolysis of switchgrass harvested in different seasons and locations. Biotechnology for Biofuels **3:** 11.
  https://biotechnologyforbiofuels.biomedcentral.com/articles/10.1186/1754-6834-3-1
  Bals B, Wedding C, Balan V, Sendich E, Dale B (2011) Evaluating the impact of ammonia fiber expansion (AFEX) pretreatment conditions on the cost of ethanol production. Bioresource Technology **102:** 1277-1283.
  http://www.sciencedirect.com/science/article/pii/S0960852410014185

- **Enzyme mixtures for various pretreatments of different feedstocks.** Here we studied several combinations of enzymes during AHP and AFEX pretreatment of corn stover using GENPLAT, a high-throughput biomass digestion platform that can be used to rapidly produce enzyme cocktails for specific pretreatment-biomass combinations. The technique assists in identifying optimal combinations for biomass deconstruction.
  Banerjee G, Car S, Scott-Craig J, Borrusch M, Walton J (2010) Rapid optimization of enzyme mixtures for deconstruction of diverse pretreatment/biomass feedstock combinations. Biotechnology for Biofuels **3:** 22.
  http://www.biotechnologyforbiofuels.com/content/3/1/22
  Banerjee G, Car S, Scott-Craig JS, Borrusch MS, Aslam N, Walton JD (2010) Synthetic enzyme mixtures for biomass deconstruction: production and optimization of a core set. Biotechnology and Bioengineering **106:** 707-720.
  http://onlinelibrary.wiley.com/doi/10.1002/bit.22741/full
  Banerjee G, Car S, Scott-Craig JS, Borrusch MS, Bongers M, Walton JD (2010) Synthetic multi-component enzyme mixtures for deconstruction of lignocellulosic biomass. Bioresource Technology **101:** 9097-9105.
  http://www.sciencedirect.com/science/article/pii/S0960852410012162
  Banerjee G, Scott-Craig JS, Walton JD (2010) Improving enzymes for biomass conversion: a basic research perspective. BioEnergy Research **3:** 82-92.
  https://link.springer.com/article/10.1007%2Fs12155-009-9067-5
  Walton J, Banerjee G, Car S (2011) GENPLAT: an automated platform for biomass enzyme discovery and cocktail optimization. Journal of Visualized Experiments**:** e3314.
  https://www.jove.com/video/3314/genplat-an-automated-platform-for-biomass-enzyme-discovery-cocktail
- **Characterization of cell wall deconstruction during pretreatment.** Multi-scale visualization and characterization of corn stover cell walls was carried out by various microscopy, magnetic resonance, and spectroscopy techniques to elucidate the mechanism of AFEX pretreatment. It was found that AFEX results in ultrastructural and physicochemical modifications within the cell wall that enhance enzymatic hydrolysis yield by 4- to 5-fold over that of untreated cell walls.
  Chundawat SPS, Donohoe BS, da Costa Sousa L, Elder T, Agarwai UP, Lu F, Ralph J, Himmel M, Balan V, Dale BE (2011) Multi-scale visualization and characterization of plant cell wall deconstruction during thermochemical pretreatment. Energy and Environmental Science **4:** 973-984.
  http://pubs.rsc.org/en/Content/ArticleLanding/2011/EE/c0ee00574f
- **Impacts of pretreatment on the fermentability of AFEX- and dilute acid-pretreated lignocellulosic biomass**. A detailed mass balance for major cell wall decomposition products and extractables was provided for AFEX- and dilute acid- treated corn stover, finding that the development of inexpensive, low thermochemical severity pretreatments that minimize formation of biological inhibitors while maximizing cell wall deconstruction is an important objective of the cellulosic ethanol industry.
  Chundawat SPS, Vismeh R, Sharma LN, Humpula JF, daCosta Sousa L, Chambliss CK, Jones AD, Balan V, Dale BE (2010) Multifaceted characterization of cell wall decomposition products formed during ammonia fiber expansion (AFEX) and dilute-acid based pretreatments. Bioresource Technology **101:** 8429-8438.
  http://www.sciencedirect.com/science/article/pii/S0960852410010084?via=ihub
  Lau M, Gunawan C, Dale B (2009) The impacts of pretreatment on the fermentability of pretreated lignocellulosic biomass: a comparative evaluation between ammonia fiber expansion and dilute acid pretreatment. Biotechnology for Biofuels **2:** 30.
  http://www.biotechnologyforbiofuels.com/content/2/1/30

- **Two-step simultaneous saccharification and co-fermentation (SSCF) to convert AFEX switchgrass to ethanol using *Saccharomyces cerevisiae*.** To overcome the reduced yield of ethanol production from AFEX-treated switchgrass, a 2-step saccharification and co-fermentation (SSCF) process was developed in which xylan is first hydrolyzed and fermented followed by the hydrolysis and fermentation of glucan. Compared to the traditional SSCF, this process results in higher xylose consumption, higher ethanol yield, and increased sugar conversion.
  Jin M, Lau M, Balan V, Dale BE (2010) Two-step SSCF to convert AFEX-treated switchgrass to ethanol using commercial enzymes and *Saccharomyces cerevisiae* 424A (LNH-ST). Bioresource Technology **101:** 8171-8178.
  http://www.sciencedirect.com/science/article/pii/S0960852410010072
- **An insect herbivore microbiome with high plant biomass-degrading capacity.** Using a combination of sugar composition analyses, metagenomics and sequencing, it was revealed that the fungus garden microbiome of leaf-cutter ants is composed of a diverse community of bacteria with high plant biomass-degrading capacity. Understanding how large-scale and rapid plant biomass degradation occurs in this highly evolved insect can help understand deconstruction processes.
  Suen G, Scott JJ, Aylward FO, Adams SM, Tringe SG, Pinto-Tomás AA, Foster CE, Pauly M, Weimer PJ, Barry KW, Goodwin LA, Bouffard P, Li L, Osterberger J, Harkins TT, Slater SC, Donohue TJ, Currie CR (2010) An insect herbivore microbiome with high plant biomass-degrading capacity. PLOS Genetics **6:** e1001129.
  http://dx.doi.org/10.1371%2Fjournal.pgen.1001129
- **New algorithm aids in refinement of metabolic models.** One of the challenges in constructing integrated metabolic and regulatory models is limited information on transcription factor-gene target interactions and computational methods to quickly refine models based on additional datasets. Researchers developed *Gene*Force, an algorithm to identify incorrect regulatory rules and gene-protein-reaction associations in such models and showed that it improves accuracy in the ability to predict growth phenotypes. New tools for the refinement of metabolic modeling will greatly aid in systems biology approaches to biofuel production.
  Barua D, Kim J, Reed JL (2010) An automated phenotype-driven approach (*Gene*Force) for refining metabolic and regulatory models. PLOS Computational Biology **6:** e1000970.
  http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1000970
- **Ionic liquid deconstruction of biomass produces sugars in high yield.** Although the use of ionic liquids to obtain fermentable sugars from biomass has been reported, the yields are typically low. Here we report a method for high-yielding sugars from untreated corn stover involving the gradual addition of water to the ionic liquid-catalytic acid mixture. Ionic liquids represent a promising approach to biomass deconstruction, provided that there be increased efficiency of sugar production and solvent recovery.
  Binder JB, Raines RT (2010) Fermentable sugars by chemical hydrolysis of biomass. Proceedings of the National Academy of Sciences of the United States of America **107:** 4516-4521.
  http://www.pnas.org/content/107/10/4516
- **Biomass-derived gamma valerolactone (GVL) converted to liquid alkenes.** GVL, a solvent that can be obtained from biomass-derived carbohydrates, was integrated into a process for production of condensable alkenes with molecular weights that can be targeted for gasoline or jet fuel. GVL is a potentially game-changing method for biomass deconstruction that avoids the use of expensive enzymes. Moreover, the method is green and renewable as GVL can be obtained from the biomass itself.

Bond JQ, Alonso DM, Wang D, West RM, Dumesic JA (2010) Integrated catalytic conversion of γ-valerolactone to liquid alkenes for transportation fuels. Science **327:** 1110-1114.
http://science.sciencemag.org/content/327/5969/1110

- **Computational method integrates transcriptional regulatory and metabolic networks to identify gene deletion or overexpression strategies to improve biofuel production.** Limitations of currently available computational methods for metabolic engineering are that they are often based on reaction deletions rather than gene deletions and do not consider the regulatory networks that control metabolism. The new algorithm, OptORF, takes into account known regulatory information to predict optimized production of biofuel from metabolic models.
  Kim J, Reed J (2010) OptORF: optimal metabolic and regulatory perturbations for metabolic engineering of microbial strains. BMC Systems Biology **4:** 53.
  https://bmcsystbiol.biomedcentral.com/articles/10.1186/1752-0509-4-53
- **Examination of natural genetic variation in wild yeast strains identifies traits for improved ethanol tolerance.** Stress due to biofuels themselves is a major factor that limits efficient microbial fermentation. The authors of this study show that a common lab strain cannot acquire higher ethanol tolerance after a mild ethanol pretreatment whereas many wild strains are adaptable. The genetic basis for this was examined and a number of genes were observed to be differentially expressed in wild vs. lab strains, including some that were previously not known to play a role in ethanol tolerance. These results demonstrate the power of comparative genomics and natural genetic variability in designing efficient biofuel microbes.
  Lewis JA, Elkon IM, McGee MA, Higbee AJ, Gasch AP (2010) Exploiting natural variation in *Saccharomyces cerevisiae* to identify genes for increased ethanol resistance. Genetics **186:** 1197-1205.
  http://www.genetics.org/content/186/4/1197
- **Water and energy footprints of bioenergy crops on marginal lands.** Water and energy demands associated with bioenergy crop production on marginal lands are inextricably linked with land quality and land use history. To illustrate the effect of land marginality on bioenergy crop yield and associated water and energy footprints, we analyzed several large-scale sites converted from either Conservation Reserve Program (CRP) or conventional agricultural land use to no-till soybean for biofuel production. The analysis of biophysical characteristics of the sites in relation to water and energy use suggests that crops and management systems similar to CRP grasslands may provide a potential strategy to grow biofuels that would minimize environmental degradation while improving the productivity of marginal lands.
  Bhardwaj AK, Zenone T, Jasrotia P, Robertson GP, Chen J, Hamilton SK (2011) Water and energy footprints of bioenergy crop production on marginal lands. Global Change Biology – Bioenergy **3:** 208-222.
  http://onlinelibrary.wiley.com/doi/10.1111/j.1757-1707.2010.01074.x/abstract
- **Evaluation of bacterial communities in the rhizosphere of biofuel crops grown on marginal lands.** We studied bacterial communities in the rhizosphere of five biofuel crops cultivated in four locations in Michigan to determine which factors were correlated to changes in the structure of those communities. Bacterial communities grouped by location rather than by crop and their structures were correlated to soil attributes, principally pH, organic matter, and nutrients. The effect of plant species was low but significant, and interactions between locations, plant species, and soil attributes account for most of the explained variation in the structure of bacterial communities, showing a complex relationship between bacterial populations and their environment.

da C. Jesus E, Susilawati E, Smith SL, Wang Q, Chai B, Farris R, Rodrigues JLM, Thelen KD, Tiedje JM (2010) Bacterial communities in the rhizosphere of biofuel crops grown on marginal lands as evaluated by 16S rRNA gene pyrosequences. BioEnergy Research **3:** 20-27.
https://link.springer.com/article/10.1007/s12155-009-9073-7

- **Modeling of biofuel production based on efficient land use without affecting animal feed production.** Our analysis explores potential changes in agriculture that utilize new technology and approaches to meet and reconcile what appear to be competing demands for food, biofuels, and environmental services. We conclude that the United State can produce 400 billion liters of ethanol annually on farmland and reduce greenhouse gas emissions by 10% without harming food production.
Dale BE, Bals BD, Kim S, Eranki P (2010) Biofuels done right: land efficient animal feeds enable large environmental and energy benefits. Environmental Science & Technology **44:** 8385-8389.
http://pubs.acs.org/doi/abs/10.1021/es101864b
- **Understanding the microbial role in soil carbon stabilization.** Here, we describe the use of an Absorbing Markov Chain (AMC) to model the dynamics of soil C transformations among three microbial states: living microbial biomass, microbial necromass, and C removed from living and dead microbial sources. We find that AMC provides a powerful quantitative approach that allows prediction of how C will be distributed among these three states, and how long it will take for the entire amount of initial C to pass through the biomass and necromass pools and be moved into atmosphere. Our work represents a first step in attempting to quantify the flow of C through microbial pathways, and has the potential to increase our understanding of the microbial role in soil C dynamics
Liang C, Cheng G, Wixon D, Balser T (2010) An Absorbing Markov Chain approach to understanding the microbial role in soil carbon stabilization. Biogeochemistry **106:** 303-309.
https://link.springer.com/article/10.1007/s10533-010-9525-3
- **Bird communities in future bioenergy landscapes of the Upper Midwest.**
Here, we use data from the North American Breeding Bird Survey to forecast the impact of potential bioenergy crops on avian species richness and the number of bird species of conservation concern in Midwestern landscapes. Our analysis suggests that expanded production of annual bioenergy crops (e.g., corn and soybeans) on marginal land will lead to declines in avian richness between 7% and 65% across 20% of the region, and will make managing at-risk species more challenging. In contrast, replacement of annual with diverse perennial bioenergy crops (e.g., mixed grasses and forbs) is expected to bring increases in avian richness between 12% and 207% across 20% of the region, and possibly aid the recovery of several species of conservation concern.
Meehan TD, Hurlbert AH, Gratton C (2010) Bird communities in future bioenergy landscapes of the Upper Midwest. Proceedings of the National Academy of Sciences of the United States of America **107:** 18533-18538.
http://www.pnas.org/content/107/43/18533.abstract

Year 4 (Dec. 1, 2010 - Nov. 30, 2011)

- **Genome-wide maize transcription atlas.** Maize is an important model species and has also emerged as a potential feedstock and model system for bioenergy research due to recent worldwide interest in developing plant biomass-based, carbon-neutral liquid fuels. To understand how the underlying genome sequence results in specific plant phenotypes, information on the temporal and spatial transcription patterns of genes is crucial. Here we

present a comprehensive atlas of global transcription profiles across developmental stages and plant organs, creating a valuable resource for gene discovery and functional characterization in maize.
Sekhon RS, Lin H, Childs KL, Hansey CN, Buell CR, de Leon N, Kaeppler SM (2011) Genome-wide atlas of transcription during maize development. The Plant Journal **66:** 553-563.
http://onlinelibrary.wiley.com/doi/10.1111/j.1365-313X.2011.04527.x/abstract

- **Photoprobes for studying *in vitro* lignification.** Here, we report synthetic protocols for preparing fluorescent tagged analogues of coniferyl alcohol (CA) and demonstrate their compatibility with normal monolignols for forming synthetic lignins. We anticipate that fluorescence-tagged monolignols will be useful for *in vitro* and *in vivo* studies of cell wall lignification.
  Tobimatsu Y, Davidson CL, Grabber JH, Ralph J (2011) Fluorescence-tagged monolignols: synthesis, and application to studying *in vitro* lignification. Biomacromolecules **12:** 1752-1761.
  http://pubs.acs.org/doi/abs/10.1021/bm200136x
- **Xylan synthesis in *Arabidopsis*.** Xylan is the principal hemicellulose in the secondary cell walls of eudicots and in the primary and secondary cell walls of grasses and cereals. The biosynthesis of this important cell wall component has yet to be fully determined although a number of proteins have been shown to be required for xylan synthesis. To discover new genes involved in xylan biosynthesis we explored the psyllium (*Plantago ovata Forsk*) seed mucilaginous layer through EST profiling; we conclude that two genes, *IRREGULAR XYLEM* (*IRX*) *15* and *IRX15-LIKE* (*IRX15-L*), function in a redundant manner and are involved in xylan biosynthesis.
  Jensen JK, Kim H, Cocuron J-C, Orler R, Ralph J, Wilkerson CG (2011) The DUF579 domain containing proteins IRX15 and IRX15-L affect xylan synthesis in *Arabidopsis*. The Plant Journal **66:** 387-400.
  http://onlinelibrary.wiley.com/doi/10.1111/j.1365-313X.2010.04475.x/abstract;jsessionid=1C30408815FAC56321024C8F5F5DE0A2.f02t02
- **CGR3, a protein involved in pectin methylesterification.** Pectins are a large group of complex polysaccharides of the plant cell wall that are made in the Golgi and secreted to the wall. The methylesterification of pectins is believed to be an important factor for the dynamic properties of the cell wall. Here, we report on a protein of unknown function discovered using an extensive proteomics analysis of cotton Golgi; our results suggest that CGR3 plays a role in the methylesterification of homogalacturonan in *Arabidopsis*.
  Held MA, Be E, Zemelis S, Withers S, Wilkerson C, Brandizzi F (2011) CGR3: a golgi-localized protein influencing homogalacturonan methylesterification. Molecular Plant **4:** 832-844.
  http://www.sciencedirect.com/science/article/pii/S1674205214607693?via%3Dihub
- **Cellulose-degrading bacteria associated with invasive woodwasp *Sirex noctilio*: from ecosystem to enzyme structure.** We developed a detailed understanding of how the microbes in the *Sirex noctilio* ecosystem act together to degrade biomass by characterizing the Sirex-associated microbiome, and focusing on the Streptomyces sp. SirexAA-E, which has a particularly strong biomass degrading capacity.
  Adams AS, Jordan MS, Adams SM, Suen G, Goodwin LA, Davenport KW, Currie CR, Raffa KF (2011) Cellulose-degrading bacteria associated with the invasive woodwasp *Sirex noctilio*. The International Society for Microbial Ecology Journal **5:** 1323-1331.
  http://www.nature.com/ismej/journal/v5/n8/full/ismej201114a.html
- **Alkaline peroxide pretreatment of corn stover.** Alkaline hydrogen peroxide (AHP) has several attractive features as a pretreatment for lignocellulosic biomass, especially since it

works well on woody materials. We studied the feasibility of scaling-up the AHP process, examining impacts on enzyme loading, enzyme composition, and ethanol yields.
Banerjee G, Car S, Liu T, Williams DL, López Meza S, Walton JD, Hodge DB (2012) Scale-up and integration of alkaline hydrogen peroxide pretreatment, enzymatic hydrolysis, and ethanolic fermentation. Biotechnology and Bioengineering **109:** 922-931.
http://onlinelibrary.wiley.com/doi/10.1002/bit.24385/abstract
Banerjee G, Car S, Scott-Craig J, Hodge DB, Walton JD (2011) Alkaline peroxide pretreatment of corn stover: effects of biomass, peroxide, and enzyme loading and composition on yields of glucose and xylose. Biotechnology for Biofuels **4:** 16.
http://www.biotechnologyforbiofuels.com/content/4/1/16

- **Corn harvest strategies for combined starch and cellulosic bioprocessing to ethanol.** We compared the ethanol yield of several sources of biomass to better understand the effects of whole-plant harvesting vs. traditional harvesting methods. Results suggest that whole-plant harvesting coupled with whole-plant bioconversion to ethanol is a viable alternative to the convention of separate grain and stover harvesting and bioprocessing.
  Gao J, Qian L, Thelen KD, Hao X, da Costa Sousa L, Balan V, Dale BE (2011) Corn harvest strategies for combined starch and cellulosic bioprocessing to ethanol. Agronomy Journal **103:** 844-850.
  https://dl.sciencesocieties.org/publications/aj/articles/103/3/844
- **CBP performance of *Clostridium phytofermentans* on AFEX-treated corn stover for ethanol production.** Consolidated bioprocessing (CBP) is believed to be a potentially cost-efficient and commercially viable way to produce cellulosic biofuels. We evaluated the performance of *Clostridium phytofermentans* on AFEX-treated corn stover, and found that decomposition products could help increase the ethanol yield during CBP and that particle size plays a crucial role in the enhancement of sugar conversion by CBP.
  Jin M, Balan V, Gunawan C, Dale BE (2011) Consolidated bioprocessing (CBP) performance of *Clostridium phytofermentans* on AFEX-treated corn stover for ethanol production. Biotechnology and Bioengineering **108:** 1290-1297.
  http://dx.doi.org/10.1002/bit.23059
- **Mining for new glycoside hydrolases.** From the metagenome sequences of an anaerobic microbial community actively decaying poplar biomass, we identified approximately 4,000 glycoside hydrolase (GHase) homologues. Based on homology to GHase families/activities of interest and the quality of the sequences, candidates were selected for full-length cloning and subsequent expression in *E. coli*.
  Li L-L, Taghavi S, McCorkle S, Zhang Y-B, Blewitt M, Brunecky R, Adney W, Himmel M, Brumm P, Drinkwater C, Mead D, Tringe S, van der Lelie D (2011) Bioprospecting metagenomics of decaying wood: mining for new glycoside hydrolases. Biotechnology for Biofuels **4:** 23.
  http://www.biotechnologyforbiofuels.com/content/4/1/23
- **Genome sequence of the leaf cutter ant revealed insights into its symbiotic lifestyle. GLBRC Researchers Successfully Leverage DOE Funding for Ant Genome Research.** With a Roche Diagnostics 10 Gigabase Sequencing and Transcriptomics Analysis Grant to sequence the leaf-cutter *Atta cephalotes* ant genome we found that leaf-cutters are unique among ants because they farm a specialized, mutualistic fungus that serves as their primary food source. The ants maintain fungal gardens and the waste dumps harbor other microbial symbionts including nitrogen-fixing bacteria and others that appear to help the fungus degrade plant biomass.
  Suen G, Teiling C, Li L, Holt C, Abouheif E, Bornberg-Bauer E, Bouffard P, Caldera EJ, Cash E, Cavanaugh A, Denas O, Elhaik E, Favé M-J, Gadau J, Gibson JD, Graur D, Grubbs KJ, Hagen DE, Helmkampf M, Hu H, Johnson BR, Kim J, Marsh SE, Moeller JA, Muñoz-

Torres MC, Murphy MC, Naughton MC, Nigam S, Overson R, Rajakumar R, Reese JT, Scott JJ, Smith CR, Tao S, Tsutsui ND, Viljakainen L, Wissler L, Yandell MD, Zimmer F, Harkins TT, Taylor J, Slater SC, Clifton SW, Warren WC, Elsik CG, Smith CD, Weinstock GM, Gerardo NM, Currie CR (2011) The genome sequence of the leaf-cutter ant *Atta cephalotes* reveals insights into its obligate symbiotic lifestyle. PLOS Genetics **7:** e1002007. http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1002007

- **Technoeconomic analysis of liquid hydrocarbon fuel production from lignocellulosic biomass suggests an economically competitive process.** This study developed and evaluated a novel catalytic strategy for the transformation of lignocellulosic biomass to levulinic acid (LA), LA to gamma valerolactone (GVL), and GVL to butene and other heavy alkenes. Economic evaluation indicated that the process could be economically competitive; further improvements to the process were identified that are predicted to enable additional cost savings.
  Sen MS, Henao CA, Braden DJ, Dumesic JA, Maravelias CT (2012) Catalytic conversion of lignocellulosic biomass to fuels: process development and technoeconomic evaluation. Chemical Engineering Science **67:** 57-67. http://www.sciencedirect.com/science/article/pii/S0009250911004830
- **New method to identify lignocellulose-degrading bacteria.** Environmental microbes represent an abundant and diverse source of lignocellulose-degrading enzymes however identification of such microorganisms is slow due to a lack of rapid screening methodologies. This study describes a new method that employs acrylamide rather than agar as the solidifying agent. Both Gram-positive and Gram-negative organisms possessing cellulose and hemicellulose degrading activities were identified from environmental samples.
  Gardner JG, Zeitler LA, Wigstrom WJS, Engel KC, Keating DH (2011) A high throughput solid phase screening method for identification of lignocellulose-degrading bacteria from environmental isolates. Biotechnology Letters **34:** 81-89. https://link.springer.com/article/10.1007%2Fs10529-011-0742-1
- **Fluorous ionic liquid that dissolves cellulose and is recoverable.** Ionic liquids are an attractive class of solvents for biomass deconstruction however their chemical properties hinder recovery. Here were report that of seven fluorous ionic liquids examined, 1-ethyl-3-methylimmidazolim (EMIM]Cl dissolves cellulose and can be recovered from glucose product. The ability to recover and recycle the ionic liquids is necessary due to the high cost of these promising solvents.
  Caes BR, Binder JB, Blank JJ, Raines RT (2011) Separable fluorous ionic liquids for the dissolution and saccharification of cellulose. Green Chemistry **13:** 2719-2722. http://pubs.rsc.org/en/content/articlelanding/2011/gc/c1gc15776k - !divAbstract
- **Cellular response to endogenous overproduction of free fatty acids (FFA) has a large membrane stress component.** A strain of *E. coli* that overproduced medium-chain FAs was shown to have greatly reduced inner membrane integrity and viability by the early stationary phase of growth. Membrane stresses were further implicated by gene and protein expression analyses, which indicated an increase in phage shock proteins and the marA/rob/soxS stress regulon. These studies show that endogenous overproduction of FAs is negatively correlated with viability and efforts to obtain higher titers of FAs will require mitigation of the toxic effects of FA overproduction.
  Lennen RM, Kruziki MA, Kumar K, Zinkel RA, Burnum KE, Lipton MS, Hoover SW, Ranatunga DR, Wittkopp TM, Marner WD, 2nd, Pfleger BF (2011) Membrane stresses induced by overproduction of free fatty acids in *Escherichia coli*. Applied and Environmental Microbiology **77:** 8114-8128. http://aem.asm.org/content/77/22/8114.long

- **Comparative genomics approach identifies yeast genes important for xylose utilization.** Many microbes are unable to metabolize pentose sugars such as xylose yet efficient conversion of lignocellulosic biomass requires that microbial catalysts be able to utilize both C5 and C6 sugars. Thus study compared the genomes of two xylose utilizing species of yeast (*Spathaspora passalidarum* and *Candida tenuis*) to 14 other Ascomycete genomes and identified many genes involved in xylose utilization. Several of these genes significantly improved xylose utilization when engineered into *S. cerevisiae*, indicating that comparative genomics is a useful approach to identify genes important for biofuel production.
  Wohlbach DJ, Kuo A, Sato TK, Potts KM, Salamov AA, LaButti KM, Sun H, Clum A, Pangilinan JL, Lindquist EA, Lucas S, Lapidus A, Jin M, Gunawan C, Balan V, Dale BE, Jeffries TW, Zinkel R, Barry KW, Grigoriev IV, Gasch AP (2011) Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. Proceedings of the National Academy of Sciences of the United States of America **108:** 13212-13217.
  http://www.pnas.org/content/108/32/13212.abstract
- **A spatially explicit bioeconomic modeling approach for biomass supply from alternative cellulosic and crop residues.** A new bioeconomic model predicts biomass supply and its environmental impacts; the model captures the opportunity cost of switching to new cellulosic crops. A key finding is that biomass from cellulosic crops has superior climate and water quality outcomes.
  Egbendewe-Mondzozo A, Swinton SM, Izaurralde RC, Manowitz DH, Zhang X (2011) Biomass supply from alternative cellulosic crops and crop residues: a spatially explicit bioeconomic modeling approach. Biomass and Bioenergy **35:** 4636-4647.
  http://www.sciencedirect.com/science/article/pii/S0961953411004648
- **Assessment of regional biomass processing depots.** In the first of two reports this year, we conducted comparative life cycle assessment (LCA) of distributed and centralized biomass processing systems combined with farm-scale landscapes of varying acreages allocated to a “corn-system” consisting of corn grain, stover, and rye (grown as a winter double crop) and two perennial grasses, switchgrass and miscanthus. In the second publication, to address supply chain challenges, we explored the concept of Regional Biomass Processing Depots (RBPDs), strategically distributed facilities that procure, pre-process/pre-treat and densify biomass into stable intermediate products that are compatible with existing bulk commodity logistical systems. These reports advance our knowledge of features important for a successful biofuel industry.
  Eranki PL, Dale BE (2011) Comparative life cycle assessment of centralized and distributed biomass processing systems combined with mixed feedstock landscapes. Global Change Biology – Bioenergy **3:** 427-438.
  http://onlinelibrary.wiley.com/doi/10.1111/j.1757-1707.2011.01096.x/abstract
  Eranki P, Bals BD, Dale BE (2011) Advanced regional biomass processing depots: a key to the logistical challenges of the cellulosic biofuel industry. Biofuels, Bioproducts and Biorefining **5:** 621-630.
  http://onlinelibrary.wiley.com/doi/10.1002/bbb.318/abstract
- **Relationship between agricultural landscape simplification and insecticide use in the Midwestern US.** A relationship between landscape simplification, pest pressure, and insecticide use has long been assumed, but direct evidence has been lacking. Results from this study provide unique correlative support for this relationship over an unprecedented range of cropping systems and environmental conditions, spanning a globally important farming region.

Meehan TD, Werling BP, Landis DA, Gratton C (2011) Agricultural landscape simplification and insecticide use in the Midwestern United States. Proceedings of the National Academy of Sciences of the United States of America **108:** 11500-11505.
http://www.pnas.org/content/108/28/11500.abstract

- **Virus susceptibility of native grasses modified for biofuel production.** In this study, we examined relationships between growth rates and biomass recalcitrance in five switchgrass populations, ranging from near-wildtype to highly selected cultivars, in a common garden trial. In experiments, susceptibility varied notably among switchgrass populations and was more strongly predicted by potential biomass accumulation rates than by foliar digestibility; highly selected, productive cultivars were most virus-susceptible and most preferred by aphids. Evaluation and mitigation of virus susceptibility of new biofuel crops is recommended to avert possible unintended consequences of biofuel production on regional pathogen dynamics.
  Schrotenboer AC, Allen MS, Malmstrom CM (2011) Modification of native grasses for biofuel production may increase virus susceptibility. Global Change Biology – Bioenergy **3:** 360-374.
  http://onlinelibrary.wiley.com/doi/10.1111/j.1757-1707.2011.01093.x/abstract
- **Carbon debt of Conservation Reserve Program (CRP) grasslands converted to bioenergy production.** Here we provide measurements of the greenhouse gas consequences of converting US Conservation Reserve Program (CRP) land to continuous corn, corn–soybean, or perennial grass for biofuel production. We consider five contrasting scenarios for subsequent management: continuous corn and corn-soybean rotations, each either tilled or in permanent no-till; a fifth scenario is CRP grassland harvested for cellulosic ethanol production. We present the permanent no-till scenario as the best-practice option, agronomically realistic with the proper incentives.
  Gelfand I, Zenone T, Jasrotia P, Chen J, Hamilton SK, Robertson GP (2011) Carbon debt of Conservation Reserve Program (CRP) grasslands converted to bioenergy production. Proceedings of the National Academy of Sciences of the United States of America **108:** 13864-13869.
  http://www.pnas.org/content/108/33/13864.abstract

Year 5 (Dec. 1, 2011 - Nov. 30, 2012)

- **Acylation of grass monolignols with *p*-coumarate.** In grasses, monolignols can be enzymatically preacylated and incorporated into lignin with unknown effects on lignin function. Here we show that the grass-specific acyltransferase enzyme OsPMT, expressed in *Escherichia coli*, acylated monolignols with *p*-coumarate; thus, OsPMT likely encodes an enzyme responsible for acylation of monolignols in grasses. With a greater understanding of monolignol *p*-coumarate conjugates, grass lignins could be engineered to contain fewer pendent *p*-coumarate groups and more monolignol conjugates that improve lignin cleavage.
  Withers S, Lu F, Kim H, Zhu Y, Ralph J, Wilkerson CG (2012) Identification of grass-specific enzyme that acylates monolignols with *p*-coumarate. The Journal of Biological Chemistry **287:** 8347-8355.
  http://www.jbc.org/content/287/11/8347.long
- **C-lignin produced naturally in the Vanilla orchid.** Here we report a lignin in the monocotyledonous angiosperm Vanilla orchid (*Vanilla planifolia*) that is naturally biosynthesized from the unusual C monolignol, caffeyl alcohol. Similar polymers are found in the seeds of other vanilla species and several species of cacti (which are dicots). The *V. planifolia* polymer was structurally characterized by various chemical methods, 2D NMR

spectroscopic techniques, and gel-permeation chromatography (GPC); all evidence indicates that the C-lignin is formed by combinatorial oxidative radical coupling under simple chemical control, a mechanism analogous to that occurring in classic lignification.
Chen F, Tobimatsu Y, Havkin-Frenkel D, Dixon RA, Ralph J (2012) A polymer of caffeyl alcohol in plant seeds. Proceedings of the National Academy of Sciences of the United States of America **109:** 1772-1777.
http://www.pnas.org/content/109/5/1772.full

- **MYB46, master regulator of secondary cell wall synthesis.** While many aspects of primary cell wall have been extensively elucidated, our current understanding of secondary wall biosynthesis is limited. Recently, transcription factor MYB46 has been identified as a master regulator of secondary wall biosynthesis in *Arabidopsis thaliana*. To gain better understanding of this MYB46-mediated transcriptional regulation, we conducted several lines of research related to MYB46, resulting in the three publications listed below for this year.
  Kim W-C, Ko J-H, Han K-H (2012) Identification of a *cis*-acting regulatory motif recognized by MYB46, a master transcriptional regulator of secondary wall biosynthesis. Plant Molecular Biology **78:** 489-501.
  https://link.springer.com/article/10.1007%2Fs11103-012-9880-7
  Ko J-H, Kim W-C, Kim J-Y, Ahn S-J, Han K-H (2012) MYB46-mediated transcriptional regulation of secondary wall biosynthesis. Molecular Plant **5:** 961-963
  http://www.sciencedirect.com/science/article/pii/S1674205214600617
  Kim W-C, Ko J-H, Kim J-Y, Kim J-M, Bae H-J, Han K-H (2013) MYB46 directly regulates the gene expression of secondary wall-associated cellulose synthases in Arabidopsis. The Plant Journal **73:** 26-36.
  http://onlinelibrary.wiley.com/doi/10.1111/j.1365-313x.2012.05124.x/abstract
- **Galactomannan biosynthesis.** Galactomannans, hemicellulosic polysaccharides, are entirely composed of yeast-fermentable hexoses and are easily digestible, making them an ideal polymer to provide sugars for biofuel production from plant biomass. In our first report this year, to better understand the galactomannan biosynthetic pathway and its regulatory mechanism, we conducted deep EST sequencing from cDNA libraries using various stages of developing fenugreek seeds. In a second report, we identified a likely glycosyltransferase important for mannan biosynthesis.
  Wang Y, Alonso A, Wilkerson C, Keegstra K (2012) Deep EST profiling of developing fenugreek endosperm to investigate galactomannan biosynthesis and its regulation. Plant Molecular Biology **79:** 243-258.
  https://link.springer.com/article/10.1007%2Fs11103-012-9909-y
  Wang Y, Mortimer JC, Davis J, Dupree P, Keegstra K (2012) Identification of an additional protein involved in mannan biosynthesis. The Plant Journal **73:** 105-117.
  http://onlinelibrary.wiley.com/doi/10.1111/tpj.12019/full
- **Influence of variable species composition on the saccharification of AFEX pretreated biomass.** We evaluated the impact of AFEX pretreatment conditions on hydrolysis sugar yields for various old-field treatments comprised of different mixtures of annual forbs and grass species to corn stover. We found that the grass-dominated feedstocks were as digestible as corn stover, but corn stover had higher total glucose and xylose yields.
  Garlock RJ, Bals B, Jasrotia P, Balan V, Dale BE (2012) Influence of variable species composition on the saccharification of AFEX™ pretreated biomass from unmanaged fields in comparison to corn stover. Biomass and Bioenergy **37:** 49-59.
  http://www.sciencedirect.com.ezproxy.library.wisc.edu/science/article/pii/S0961953411006556

- **An integrated biological process for ethanol production featuring enzyme recycling.** We developed a process that saves time by quickly fermenting xylose, processing the easily digestible biomass first to fully utilize the high enzymatic hydrolysis rate period, and hydrolyzing the more recalcitrant part of biomass with less inhibition by degradation products and sugar, enhancing the process ethanol productivity. This process also allows for better use of biocatalysts resources by recycling yeast cells and enzymes and reducing overall processing cost.
  Jin M, Gunawan C, Uppugundla N, Balan V, Dale BE (2012) A novel integrated biological process for cellulosic ethanol production featuring high ethanol productivity, enzyme recycling and yeast cells reuse. Energy & Environmental Science **5:** 7168-7175.
  http://dx.doi.org/10.1039/C2EE03058F
- **Integrated model for cellulosic biorefineries.** We demonstrated a cellulosic biorefinery model, which produces ethanol and food precursors using lignocellulosic biomass as the exclusive source of carbohydrates and minerals. This biorefinery model includes in-house saccharolytic enzyme production using AFEX-pretreated corn stover as carbohydrate sources, which reduces the dependence on commercial enzymes.
  Lau MW, Bals BD, Chundawat SPS, Jin M, Gunawan C, Balan V, Jones AD, Dale BE (2012) An integrated paradigm for cellulosic biorefineries: utilization of lignocellulosic biomass as self-sufficient feedstocks for fuel, food precursors and saccharolytic enzyme production. Energy & Environmental Science **5:** 7100-7110.
  http://dx.doi.org/10.1039/C2EE03596K
- **Structural characterization of AHP-treated grasses with diverse lignin phenotypes.** We determined that the digestibility of four grasses with relatively diverse lignin phenotypes could be linked to quantifiable changes in the cell wall composition and properties of the lignin of the grasses, while S/G ratios did not appear to contribute to the enzymatic digestibility of delignification.
  Li M, Foster CE, Pu Y, Holmes D, Saffron C, Ragauskas A, Hodge DB (2012) Structural characterization of alkaline hydrogen peroxide pretreated grasses exhibiting diverse lignin phenotypes. Biotechnology for Biofuels **5:** 38.
  http://www.biotechnologyforbiofuels.com/content/5/1/38
- **Techno-Economic Analysis (TEA) of butene oligomer production from lignocellulosic biomass.** We developed and evaluated an integrated process for the conversion of lignocellulose to liquid fuels through the esterification of levulinic acid (LA). We performed TEA and our model shows that the biomass feedstock price is the main cost driver for the lignocellulose conversion.
  Sen M, Gurbuz EI, Wettstein SG, Alonso DM, Dumesic JA, Maravelias CT (2012) Production of butene oligomers as transportation fuels using butene for esterification of levulinic acid from lignocellulosic biomass: process synthesis and technoeconomic evaluation. Green Chemistry **14:** 3289-3294.

http://pubs.rsc.org/en/content/articlelanding/2012/gc/c2gc35881f

- **Solvent derived from lignin used in catalytic conversion of cellulose and hemicellulose biomass fractions.** Catalytic depolymerization of lignin was used to produce a lignin-derived solvent, shown to be effective for selective biomass conversion processes. Like biomass-derived gamma valerolactone, the ability to derive solvent from lignin represents a green, renewable process for production of fuels and chemicals.
  Azadi P, Carrasquillo-Flores R, Pagan-Torres YJ, Gurbuz EI, Farnood R, Dumesic JA (2012) Catalytic conversion of biomass using solvents derived from lignin. Green Chemistry **14:** 1573-1576.
  http://pubs.rsc.org/en/content/articlelanding/2012/gc/c2gc35203f - !divAbstract

- **An improved computational method for predicting the effects of metabolic and regulatory perturbations in systems biology.** Predicting cellular responses to perturbations is an important goal in systems biology. The authors of this study describe a new approach, RELATCH, which uses flux and gene expression data from a reference state to predict metabolic responses in a genetically or environmentally perturbed state. The generation of accurate genome-scale models of microbial metabolism will greatly aid host strain engineering and biofuel production.
  Kim J, Reed JL (2012) RELATCH: relative optimality in metabolic networks explains robust metabolic and regulatory responses to perturbations. Genome Biology **13:** R78.
  https://genomebiology.biomedcentral.com/articles/10.1186/gb-2012-13-9-r78
- **Unique ability of *Spathaspora* yeast to co-ferment sugars provides insight into regulatory mechanisms that limit conversion of lignocellulosic biomass.** For many microorganisms the ability to co-utilize sugars is limited by distinct regulatory mechanisms, with glucose generally preferred over other carbon sources. However *Spathaspora passalidarum*, a native xylose-fermenting yeast, is unique in its ability to co-ferment glucose, xylose, and cellobiose and analyses indicated there was increased glycolytic flux in cultures grown on xylose compared to glucose. Study of this yeast's unique metabolism could provide insight into ways in which cellular metabolism may be rewired for increased conversion of sugars to biofuels.
  Long TM, Su Y-KK, Headman J, Higbee A, Willis LB, Jeffries TW (2012) Cofermentation of glucose, xylose, and cellobiose by the beetle-associated yeast, *Spathaspora passalidarum*. Applied and Environmental Microbiology **78:** 5492-54500.
  http://aem.asm.org/content/78/16/5492.abstract?sid=8fe0097c-37ac-4f8d-bfe3-887728712884
- **Fermentative performance and ethanol production in AFEX corn stover hydrolysate (ACSH) is limited by multiple stress responses in *E. coli*.** Fermentation of ACSH was performed and the effects on *E. coli* growth, sugar utilization, gene expression, and biofuel production were monitored. The results suggest that the high energetic cost of mitigating numerous stressors limits growth and biofuel production in lignocellulosic hydrolysates and identifies genetic targets for strain improvement.
  Schwalbach MS, Keating DH, Tremaine M, Marner WD, 2nd, Zhang YH, Bothfeld WH, Higbee AJ, Grass JA, Cotten C, Reed JL, da Costa Sousa L, Jin M, Balan V, Ellinger JJ, Dale B, Kiley PJ, Landick R (2012) Complex physiology and compound stress responses during fermentation of alkali-pretreated corn stover hydrolysate by an *Escherichia coli* ethanologen. Applied and Environmental Microbiology **78:** 3442-3457.
  http://aem.asm.org/content/78/9/3442.abstract
- **Yields of free fatty acid (FA) are higher in continuous culture compared to batch culture.** A plasmid-free strain of *E. coli* expressing three heterologous copies of a thioesterase gene was grown in continuous culture under carbon-limiting conditions and compared to batch culture. The yields of free FAs were 15% higher in continuous culture at low dilution rate as compared to batch culture, and could be further increased to ~40% when carbon was no longer limiting. Modeling suggests that maintenance requirements for the FA-producing strain are much higher than wild-type *E. coli.*
  Youngquist JT, Lennen RM, Ranatunga DR, Bothfeld WH, Marner II WD, Pfleger BF (2011) Kinetic modeling of free fatty acid production in *Escherichia coli* based on continuous cultivation of a plasmid free strain. Biotechnology and Bioengineering **109:** 1518-1527.
  http://onlinelibrary.wiley.com/doi/10.1002/bit.24420/abstract
- **Hierarchical marginal land assessment framework for land use planning and management.** The objective of this study was to develop a hierarchical marginal land

assessment framework for land use planning and management. The hierarchical assessment framework has advantages of quantitatively reflecting land functions and multiple concerns. This provides a foundation upon which focused studies can be identified in order to improve the assessment framework by quantifying high-resolution land functions associated with environment and ecosystem services as well as their criteria needed to improve the assessment framework.
Kang S, Post WM, Wang D, Nichols J, Bandaru VP (2013) Hierarchical marginal land assessment for land use planning. Land Use Policy **30:** 106-113.
http://www.sciencedirect.com/science/article/pii/S0264837712000312

- **Soil microbial communities under biofuel cropping systems in southern Wisconsin.** In the first of two papers, in which we analyzed microbial lipids and various soil physicochemical factors under model biofuel cropping systems of corn, switchgrass, and mixed prairie in southern Wisconsin, we conclude that the cropping system shifted the microbial community composition at this regional scale, which may also affect the microbial processes associated with these differing communities. In the second report, we evaluated the impact of soil attributes, microbial functional group biomass, and cropping system type on soil amino sugar profiles in three model biofuel cropping systems in southern Wisconsin; our results highlight some of the complications present in using and interpreting time-integrative measures of ecosystem properties such as amino sugar profiles (microbial residues), in contrast to more immediately responsive metrics such as microbial lipid profiles (microbial biomass).
  Liang C, Jesus EdC, Duncan DS, Jackson RD, Tiedje JM, Balser TC (2012) Soil microbial communities under model biofuel cropping systems in southern Wisconsin, USA: impact of crop species and soil properties. Applied Soil Ecology **54:** 24-31.
  http://www.sciencedirect.com/science/article/pii/S0929139311003209
  Liang C, Duncan DS, Balser TC, Tiedje JM, Jackson RD (2012) Soil microbial residue storage linked to soil legacy under biofuel cropping systems in southern Wisconsin, USA. Soil Biology and Biochemistry **57:** 939-942.
  http://www.sciencedirect.com/science/article/pii/S0038071712003549
- **Pest suppression potential of Midwestern landscapes under contrasting bioenergy scenarios.** In this study we use predation rates of three sentinel crop pests to develop a biocontrol index (BCI) summarizing pest-suppression potential in corn and perennial grass-based bioenergy crops in southern Wisconsin, lower Michigan, and northern Illinois. We show that BCI is higher in perennial grasslands than in corn, and increases with the amount of perennial grassland in the surrounding landscape. Through comparisons with other independent studies, we find that our biocontrol index is negatively related to insecticide use across the Midwest, suggesting that strategically positioned, perennial bioenergy crops could reduce insect damage and insecticide use on neighboring food and forage crops.
  Meehan TD, Werling BP, Landis DA, Gratton C (2012) Pest-suppression potential of Midwestern landscapes under contrasting bioenergy scenarios. PLOS ONE **7:** e41728.
  http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0041728
- **Pastureland conversion effects on soil greenhouse gas fluxes.** We assessed the short-term effects of converting pastureland to hybrid poplar and willow bioenergy plantation on soil greenhouse gas (GHG) fluxes and nitrogen (N) leaching in northern Michigan. Our results demonstrate the need to include soil disturbance impacts on the N cycle in future life cycle assessment of these bioenergy crops.
  Nikièma P, Rothstein DE, Miller RO (2012) Initial greenhouse gas emissions and nitrogen leaching losses associated with converting pastureland to short-rotation woody bioenergy crops in northern Michigan, USA. Biomass and Bioenergy **39:** 413-426.
  http://www.sciencedirect.com/science/article/pii/S0961953412000475

- **Devising a new data structure for metagenome assembly.** In this work, we describe a simple probabilistic representation for storing short-read sequencing de Bruijn graphs in memory; we apply this graph representation to reduce the memory needed to assemble a soil metagenome sample through the use of read partitioning. By applying the probabilistic de Bruijn graph representation to the problem of partitioning, we achieve a dramatic decrease of nearly 40-fold in the memory required for assembly of a soil metagenome. This probabilistic graph representation is a significant theoretical advance in storing assembly graphs and also yields immediate leverage on metagenomic assembly.
  Pell J, Hintze A, Canino-Koning R, Howe A, Tiedje JM, Brown CT (2012) Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. Proceedings of the National Academy of Sciences of the United States of America **109:** 13272-13277.
  http://www.pnas.org/content/109/33/13272

Year 6 (Dec. 1, 2012 - Nov. 30, 2013)

- **Ectopic expression of a diacylglycerol acyltransferase results in lipids with increased energy density.** Enhancement of acyl-CoA–dependent triacylglycerol (TAG) synthesis in vegetative tissues is widely discussed as a potential avenue to increase the energy density of crops. Here, we report the identification and characterization of *Chlamydomonas reinhardtii* diacylglycerol acyltransferase type two (DGTT) enzymes and use DGTT2 to alter acyl carbon partitioning in plant vegetative tissues. The nutritional value and/or energy density of the transgenic lines was increased by ectopic expression of *DGTT2* and acyl groups were diverted from different pools into TAGs, demonstrating the interconnectivity of acyl metabolism in leaves.
  Sanjaya, Miller R, Durrett TP, Kosma DK, Lydic TA, Muthan B, Koo AJK, Bukhman YV, Reid GE, Howe GA, Ohlrogge J, Benning C (2013) Altered lipid composition and enhanced nutritional value of *Arabidopsis* leaves following introduction of an algal diacylglycerol acyltransferase 2. The Plant Cell **25:** 677-693.
  http://www.plantcell.org/content/25/2/677.long
- **New maize sequencing information complements existing databases.** Here we provide two reports: 1) optimizing read depth to obtain desired marker coverage when using genotyping-by-sequencing (GBS), and 2) analysis of RNA-Seq data to enhance the coverage and resolution of the maize gene atlas.
  Beissinger TM, Hirsch CN, Sekhon RS, Foerster JM, Johnson JM, Muttoni G, Vaillancourt B, Buell CR, Kaeppler SM, de Leon N (2013) Marker density and read-depth for genotyping populations using genotyping-by-sequencing. Genetics **193:** 1073-1081.
  http://www.genetics.org/content/193/4/1073
  Sekhon RS, Briskine R, Hirsch CN, Myers CL, Springer NM, Buell CR, de Leon N, Kaeppler SM (2013) Maize gene atlas developed by RNA sequencing and comparative evaluation of transcriptomes based on RNA sequencing and microarrays. PLOS ONE **8:** e61005.
  http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0061005
- **Dynamic metabolic flux analysis of plant cell wall synthesis.** A dynamic metabolic flux model was developed based on pulse labeling experiments in *Arabidopsis*. Candidates for engineering cell wall synthesis rates and composition were identified.
  Chen X, Alonso AP, Shachar-Hill Y (2013) Dynamic metabolic flux analysis of plant cell wall synthesis. Metabolic Engineering **18:** 78-85.
  http://www.sciencedirect.com/science/article/pii/S1096717613000487
- **Unconventional lignin identified in a *Medicago* mutant.** Here, we describe the effect of cinnamyl alcohol dehydrogenase (CAD) gene knockout in the model legume *Medicago*

truncatula. Retrotransposon insertions in the *M. truncatula CAD1* (*MtCAD1*) gene result in stable mutant plants that grow normally under standard growth conditions. However, 2D NMR analysis revealed that lignins in *MtCAD1* mutants are, surprisingly, composed almost exclusively (~95%) of hydroxycinnamaldehyde-derived units. The almost exclusive derivation of lignin polymers in the *cad1* mutants from nontraditional lignin monomers extends the scope of modifications that we may yet consider for lignin modification toward improved biomass processing.
Zhao Q, Tobimatsu Y, Zhou R, Pattathil S, Gallego-Giraldo L, Fu C, Jackson LA, Hahn MG, Kim H, Ralph J, Chen F, Dixon RA (2013) Loss of function of cinnamyl alcohol dehydrogenase 1 leads to unconventional lignin and a temperature-sensitive growth defect in *Medicago truncatula*. Proceedings of the National Academy of Sciences of the United States of America **110:** 13660-13665.
http://www.pnas.org/content/110/33/13660.full

- **Identification of a new enzyme in lignin biosynthesis.** Lignin is a major component of plant secondary cell walls. Here we have identified a new step in the biosynthetic pathway of lignin in *Arabidopsis* in which caffeoyl shikimate esterase (CSE) is a central enzyme. Our data necessitate the revision of currently accepted models of the lignin biosynthetic pathway.
  Vanholme R, Cesarino I, Rataj K, Xiao Y, Sundin L, Goeminne G, Kim H, Cross J, Morreel K, Araujo P, Welsh L, Haustraete J, McCellan C, Vanholme B, Ralph J, Simpson GG, Halpin C, Boerjan W (2013) Caffeoyl shikimate esterase (CSE) is an enzyme in the lignin biosynthetic pathway in *Arabidopsis*. Science **341:** 1103-1106.
  http://science.sciencemag.org/content/341/6150/1103.long
- **Demonstrating biomass deconstruction of *Streptomyces* sp. SirexAA-E.** When grown on plant biomass, ActE secretes a suite of enzymes including endo- and exo-cellulases and hemicellulases. We performed extensive analyses of this enzyme to provide insight into its function. Transcriptomic and proteomic analysis have revealed the key enzymes used in the biomass deconstruction process, and we found it is comparable to a cellulolytic enzyme cocktail from *Trichoderma reesei*.
  Bianchetti CM, Harmann CH, Takasuka TE, Hura GL, Dyer K, Fox BG (2013) Fusion of dioxygenase and lignin-binding domains in a novel secreted enzyme from cellulolytic *Streptomyces* sp. SirexAA-E. Journal of Biological Chemistry **288:** 18574-18587.
  http://www.jbc.org/content/288/25/18574.abstract
  Takasuka TE, Book AJ, Lewin GR, Currie CR, Fox BG (2013) Aerobic deconstruction of cellulosic biomass by an insect-associated *Streptomyces*. Scientific Reports **3:** 1030.
  http://www.nature.com/srep/2013/130107/srep01030/full/srep01030.html
- **Increased enzyme binding to substrate is not necessary for more efficient cellulose hydrolysis.** We found that altering the crystalline structure of plant-derived cellulose I to III can lower fungal cellulose loading by 5- fold to achieve comparable saccharification yields, despite a reduced effective enzyme affinity for the III substrate. We developed a mechanistic kinetic model coupling enzyme binding, cellulose surface chain extraction, and glycosidic bond hydrolysis to explain our findings. This can help engineer more efficient cellulases to work in native and non-native (i.e. chemically pretreated) celluloses.
  Gao D, Chundawat SPS, Sethi A, Balan V, Gnanakaran S, Dale BE (2013) Increased enzyme binding to substrate is not necessary for more efficient cellulose hydrolysis. Proceedings of the National Academy of Sciences of the United States of America **110:** 10922-10927.
  http://www.pnas.org/content/110/27/10922.full
- **Hydrolysis of AFEX-pretreated corn stover. Effects of supply and storage conditions.** We investigated the effects of storage conditions on the composition and fermentability of

hydrolysate prepared from AFEX-pretreated corn stover, including pelletized biomass as a source using high solid loadings. We found that there is no significant difference in the fermentability between fresh hydrolysate and stored hydrolysate, and that the slurries resulting from pelletized stover remained well mixed. Furthermore, pelletization slightly increased the initial rate of hydrolysis compared to unpelletized biomass, suggesting that pelletization after AFEX pretreatment could have additional advantages beyond the logistical handling of biomass.
Bals BD, Gunawan C, Moore J, Teymouri F, Dale BE (2013) Enzymatic hydrolysis of pelletized AFEX™-treated corn stover at high solid loadings. Biotechnology and Bioengineering **111:** 264-271.
http://onlinelibrary.wiley.com/doi/10.1002/bit.25022/abstract
Jin M, Bothfeld W, Austin S, Sato TK, LaReau A, Li H, Foston M, Gunawan C, LeDuc RD, Quensen JF, McGee M, Nuppugundia N, Higbee A, Ranatunga R, Donald CW, Bone G, Raguskas AJ, Tiedje JM, Noguera DR, Dale BE, Zhang Y, Balan V (2013) Effect of storage conditions on the stability and fermentability of enzymatic lignocellulosic hydrolysate. Bioresource Technology **147:** 212-220.
http://dx.doi.org/10.1016/j.biortech.2013.08.018

- **Framework for biomass-to-fuel conversion strategies.** We developed a framework for the identification and evaluation of biomass-to-fuel production strategies; a technology superstructure consisting of a wide range of conversion technologies along with the corresponding feedstocks, intermediates, and final products. The proposed framework can be used to study a range of questions including "What is the best strategy for the production of a specific fuel? What is the best use strategy for a specific feedstock? We illustrated our methodology using the production of ethanol from hard woody biomass as a case study.
Kim J, Sen SM, Maravelias CT (2013) An optimization-based assessment framework for biomass-to-fuel conversion strategies. Energy & Environmental Science **6:** 1093-1104.
http://pubs.rsc.org/en/Content/ArticleLanding/2013/EE/C3EE24243A
- **Pretreatment of woody biomass via Alkaline Hydrogen Peroxide catalyzed by a metal complex.** We discovered that AHP Cu^{II}(bpy) significantly improves the sugar release from poplar relative to uncatalyzed AHP pretreatment, and we characterized the relationship between pretreatment conditions and enzymatic sugar release.
Li Z, Chen CH, Hegg EL, Hodge DB (2013) Rapid and effective oxidative pretreatment of woody biomass at mild reaction conditions and low oxidant loadings. Biotechnology for Biofuels **6:** 119.
http://www.biotechnologyforbiofuels.com/content/6/1/119
Li Z, Chen CH, Liu T, Mathrubootham V, Hegg EL, Hodge DB (2013) Catalysis with Cu^{II}(bpy) improves alkaline hydrogen peroxide pretreatment. Biotechnology and Bioengineering **110:** 1078-1086.
http://dx.doi.org/10.1002/bit.24793
- **Algorithm for high-resolution identification of transcription factor binding sites in ChIP-seq data.** Chromatin-immunoprecipitation followed by high-throughput sequencing (ChIP-seq) is a powerful technique to identify transcription factor binding sites throughout the genome. Microbial genomes often contain closely spaced or overlapping promoters and it can be difficult to identify binding sites with a high degree of resolution. The authors of this study developed the algorithm dPeak, which can estimate the locations of binding events with higher resolution than standard methods. High resolution mapping of promoter binding sites is an important tool for synthetic biology and biofuel host strain development.
Chung D, Park D, Myers K, Grass J, Kiley P, Landick R, Keleş S (2013) dPeak: High resolution identification of transcription factor binding sites from PET and SET ChIP-Seq data. PLOS Computational Biology **9:** e1003246.
http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1003246

- **Identification of pathway utilized for microbial metabolism of meta-hydroxy aromatic compounds.** Researchers used a genetic approach to show that metabolism of meta-hydroxy-aromatic acids by *R. palustris* occurs via induction of the native benzyol-CoA pathway. The results open the possibility of *R. palustris* metabolizing aromatic compounds from lignin and the ability to derive greater value from all of the major components of biomass.
  Gall DL, Ralph J, Donohue TJ, Noguera DR (2013) Benzoyl coenzyme A pathway-mediated metabolism of *meta*-hydroxy-aromatic acids in *Rhodopseudomonas palustris*. Journal of Bacteriology **195:** 4112-4120.
  http://jb.asm.org/content/195/18/4112.long
- **Genome-scale mapping of transcription factor binding sites provide insights into the global response to oxygen.** Two studies utilized ChIP-seq to map promoter occupancy of the *Escherichia coli* transcription factors FNR and ArcA in response to oxygen availability. Interestingly, FNR promoter occupancy was strongly influenced by nucleoid associated proteins, which in several cases appear to restrict promoter access by FNR. In the case of ArcA, an abundance of non-cannonical binding sites within promoters dictates the length and concentration-sensitive occupancy of DNA. Knowledge of promoter architecture and the mechanisms that govern global gene regulation informs synthetic biology approaches for improved biofuel production.
  Myers KS, Yan H, Ong IM, Chung D, Liang K, Tran F, Keles S, Landick R, Kiley PJ (2013) Genome-scale analysis of *Escherichia coli* FNR reveals complex features of transcription factor binding. PLOS Genetics **9:** e1003565.
  http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1003565
  Park DM, Akhtar MS, Ansari AZ, Landick R, Kiley PJ (2013) The bacterial response regulator ArcA uses a diverse binding site architecture to regulate carbon oxidation globally. PLOS Genetics **9:** e1003839.
  http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1003839
- **New method of alcohol oxidation in lignin.** An efficient organocatalytic method for chemoselective aerobic oxidation of secondary benzylic alcohols within lignin model compounds has been identified. Extension to selective oxidation of natural lignins has also been demonstrated. Preliminary studies highlight the prospect of combining this method with a subsequent oxidation step to achieve C–C bond cleavage.
  Rahimi A, Azarpira A, Kim H, Ralph J, Stahl SS (2013) Chemoselective metal-free aerobic alcohol oxidation in lignin. Journal of the American Chemical Society **135:** 6415-6418
  http://pubs.acs.org/doi/abs/10.1021/ja401793n
- **Multiomics data sets provide estimation of *in vivo* kinetic parameters for constraint-based metabolic models.** Constraint-based models typically omit kinetic considerations due to limitations in determining kinetic information for an entire metabolic network. To overcome these limitations, researchers produced a method for *in vivo* kinetic parameter estimation, using multi-omic data sets for *Escherichia coli*. The result was a simplified kinetic model, with rate laws for a subset of metabolic enzymes. These results demonstrate the utility of multiomic data sets for identifying metabolic bottlenecks for biofuel production.
  Cotten C, Reed JL (2013) Mechanistic analysis of multi-omics datasets to generate kinetic parameters for constraint-based metabolic models. BMC Bioinformatics **14:** 32.
  https://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-14-32
- **Net primary production in three bioenergy crop systems following land conversion.** This is the first study of this kind to investigate and compare production on two common types of land available for bioenergy production in the Midwest. The results lead to the conclusion that there was no significantly higher production in lands that were converted

from the conservation reserve program (CRP) as originally hypothesized. This study should be followed up with a more comprehensive investigation evaluating these differences in a long-term field trial, with increased replication, simultaneous microclimate study and analysis of CO_2, H_2O and energy flux coupled with NPP.
Deal MW, Xu J, John R, Zenone T, Chen J, Jasrotia P, Kahmark K, Bossenbroek J, Mayer C (2014) Net primary production in three bioenergy crop systems following land conversion. Journal of Plant Ecology **7:** 451-460.
https://academic.oup.com/jpe/article/7/5/451/939272/Net-primary-production-in-three-bioenergy-crop?related-urls=yes&legid=jpe;rtt057v1

- **Sustainable bioenergy production from marginal lands in the US Midwest.** Here we evaluate the potential for marginal lands in ten Midwestern US states to produce sizeable amounts of biomass and concurrently mitigate greenhouse gas (GHG) emissions. In a comparative assessment of six alternative cropping systems over 20 years, we found that successional herbaceous vegetation, once well established, has a direct GHG emissions mitigation capacity that rivals that of purpose-grown. Our results suggest that such vegetation could produce about 21 gigalitres of ethanol per year from around 11 million hectares, or approximately 25 per cent of the 2022 target for cellulosic biofuel mandated by the US Energy Independence and Security Act of 2007, with no initial carbon debt nor the indirect land-use costs associated with food-based biofuels.
  Gelfand I, Sahajpal R, Zhang X, Izaurralde RC, Gross KL, Robertson GP (2013) Sustainable bioenergy production from marginal lands in the US Midwest. Nature **493:** 514-517.
  https://www.nature.com/articles/nature11811
- **Miscanthus establishment and overwintering in the Midwest.** This study described a dataset for annual extreme minimum temperatures across the Midwest US for both soils that are managed without leaving residue on the soil surface after harvest of crops as well as for soils that have a full cover (5 cm thick prostrate residue layer for maize in place, and for varying thicknesses of miscanthus straw). Our results indicated that strategic residue management in the region has potential to help increase extreme minimum soil temperatures that can threaten overwintering of miscanthus rhizomes in the first year of establishment and potentially in later years; also, the thickness of that residue layer has significant bearing on the insulating effect.
  Kucharik CJ, VanLoocke A, Lenters JD, Motew MM (2013) Miscanthus establishment and overwintering in the Midwest USA: a regional modeling study of crop residue management on critical minimum soil temperatures. PLOS ONE **8:** e68847.
  http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0068847
- **Initial N_2O, CO_2, and methane costs of converting CRP grassland to row crops under no-till vs. conventional tillage.** In our earlier work by Gelfand *et al*. (in Year 4), we reported that the conversion of Conservation Reserve Program (CRP) land to no-till soybean production released significant amounts of CO_2 and N_2O and had little effect on CH_4 oxidation rates. Here, we extend the results to examine the impact of conventional tillage practices on greenhouse gas (GHG) fluxes during conversion. Of particular note, we conclude that no-till management can reduce GHG costs by ~60% compared to conventional tillage during initial CRP conversion. **Ruan L, Robertson GP** (2013) Initial nitrous oxide, carbon dioxide, and methane costs of converting conservation reserve program grassland to row crops under no-till vs. conventional tillage. Global Change Biology **19:** 2478-2489.
  http://onlinelibrary.wiley.com/doi/10.1111/gcb.12216/abstract
- **Effects of land use change on carbon balance.** We studied the effect of agricultural land-use change on two historical land use types for three different cropping systems using eddy

covariance and ecosystem carbon balance approaches. We evaluated the impact of the crop choices and yields together with biomass end-use to show the relative effects of these factors on the carbon balance of the converted ecosystems. These results can be readily incorporated into management recommendations for future establishment of biofuels feedstock and row agriculture systems with different management intensities.
Zenone T, Gelfand I, Chen J, Hamilton SK, Robertson GP (2013) From set-aside grassland to annual and perennial cellulosic biofuel crops: effects of land use change on carbon balance. Agricultural and Forest Meteorology **182-183:** 1-12.
http://www.sciencedirect.com/science/article/pii/S0168192313001950

Year 7 (Dec. 1, 2013 - Nov. 30, 2014)

- **PMT acts specifically in monolignol acylation.** In this study we tested the authenticity of *p*-coumaroyl-CoA:monolignol transferase (PMT) as a lignin biosynthetic pathway enzyme, by examining *Brachypodium distachyon* plants with altered *BdPMT* gene function. Using newly developed cell wall analytical methods, we determined that the transferase was involved specifically in monolignol acylation. Our data are consistent with a defined role for grass PMT genes in encoding BAHD acyltransferases that specifically acylate monolignols with *p*-coumarate (*p*CA) and produce monolignol *p*-coumarate conjugates that are used for lignification *in planta.*
Petrik DL, Karlen SD, Cass CL, Padmakshan D, Lu F, Liu S, Le Bris P, Antelme S, Santoro N, Wilkerson CG, Sibout R, Lapierre C, Ralph J, Sedbrook JC (2014) *p*-Coumaroyl-CoA:monolignol transferase (PMT) acts specifically in the lignin biosynthetic pathway in *Brachypodium distachyon*. The Plant Journal **77:** 713-726.
http://onlinelibrary.wiley.com/doi/10.1111/tpj.12420/abstract
- **Photoperiodic flowering time in *Brachypodium*.** In this year we published two papers on flowering time in *Brachypodium*. In the first report, our results indicate there is rich natural diversity in photoperiod and vernalization requirements to exploit for understanding gene networks controlling flowering; further, we provide evidence for conserved roles of *VRN1* and *FT* in promoting flowering, whereas the role of *VRN2* is less clear. In the second report, we show that *PHYC* is required for the transcriptional activation of several photoperiod-pathway genes, including *PPD1*, *CO*, and *FT*, and that loss of *PHYC* alters the expression of certain circadian input and output genes, revealing a difference in how light is perceived for the photoinduction of flowering between the well-studied plants *Arabidopsis* and rice compared to the temperate grass *Brachypodium*.
Ream T, Woods D, Schwartz C, Sanabria C, Mahoy J, Walters E, Kaeppler H, Amasino R (2013) Interaction of photoperiod and vernalization determine flowering time of *Brachypodium distachyon*. Plant Physiology **164:** 694-709.
http://www.plantphysiol.org/content/164/2/694.long
Woods DP, Ream TS, Minevich G, Hobert O, Amasino RM (2014) PHYTOCHROME C is an essential light receptor for photoperiodic flowering in the temperate grass, *Brachypodium distachyon*. Genetics **198:** 397-408.
http://www.genetics.org/content/198/1/397
- **Maize pan-genome and pan-transcriptome.** Genomes at the species level are dynamic, with genes present in every individual (core) and genes in a subset of individuals (dispensable) that collectively constitute the pan-genome. Using transcriptome sequencing of seedling RNA from maize (*Zea mays*) inbred lines to characterize the maize pan-genome, we identified 8681 representative transcript assemblies (RTAs) with 16.4% expressed in all lines and 82.7% expressed in subsets of the lines; furthermore, genome-wide association studies based on single nucleotide polymorphisms (SNPs) and transcript abundance in the

pan-genome revealed loci associated with the timing of the juvenile-to-adult vegetative and vegetative-to-reproductive developmental transitions, two traits important for fitness and adaptation. This study revealed the dynamic nature of the maize pan-genome and demonstrated that a substantial portion of variation may lie outside the single reference genome for a species.
Hirsch CN, Foerster JM, Johnson JM, Sekhon RS, Muttoni G, Vaillancourt B, Peñagaricano F, Lindquist E, Pedraza MA, Barry K, de Leon N, Kaeppler SM, Buell CR (2014) Insights into the maize pan-genome and pan-transcriptome. The Plant Cell **26:** 121-135.
http://www.plantcell.org/content/26/1/121

- **Zip-lignin poplar.** Redesigning lignin, the aromatic polymer fortifying plant cell walls, to be more amenable to chemical depolymerization can lower the energy required for industrial processing. We have engineered poplar trees to introduce ester linkages into the lignin backbone by augmenting the monomer pool with monolignol ferulate conjugates, and demonstrate that the resulting "zip-lignin" poplar trees showed no difference in growth habit under greenhouse conditions, but that their lignin showed improved digestibility. Tailoring plants to use such conjugates during cell wall biosynthesis is s promising way to produce plants that are designed for deconstruction.
Wilkerson CG, Mansfield SD, Lu F, Withers S, Park J-Y, Karlen SD, Gonzales-Vigil E, Padmakshan D, Unda F, Rencoret J, Ralph J (2014) Monolignol ferulate transferase introduces chemically labile linkages into the lignin backbone. Science **344:** 90-93.
http://science.sciencemag.org/content/344/6179/90
- **Sorghum modeling of genetics maps.** Here, we build off an existing model of differential zygotic viability to incorporate a heterozygosity maintenance term for plant recombinant inbred populations and find a new solution for the genotype probabilities used to calculate recombination frequencies. Using sorghum, this modeling allows more accurate generation of genetic maps and retention of more genetic information by accounting for the biological phenomenon of differential fitness of heterozygous loci. More accurate estimations of recombination fractions, and thus linkage, will improve the accuracy of methods that use linkage information to detect and use causal genetic variants.
Truong SK, McCormick RF, Morishige DT, Mullet JE (2014) Resolution of genetic map expansion caused by excess heterozygosity in plant recombinant inbred populations. G3: Genes | Genomes | Genetics **4:** 1963-1969.
http://www.g3journal.org/content/4/10/1963
- **Evolution of substrate specificity in bacterial lytic polysaccharide monooxygenases (LPMOs).** We analyzed the sequences, structures, and evolution of LPMOs to understand the factors that may influence substrate specificity within and between these enzyme families. We found that these families share an ancient ancestral protein, but the different clades have specialized their selection towards different substrate bindings. Our work provided a phylogenetic basis for identifying and classifying these LPMOs.
Book AJ, Yennamalli RM, Takasuka TE, Currie CR, Phillips GN, Fox BG (2014) Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. Biotechnology for Biofuels **7:** 109.
http://www.biotechnologyforbiofuels.com/content/7/1/109
- **Comparison of enzymatic reactivity from corn stover pretreated via three different pretreatments.** In a biorefinery, biomass pretreatment will significantly influence the efficacy of enzymatic hydrolysis and fermentation. In this BRC collaboration, we compared the effects of three pretreatments (dilute acid, AFEX, and ionic liquid) on downstream operations. We found that AFEX treated corn stover showed no significant change in composition, whereas 85% of the hemicellulose was solubilized after dilute acid

pretreatment, and about 90% of the lignin was removed after ionic liquid pretreatment. We also found that no single factor absolutely dominated the early and long-term sugar yields from enzymatic hydrolysis.
Gao X, Kumar R, Singh S, Simmons B, Balan V, Dale B, Wyman CE (2014) Comparison of enzymatic reactivity of corn stover solids prepared by dilute acid, AFEX™, and ionic liquid pretreatments. Biotechnology for Biofuels **7:** 71.
http://www.biotechnologyforbiofuels.com/content/7/1/71
Uppugundla N, Sousa L, Chundawat SPS, Yu X, Simmons B, Singh S, Gao X, Kumar R, Wyman CE, Dale BE, Balan VA (2014) A comparative study of ethanol production using dilute acid, ionic liquid and AFEX™ pretreated corn stover. Biotechnology for Biofuels **7:** 72.
http://www.biotechnologyforbiofuels.com/content/7/1/72/abstract

- **Pyrolysis of grass species in North America.** We analyzed various North American native grass species to understand the effects of feedstock compositional variability on fast pyrolysis and associated products. The grasses studied were: big bluestem, coastal panicgrass, deertongue, indiangrass, Miscanthus, prairie sandreed, sideoats grama, and switchgrass. We identified significant variability in the pyrolysis products but could find no connection to the taxonomic tribe. The results help identify which grasses might be better suited for different biofuels technologies.
  Kelkar S, Li Z, Bovee J, Thelen KD, Kriegel RM, Saffron CM (2014) Pyrolysis of North-American grass species: effect of feedstock composition and taxonomy on pyrolysis products. Biomass and Bioenergy **64:** 152-161.
  http://www.sciencedirect.com/science/article/pii/S0961953414001500?via=ihub
- **Bacterial enzyme sheds light on cellulose deconstruction.** Using a CBM first isolated from a highly cellulolytic actinobacterium discovered by our own researchers, we described a simple strategy to produce fully functional bacterial CBMs, showing that, unlike previous studies of bacterial CBMs, these bacterial CBMs bind reversibly to cellulose.
  Lim S, Chundawat SPS, Fox BG (2014) Expression, purification and characterization of a functional carbohydrate-binding module from *Streptomyces* sp. SirexAA-E. Protein Expression and Purification **98:** 1-9.
  http://www.sciencedirect.com/science/article/pii/S1046592814000473
- **The RaBIT process: Rapid bioconversion of lignocellulosic sugars into ethanol using high cell density fermentations with enzyme recycling.** We developed a process called RaBIT (Rapid Bioconversion with Integrated recycle Technology) that reduces capital costs, processing times, and biocatalyst cost for biochemical conversion of cellulosic biomass to biofuels. The process reduces total bioprocessing time to 48 h, increases biofuel productivity 2-fold, and recycles biocatalysts using 24-h high cell density fermentations along with cell recycling to solve the slow/incomplete xylose fermentation issue. We tested various microbial strains in the fermentation process, and while not all of them are capable of effectively performing in the RaBIT process, we found that their performance is largely correlated to the specific xylose consumption rate.
  Sarks C, Jin M, Sato TK, Balen V, Dale BE (2014) Studying the rapid bioconversion of lignocellulosic sugars into ethanol using high cell density fermentations with cell recycle. Biotechnology for Biofuels **7:** 73.
  http://www.biotechnologyforbiofuels.com/content/7/1/73
- **Ethanol shown to target transcriptional and translational machinery in *E. coli*.** Various omics methods, including ribosome profiling, were used to characterize ethanol-tolerant mutants to show that biofuel directly targets central dogma processes. These findings provide conceptual frameworks for the study of ethanol toxicity in microbes and for the engineering of ethanol tolerance that may be extensible to other microbes and to other short-chain alcohols.

Haft, R. J. F., Keating, D. H., Schwaegler, T., S., S. M., Vinokur, J., Tremaine, M., Peters, J. M., Kotlajich, M. V., Pohlmann, E. L., Ong, I. M., Grass, J. A., Kiley, P. J., and Landick, R. (2014) Correcting direct effects of ethanol on translation and transcription machinery confers ethanol tolerance in bacteria. *Proceedings of the National Academy of Sciences of the United States of America* **111**, E2576-E2585. http://www.pnas.org/content/111/25/E2576.long

- **Aromatic inhibitors derived from lignocellulosic biomass hinder bacterial ethanologensis by activating energy-depleting stress-response and detoxification pathways.** This studied utilized transcriptomic, proteomic, and metabolomic approaches to investigate inhibitor toxicity and microbial response mechanisms in the model bacterium *E. coli*. The findings indicate that the major regulatory responses to lignocellulose-derived inhibitors are mediated by transcriptional rather than translational regulators and that energy consumed for inhibitor efflux and detoxification may limit biofuel production.
  Keating, D. H., Zhang, Y., Ong, I. M., McIlwain, S., Morales, E. H., Grass, J. A., Tremaine, M., Bothfeld, W., Higbee, A., Ulbrich, A., Balloon, A., Westphall, M. S., Aldrich, J., Lipton, M., Kim, J., Moskvin, O. V., Bukhman, Y. V., Coon, J., Kiley, P. J., Bates, D. M., and Landick, R. (2014) Aromatic inhibitors derived from ammonia-pretreated lignocellulose hinder bacterial ethanologenesis by activating regulatory circuits controlling inhibitor efflux and detoxification. *Frontiers in Microbiology* **5**, 402. http://journal.frontiersin.org/article/10.3389/fmicb.2014.00402/full
- **Examination of bacterial lipid production reveals a novel furan-containing fatty acid that could potentially serve as a biofuel precursor or additive.** A previously undescribed pathway for furan-containing fatty acid synthesis in *Rhodobacter sphaeroides* was discovered. The oxygen atom in the furan ring is reactive and could have potentially useful applications either as a fuel or fuel additive.
  Lemke, R. A. S., Peterson, A. C., Ziegelhoffer, E. C., Westphall, M. S., Tjellström, H., Coon, J. J., and Donohue, T. J. (2014) Synthesis and scaveging role of furan fatty acids. *Proceedings of the National Academy of Sciences of the United States of America* **111**, E3450-E3457. http://www.pnas.org/content/early/2014/07/31/1405520111.full.pdf+html?sid=dc6a6a79-baa9-4d4d-8510-16bc677a028b
- **GVL-based deconstruction method for high-yielding sugars.** This novel deconstruction method produces both C5 and C6 sugars from biomass in high yield without the use of enzymes. It is also a green, renewable technology since GVL may be derived from the biomass itself and recycled. The ability to bypass the use of enzymes to deconstruct biomass could provide a substantial cost-savings and thus is a promising new technology.
  Luterbacher, J. S., Rand, J. M., Martin Alonso, D., Han, J., Youngquist, J. T., Maravelias, C. T., Pfleger, B. F., and Dumesic, J. A. (2014) Non-enzymatic sugar production from biomass using biomass-derived γ-valerolactone. *Science* **343**, 277-280. http://www.sciencemag.org/content/343/6168/277.abstract
- **Lignin depolymerization method increases monomeric yield.** Oxidation of a C-O bond adjacent to the β-aryl ether bond in lignin enhances depolymerization and aromatic monomer yield. This study demonstrates a more efficient process that may potentially enhance the lignin value chain and improve the commercial and economic viability of lignocellulosic biofuels.
  Rahimi, A., Ulbrich, A., Coon, J. J., and Stahl, S. S. (2014) Formic-acid-induced depolymerization of oxidized lignin to aromatics. *Nature* **515**, 249-252. http://www.nature.com/nature/journal/v515/n7526/full/nature13867.html
- **Tackling soil diversity with the assembly of large, complex metagenomes.** Investigations of complex environments rely on large volumes of sequence data to

adequately sample the genetic diversity of a microbial community. We present approaches that make *de novo* assembly of complex metagenomes more accessible; these approaches scale data size with community richness and subdivide the data into tractable subsets representing individual species. We applied these methods toward the assembly of two large soil metagenomes to identify important metagenomic references and show that considerably more data are needed to study the terrestrial microbiome comprehensively. **Howe AC, Jansson JK, Malfatti SA, Tringe SG, Tiedje JM, Brown CT** (2014) Tackling soil diversity with the assembly of large, complex metagenomes. Proceedings of the National Academy of Sciences of the United States of America **111:** 4904-4909. http://www.pnas.org/content/111/13/4904

- **Modeling a biorefinery for production of furfural and furfuryl alcohol in a green, high-yield process.** The biodetoxification pathway for the reduction of the fermentation inhibitor furfural was utilized to produce furfuryl alcohol using both a commercial Bakers' yeast and six other native strains, selected for their high tolerance towards the inhibitory effects of furfural. This study explores the potential of the microbial method as an environmentally-benign alternative to the conventional catalytic hydrogenation process for producing furfuryl alcohol used extensively in industry. Results showed that the yields of furfuryl alcohol using the laboratory yeast strains exceeded 90% of the theoretical yield at a furfural concentration of 25 g l^{-1}, which are comparable to yields obtained using the catalytic process; thus, piecing together novel high-yield conversion processes for furfural and furfuryl alcohol, an integrated biorefinery model based on the production of furans has been envisioned.
  Mandalika A, Qin L, Sato TK, Runge T (2014) Integrated biorefinery model based on production of furans using open-ended high yield processes. Green Chemistry **16:** 2480-2489.
  http://pubs.rsc.org/en/content/articlelanding/2014/gc/c3gc42424c#!divAbstract
- **Nitrous oxide (N_2O) in soil.** We have published two notable soil N_2O reports in Year 7; the first provides results showing that it is possible to estimate N_2O diffusivity with sparse measurements, and that accuracy can likely be further improved with knowledge of soil moisture and texture in the immediate vicinity of the injection and sampling ports, as uncertainty in water modeling is reduced. In our second report, we clarify the response of the greenhouse gas nitrous oxide (N_2O) to nitrogen (N) fertilizer additions, a topic of considerable debate; our results suggest a general trend of exponentially increasing N_2O emissions as N inputs increase to exceed crop needs. Use of this knowledge in greenhouse gas inventories should improve assessments of fertilizer-derived N_2O emissions, help address disparities in the global N_2O budget, and refine the accuracy of N_2O mitigation protocols.
  Shcherbak I, Philip Robertson G (2014) Determining the diffusivity of nitrous oxide in soil using in situ tracers. Soil Science Society of America Journal **78:** 79-88.
  https://dl.sciencesocieties.org/publications/sssaj/abstracts/78/1/79
  Shcherbak I, Millar N, Robertson GP (2014) Global metaanalysis of the nonlinear response of soil nitrous oxide (N_2O) emissions to fertilizer nitrogen. Proceedings of the National Academy of Sciences of the United States of America **111:** 9199-9204.
  http://www.pnas.org/content/111/25/9199.abstract
- **Mechanism of soil carbon accrual and storage in bioenergy cropping systems.** Annual row cropping systems converted to perennial bioenergy crops tend to accrue soil carbon (C), likely a function of increased root production and decreased frequency of tillage. To address this uncertainty, we assessed the formation and stability of aggregates and soil organic C (SOC) pools under switchgrass, giant miscanthus, and native perennial grass mix, and continuous corn treatments in Michigan and Wisconsin soils differing in both texture and mineralogy. Our results help explain cross-site variability in soil C accrual under

perennial bioenergy crops by demonstrating how interactions between belowground productivity, soil type, aggregation processes and microbial communities influence the rates and extent of SOC stabilization.
Tiemann LK, Stuart Grandy A (2015) Mechanisms of soil carbon accrual and storage in bioenergy cropping systems. Global Change Biology – Bioenergy **7:** 161-174.
http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12126/abstract

- **The impact of perennial grasslands in bioenergy landscapes.** Science-based polices are needed to inform sustainable bioenergy landscape design. Our key finding is that the linkage between biodiversity and ecosystem services is dependent not only on the choice of bioenergy crop but also on its location relative to other habitats; the implication is that careful design of bioenergy landscapes has the potential to enhance multiple services in food and energy crops, leading to important synergies that have not yet informed the ongoing bioenergy debate. This study is especially timely as high commodity prices are driving conversion of marginal lands to annual crop production, reducing future flexibility.
  Werling BP, Dickson TL, Isaacs R, Gaines H, Gratton C, Gross KL, Liere H, Malmstrom CM, Meehan TD, Ruan L, Robertson BA, Robertson GP, Schmidt TM, Schrotenboer AC, Teal TK, Wilson JK, Landis DA (2014) Perennial grasslands enhance biodiversity and multiple ecosystem services in bioenergy landscapes. Proceedings of the National Academy of Sciences of the United States of America **111:** 1652-1657.
  http://www.pnas.org/content/111/4/1652.abstract

Year 8 (Dec. 1, 2014 - Nov. 30, 2015)

- **Ac-TAGs from transgenic *Camelina*.** In these two studies, we report the engineering and subsequent field production of acetyl-triacylglycerol (acetyl-TAG) in *Camelina*. The first study produced multi-liter quantities of conventional oils suitable for testing in a range of applications and with different fatty acid compositions, whereas the second study resulted in the highest accumulation of unusual oil achieved so far in transgenic plants.
  Liu J, Tjellström H, McGlew K, Shaw V, Rice A, Simpson J, Kosma D, Ma W, Yang W, Strawsine M, Cahoon E, Durrett TP, Ohlrogge J (2015) Field production, purification and analysis of high-oleic acetyl-triacylglycerols from transgenic *Camelina sativa*. Industrial Crops and Products **65:** 259-268.
  http://www.sciencedirect.com/science/article/pii/S0926669014007067
  Liu J, Rice A, McGlew K, Shaw V, Park H, Clemente T, Pollard M, Ohlrogge J, Durrett TP (2015) Metabolic engineering of oilseed crops to produce high levels of novel acetyl glyceride oils with reduced viscosity, freezing point and calorific value. Plant Biotechnology Journal **13:** 858-865.
  http://onlinelibrary.wiley.com/doi/10.1111/pbi.12325/full
- **Topology of the MLG synthase BdCLSF6.** In our studies to better understand the biosynthesis of mixed-linkage glucan (MLG), a major carbon source for grass-based biofuel production, we sought to establish the topology of the BdCLSF6 enzyme. Our results demonstrate BdCLSF6 localization in the Golgi and supports a model where: BdCLSF6 alone can synthesize MLG using UDP-glucose in the cytoplasm, and MLG is channeled through the biosynthetic membranes of the Golgi and secreted into the cell wall through the default pathway. While the evidence supports our proposed model, the results do not preclude the possibility of other isoforms expressed in other cellular locations.
  Kim S-J, Zemelis S, Keegstra K, Brandizzi F (2015) The cytoplasmic localization of the catalytic site of CSLF6 supports a channeling model for the biosynthesis of mixed-linkage glucan. The Plant Journal **81:** 537-547.
  http://onlinelibrary.wiley.com/doi/10.1111/tpj.12748/abstract

- **Maize cell-wall properties contributing to improved deconstruction and hydrolysis.** To gain a better understanding of how maize cell-wall properties impact initial recalcitrance as well as alkaline pre-treatment, we investigated correlations between cell-wall properties and hydrolysis yields. We found that several properties did not correlate with yield, indicating that while enzymatic hydrolysis yields may be set by the cell-wall lignin content, the cell wall's response to delignifying pre-treatment is not necessarily set by the initial lignin content. This knowledge may inform strategies for plant breeding or genetic engineering that may improve cell-wall deconstruction, thereby improving bioenergy production.
  Li M, Heckwolf M, Crowe JD, Williams DL, Magee TD, Kaeppler SM, de Leon N, Hodge DB (2015) Cell-wall properties contributing to improved deconstruction by alkaline pre-treatment and enzymatic hydrolysis in diverse maize (*Zea mays* L.) lines. Journal of Experimental Botany **66:** 4305-4315.
  https://academic.oup.com/jxb/article-lookup/doi/10.1093/jxb/erv016
- **CGR2 and CGR3 are involved in pectin methylesterification.** To gain a better understanding of pectin biosynthesis and methylesterification and their effects on cell wall features critical for plant growth and development, we conducted various genetic and biochemical analyses of *Arabidopsis* CGR2 and CGR3. Our results indicate that CGR2 and CGR3 share high sequence similarity, are localized to the Golgi, and are type II membrane proteins with the bulk of the protein, including the methyltransferase domain, exposed to the Golgi lumen where pectin methylesterification occurs; further, *cgr2-1 cgr3-1* double mutants exhibit dwarfism and apparent reduced pectin methylesterification, while overexpression lines demonstrate the opposite phenotypes, suggesting overlapping roles in plant growth and development for the CGR2 and CGR3 proteins. This knowledge may inform the design of new bioenergy crops with altered cell wall properties.
  Kim S-J, Held MA, Zemelis S, Wilkerson C, Brandizzi F (2015) CGR2 and CGR3 have critical overlapping roles in pectin methylesterification and plant growth in *Arabidopsis thaliana*. The Plant Journal **82:** 208-220.
  http://onlinelibrary.wiley.com/doi/10.1111/tpj.12802/abstract
- **Tricin: the first phenolic from outside the lignin biosynthetic pathway to be discovered in the lignin polymer.** After tricin had been found in lignin preparations from wheat and all monocots examined, we sought to provide proof that tricin is involved in lignification and to establish the mechanism by which it incorporates into the lignin polymer. We demonstrated that tricin is able to couple with monolignols and participate in lignification, and regularly does so in monocots where tricin is found covalently bound within the lignin polymer itself; further, tricin acts as an initiator, as it is only found at the beginning of the polymer chain. Incorporation of tricin into monocot lignins provides a new, extractable source of this valuable flavonoid, recognized for its antioxidant, antiaging, anticancer, and cardioprotective properties.
  Lan W, Lu F, Regner M, Zhu Y, Rencoret J, Ralph SA, Zakai UI, Morreel K, Boerjan W, Ralph J (2015) Tricin, a flavonoid monomer in monocot lignification. Plant Physiology **167:** 1284-1295.
  http://www.plantphysiol.org/content/167/4/1284
- **Exome capture sequencing of switchgrass.** Switchgrass is present primarily in two ecotypes: a northern upland ecotype, and a southern lowland ecotype. We employed high-coverage exome capture sequencing to genotype 537 individuals from 45 upland and 21 lowland ecotypes. In total, 45,719 genes were affected by nucleotide variants across the panel, providing a firm foundation to identify functional variation associated with phenotypic traits of interest for biofuel feedstock production.

Evans J, Crisovan E, Barry K, Daum C, Jenkins J, Kunde-Ramamoorthy G, Nandety A, Ngan CY, Vaillancourt B, Wei C-L, Schmutz J, Kaeppler SM, Casler MD, Buell CR (2015) Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. The Plant Journal **84:** 800-815.
http://onlinelibrary.wiley.com/doi/10.1111/tpj.13041/full

- **Improving alkaline hydrogen peroxide pretreatment of woody biomass via transition metals.** Having previously demonstrated that the Cu-catalyzed AHP pretreatment of hybrid poplar resulted in substantial improvement of sugar yields after enzymatic hydrolysis, we correlated biomass properties to pretreatment efficacy by comparing enzymatic hydrolysis yields after AHP pretreatment of four different hardwoods and correlated these results with various cell wall properties, finding that lignin removal was correlated with an increase in enzymatic hydrolysis yields. We also demonstrated the role of cell wall-associated redox-active transition metals in impacting the effectiveness of AHP pretreatment, finding that transition metals can play a positive role in oxidative cell wall deconstruction.
  Bansal N, Bhalla A, Pattathil S, Adelman SL, Hahn MG, Hodge DB, Hegg EL (2015) Cell wall-associated transition metals improve alkaline-oxidative pretreatment in diverse hardwoods. Green Chemistry **18:** 1405-1415.
  http://pubs.rsc.org/en/content/articlelanding/2016/gc/c5gc01748c#!divAbstract
- **Active site and laminarin hydrolysate in glycosidase hydrolase family 55 (GH55).** In collaboration with JGI, we used a combination of gene synthesis, cell-free protein translation, catalytic assays, and X-ray crystallography to provide a correlated biochemical and structural characterization of the GH55 family. The high resolution crystal structures with substrates bound and ensemble refinement suggest a simple new mechanism for promoting processive reactivity, which is a new way to annotate bioenergy phylogenetic space.
  Bianchetti CM, Takasuka TE, Deutsch S, Udell HS, Yik EJ, Bergeman LF, Fox BG (2015) Active site and laminarin binding in glycoside hydrolase family 55. Journal of Biological Chemistry **290:** 11819-11832.
  http://www.jbc.org/content/290/19/11819.long
- **Use of Nanostructure-initiator Mass Spectrometry (NIMS) to deduce selectivity of reaction in glycoside hydrolases.** In collaboration with JBEI, we used chemically synthesized NIMS to study the reactivity of several enzymes representative of the glycoside hydrolase (GH) function. We modeled time-dependent reactions of these enzymes in order to provide a quantitative basis to make functional distinctions among reactive properties, thus offering a new approach to enhance the annotation of GH phylogenetic trees with functional measurements.
  Deng K, Takasuka TE, Heins R, Cheng X, Bergeman LF, Shi J, Aschenbrener R, Deutsch S, Singh S, Sale KL, Simmons BA, Adams PD, Singh AK, Fox BG, Northen TR (2014) Rapid kinetic characterization of glycosyl hydrolases based on oxime derivatization and nanostructure-initiator mass spectrometry (NIMS). ACS Chemical Biology **9:** 1470-1479.
  http://pubs.acs.org/doi/abs/10.1021/cb5000289
  Deng K, Guenther JM, Gao J, Bowen BP, Tran H, Reyes-Ortiz V, Cheng X, Sathitsuksanoh N, Heins R, Takasuka TE, Bergeman LF, Geertz-Hansen H, Deutsch S, Loque D, Sale K, Simmons B, Adam PD, Singh AK, Fox BG, Northen TR (2015) Development of a high throughput platform for screening glycoside hydrolases based on oxime-NIMS. Frontiers in Bioengineering and Biotechnology **3:** 153.
  http://journal.frontiersin.org/article/10.3389/fbioe.2015.00153/full
  Deng K, Takasuka TE, Bianchetti CM, Bergeman LF, Adam PD, Northen TR, Fox BG (2015) Use of nanostructure initiator mass spectrometry to deduce selectivity of reaction in glycoside hydrolases. Frontiers in Bioengineering and Biotechnology **3:** 165

http://journal.frontiersin.org/article/10.3389/fbioe.2015.00165/abstract

- **Effects of lignin on cellulase during lignocellulosic biomass saccharification.** We used a fast protein liquid chromatography (FPLC)-based methodology to quantify free *Trichoderma reesei* cellulases (namely CBH I, CBH II, and EG I) concentration within a complex hydrolyzate mixture during the varying time course of biomass saccharification resulting from corn stover samples pretreated via AFEX, dilute acid, and ionic liquids. We showed that family 1 CBMs are highly implicated in the binding of full-length *T. reesei* cellulases to lignin, which aids in further understanding the complex mechanisms of non-productive binding of cellulases to pretreated lignocellulosic biomass.
  Gao D, Haarmeyer C, Balan V, Whitehead TA, Dale BE, Chundawat SPS (2014) Lignin triggers irreversible cellulase loss during pretreated lignocellulosic biomass saccharification. Biotechnology for Biofuels **7:** 175.
  http://www.biotechnologyforbiofuels.com/content/7/1/175
- **Using a designer synthetic media to study inhibitors effect in biomass conversion.** We characterized the plant-derived decomposition products present in AFEX-pretreated corn stover hydrolysate (ACH), and a synthetic hydrolysate (SH) was formulated based on that ACH composition and further used to evaluate the inhibitory effects of various families of decomposition products during fermentation using a strain of *S. cerevisiae*. The SH did not entirely match the ACH performance, but the major groups of inhibitory compounds were identified and used for further evaluation, finding that amides are significantly less inhibitory to both glucose and xylose fermentation, suggesting ACH would be easily fermentable by yeast without any further detoxification.
  Tang X, da Costa Sousa L, Jin M, Chundawat SPS, Chambliss CK, Lau MW, Xiao Z, Dale BE, Balan V (2014) Designer synthetic media for studying microbial-catalyzed biofuel production. Biotechnology for Biofuels **8:** 1.
  http://www.biotechnologyforbiofuels.com/content/8/1/1/abstract
- **Design of biofuel supply chains with regional depots.** We developed optimization models for the design and operational planning of biofuel supply chains including regional depots. These models can be modified to yield solutions where biomass from a harvesting site is shipped to different depots depending on the amount of feedstock available and the needs of the biorefinery, which could lead to a better "steady-state" configuration more aligned with the reality of a biofuel supply chain operation. The proposed models can aid decision-makers studying the trade-offs in biofuel supply chains.
  Ng RTL, Maravelias CT (2016) Design of cellulosic ethanol supply chains with regional depots. Industrial and Engineering Chemistry Research **55:** 3420-3432.
  http://pubs.acs.org.ezproxy.library.wisc.edu/doi/abs/10.1021%2Facs.iecr.5b03677
  Ng RTL, Maravelias CT (2017) Design of biofuel supply chains with variable regional depot and biorefinery locations. Renewable Energy **100:** 90-102.
  http://www.sciencedirect.com/science/article/pii/S0960148116304190
  Kim S, Dale BE (2016) A distributed cellulosic biorefinery system in the US Midwest based on corn stover. Biofuels, Bioproducts and Biorefining **10:** 819-832.
  http://onlinelibrary.wiley.com/doi/10.1002/bbb.1712/abstract
- **Microbes metabolize aromatic compounds in lignocellulosic hydrolysate, producing easily fermentable sugars.** Many aromatic compounds are toxic to biofuel microbes whereas *R. palustris* is able to metabolically remove these compounds from hydrolysate via a specific pathway. Moreover, the use of mutant strains with blocks in specific steps of the pathway can allow for enrichment of aromatic intermediates that may be recoverable as bioproducts.
  Austin, S., Kontur, W. S., Ulbrich, A., Oshlag, J. Z., Zhang, W., Higbee, A., Zhang, Y., Coon, J. J., Hodge, D. B., Donohue, T. J., and Noguera, D. R. (2015) Metabolism of multiple

aromatic compounds in corn stover hydrolysate by *Rhodopseudomonas palustris*. *Environmental Science & Technology* **49**, 8914-8922. http://pubs.acs.org/doi/abs/10.1021/acs.est.5b02062

- **Integrative approach to identify genome-scale transcriptional regulatory networks.** This study combines comparative genomics, motif analysis, and gene expression-based methods to improve the predictive power and information content of transcriptional regulatory networks, informing synthetic biology approaches to design of biofuel microbes. **Imam, S., Noguera, D. R., and Donohue, T. J.** (2015) An integrated approach to reconstructing genome-scale transcriptional regulatory networks. *PLOS Computational Biology* **11**, e1004103. http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004103
- **Production of GVL-derived lignin expands deconstruction platform to three biomass fractions.** Lignin was isolated using the GVL method and shown to retain a native-like structure. After hydrogenolysis over a catalyst a significant portion of lignin carbon was converted to monomers. These findings show that the GVL platform could allow easy and efficient upgrading of all three biomass fractions: C5/C6 sugars and lignin. **Luterbacher, J. S., Azarpira, A., Motagamwala, A. H., Lu, F., Ralph, J., and Dumesic, J. A.** (2015) Lignin monomer production integrated into the γ-valerolactone sugar platform. *Energy & Environmental Science* **8**, 2657-2663. http://pubs.rsc.org/en/content/articlelanding/2015/ee/c5ee01322d - !divAbstract
- **Biofuels research uncovers a natural bioproduct with fungicidal properties.** Plant-derived fermentation inhibitors are a challenge to efficient biofuel production yet they may also have added value as bioproducts. In this study a combination of yeast chemical genomics and microscopic profiling was used to identify the cellular target of poacic acid, a compound present in lignocellulosic hydrolysates of grasses. Poacic acid was shown to target the glucan layer in fungal cell walls and protects soybean leaves from the broad-range fungal pathogen *S. sclerotiorum*. This study demonstrates that biofuel research can sometimes reveal potentially useful bioproducts of value, enhancing the economics of biorefineries. **Piotrowski, J. S., Okada, H., Lu, F., Li, S. C., Hinchman, L., Ranjan, A., Smith, D. L., Higbee, A. J., Ulbrich, A., Coon, J. J., Deshpande, R., Bukhman, Y. V., McIlwain, S., Ong, I. M., Myers, C. L., Boone, C., Landick, R., Ralph, J., Kabbage, M., and Ohya, Y.** (2015) Plant-derived antifungal agent poacic acid targets β-1,3-glucan. *Proceedings of the National Academy of Sciences of the United States of America* **112**, E1490-E1497. http://www.pnas.org/content/112/12/E1490.abstract?sid=45276789-834f-4a5c-947a-62eea82daf15
- **Phenolic amides inhibit *de novo* nucleotide biosynthesis.** This study utilized metabolomics, isotopic tracer methods, and biochemical assays to identify the cellular targets of amide inhibition in the model bacterium *E. coli*. Results indicate that phenolic amides directly inhibit a key enzyme involved in nucleotide biosynthesis. Knowledge of the mechanistic effects of hydrolysate inhibitors will inform efforts to engineer new biocatalysts with improved bioconversion efficiencies. **Pisithkul, T., Jacobson, T. B., O'Brien, T. J., Stevenson, D. M., and Amador-Noguez, D.** (2015) Phenolic amides are potent inhibitors of *de novo* nucleotide biosynthesis. *Applied and Environmental Microbiology* **81**, 5761-5772. http://aem.asm.org/content/early/2015/06/08/AEM.01324-15.abstract
- **Influence of cropping systems on soil microbial communities.** We characterized and compared soil microbial communities under restored prairie and three potential cellulosic biomass crops (corn, switchgrass, and mixed prairie grasses) in two spatial experimental designs – side-by-side plots where plant communities were in their second year since

establishment and regionally distributed fields where plant communities had been in place for at least 10 years. We conclude that location, a proxy primarily for soil type but also including site history, landscape, and climate, was the major factor determining microbial communities in our 2-year-old intensive sites and that these study sites were not under cultivation long enough for the crop to impose a strong signature on the microbial communities; in contrast, when the same crop had been grown on a site for 10 years or longer, a crop effect was observed, with communities under corn clearly differentiated from those under perennial grasses. Both presence of perennial plants and higher plant diversity likely favored the accumulation of microbial biomass and fungi, especially arbuscular mycorrhizal fungi (AMF), under switchgrass, mixed grasses, and prairie, leading to a more stable environment and highlighting that these alternatives to corn for biofuels may improve soil functional stability and sustainability.
da C. Jesus E, Liang C, Quensen JF, Susilawati E, Jackson RD, Balser TC, Tiedje JM (2016) Influence of corn, switchgrass, and prairie cropping systems on soil microbial communities in the upper Midwest of the United States. Global Change Biology – Bioenergy **8:** 481-494.
http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12289/abstract

- **Comparative water use by maize, perennial crops, restored prairie, and poplar trees in the US Midwest.** We measured growing-season evapotranspiration (ET) based on daily changes in soil profile water contents in five perennial systems—switchgrass, miscanthus, native grasses, restored prairie, and hybrid poplar—and in annual maize (corn) in a temperate humid climate (Michigan, USA). Our result show that measured water use by perennial systems was similar to maize across normal and drought years, contrasting with earlier modeling studies and suggesting that rain-fed perennial biomass crops in this climate have little impact on landscape water balances, whether replacing rain-fed maize on arable lands or successional vegetation on marginal lands. Results also suggest that crop ET rates, and thus groundwater recharge, streamflow, and lake levels, may be less sensitive to climate change than has been assumed.
  Hamilton SK, Hussain MZ, Bhardwaj AK, Basso B, Robertson GP (2015) Comparative water use by maize, perennial crops, restored prairie, and poplar trees in the US Midwest. Environmental Research Letters **10:** 064015.
  http://iopscience.iop.org/article/10.1088/1748-9326/10/6/064015/meta;jsessionid=CB6BCD3D5CE3285C1AB068B6E9B18EB5.c1
- **Potential of electrified vehicles to contribute to petroleum and climate goals and implications for biofuels.** We are interested in the extent to which electrified vehicles could reduce petroleum consumption and greenhouse gas (GHG) emissions and the sensitivity of these impacts across a range of travel demand and technology scenarios. We find that petroleum consumption and GHG emissions are highly sensitive to these inputs, with resulting petroleum consumption and GHG emissions varying widely. The implication for biofuels is important, to the extent they are aimed at meeting climate and petroleum use reduction goals; and to put these implications into perspective, we further estimate the volume of Renewable Fuel Standard (RFS)-compliant advanced biofuel (e.g., cellulosic biofuel) needed to meet petroleum and climate goals.
  Meier PJ, Cronin KR, Frost EA, Runge TM, Dale BE, Reinemann DJ, Detlor J (2015) Potential for electrified vehicles to contribute to U.S. petroleum and climate goals and implications for advanced biofuels. Environmental Science & Technology **49:** 8277-8286.
  http://pubs.acs.org/doi/abs/10.1021/acs.est.5b01691
- **Nitrous oxide emissions during establishment phase of various bioenergy cropping systems.** We measured soil N_2O emissions and potential environmental drivers of these fluxes from a three-year establishment-phase bioenergy cropping systems experiment

replicated in southcentral Wisconsin and southwestern Michigan. Our results indicate that perennial bioenergy crops in their establishment phase emit less N_2O than annual crops, especially when not fertilized. These findings should be considered further alongside yield and other metrics contributing to important ecosystem services.
Oates LG, Duncan DS, Gelfand I, Millar N, Robertson GP, Jackson RD (2016) Nitrous oxide emissions during establishment of eight alternative cellulosic bioenergy cropping systems in the North Central United States. Global Change Biology – Bioenergy **8:** 539-549.
http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12268/abstract

- **Comparing productivity of alternative cellulosic bioenergy cropping systems.** Here, we report on the six-year production potential (above ground net primary production, ANPP), post-frost harvested biomass (yield), and gross harvest efficiency (GHE = yield/ANPP) of seven model bioenergy cropping systems in both southcentral Wisconsin (ARL) and southwest Michigan (KBS). Overall the most productive cropping systems were corn > giant miscanthus > and switchgrass, which were significantly more productive than native grasses ≈ restored prairie ≈ early successional ≈ and hybrid poplar, although some systems (e.g. hybrid poplar) differed significantly by location. Results show that well-established, dedicated bioenergy crops are capable of producing as much biomass as corn stover, but with fewer inputs.
  Sanford GR, Oates LG, Jasrotia P, Thelen KD, Robertson GP, Jackson RD (2016) Comparative productivity of alternative cellulosic bioenergy cropping systems in the North Central USA. Agriculture, Ecosystems & Environment **216:** 344-355.
  http://www.sciencedirect.com/science/article/pii/S0167880915301250

Year 9 (Dec. 1, 2015 - Nov. 30, 2016)

- **Accounting for linkage disequilibrium improves the accuracy of genomic prediction in switchgrass.** In this study we empirically evaluate accuracies of different genomic prediction methods to assess the usefulness of genomic selection in switchgrass. Results suggest that marker-data transformations and, more generally, the account of linkage disequilibrium among markers, offer valuable opportunities for improving prediction procedures in genomic selection. High prediction accuracies, particularly with given traits at given locations, should motivate the implementation of genomic selection breeding programs in switchgrass that will help to accelerate the progress needed to reach biomass yield goals.
  Ramstein GP, Evans J, Kaeppler SM, Mitchell RB, Vogel KP, Buell CR, Casler MD (2016) Accuracy of genomic prediction in switchgrass (*Panicum virgatum* L.) improved by accounting for linkage disequilibrium. G3: Genes | Genomes | Genetics **6:** 1049-1062.
  http://www.g3journal.org/content/6/4/1049.long
- **Genome-wide associations with flowering time in switchgrass using exome-capture sequencing data.** This study used exome capture sequencing to perform genome-wide association studies using flowering time data from a switchgrass association panel. Principal component analysis showed that the greater than 500 switchgrass genotypes in the study represent five genetically distinct regional gene pools. Candidate genes involved in flowering time include known flowering regulators and also genes not previously associated with the control of flowering time; furthermore, the relationship of flowering time and geographic origin indicates likely roles for genes in both photoperiod and autonomous pathways in generating switchgrass flowering time variation.
  Grabowski PP, Evans J, Daum C, Deshpande S, Barry KW, Kennedy M, Ramstein G, Kaeppler SM, Buell CR, Jiang Y, Casler MD (2017) Genome-wide associations with

flowering time in switchgrass using exome-capture sequencing data. New Phytologist **213:** 154-169.
http://onlinelibrary.wiley.com/doi/10.1111/nph.14101/abstract

- **Advances in understanding flowering time in grasses.** In our continuing studies of flowering time in the model grass *Brachypodium*, we have published two new papers: 1) we demonstrate that VRN2 is a repressor of flowering that functions broadly in grasses from rice to *Brachypodium*, and 2) we identified six quantitative trait loci (QTL) that control differences in flowering time. Furthering the molecular-level understanding of the flowering network in the model grass *Brachypodium* improves the potential to manipulate flowering time in bioenergy grass crops to increase biomass yield.
  Woods DP, McKeown MA, Dong Y, Preston JC, Amasino RM (2016) Evolution of *VRN2/Ghd7*-like genes in vernalization-mediated repression of grass flowering. Plant Physiology **170:** 2124-2135.
  http://www.plantphysiol.org/content/170/4/2124
  Woods DP, Bednarek R, Bouché F, Gordon SP, Vogel JP, Garvin DF, Amasino RM (2017) Genetic architecture of flowering-time variation in *Brachypodium distachyon*. Plant Physiology **173:** 269-279.
  http://www.plantphysiol.org/content/173/1/269
- **Native zips.** In this study we surveyed a set of plants representing the spermatophytes or “seed plants” for the presence of monolignol (ML) ferulate conjugate ester linkages (“zips”) within the lignin polymers of these plants. All gymnosperms tested showed no evidence of zip-lignin, whereas low zip-levels were present in the isolated lignins of many, but not all, angiosperms; further, FMT was shown to be specific for the production of zip-lignin; a new grass-specific FMT was identified, revealing convergent evolution as the route to produce two distinct types of FMT. Identification of plant lines with increased zip-lignin content, likely able to be more easily and economically deconstructed, could provide superior sources of biomass for conversion to biofuels and bioproducts.
  Karlen SD, Zhang C, Peck ML, Smith RA, Padmakshan D, Helmich KE, Free HCA, Lee S, Smith BG, Lu F, Sedbrook JC, Sibout R, Grabber JH, Runge TM, Mysore KS, Harris PJ, Bartley LE, Ralph J (2016) Monolignol-ferulate conjugates are naturally incorporated into plant lignins. Science Advances **2:** e1600393.
  http://advances.sciencemag.org/content/2/10/e1600393
- **Formaldehyde stabilization increases lignin monomer yield.** Extracting a soluble and uncondensed lignin substrate during biomass pretreatment could facilitate the production of lignin monomers and be compatible with current biorefining strategies. In this study we used formaldehyde to stabilize lignin during extraction, leading to near theoretical yields of lignin monomers after hydrogenolysis of the extracted product; yields were three to seven times higher than those obtained when using the analogous method without formaldehyde. Our formaldehyde stabilization results suggest that lignin upgrading could be easily integrated into current biorefinery schemes, especially considering that formaldehyde is a relatively inexpensive bulk chemical that can be produced from biomass-derived syngas or methanol, either sourced biologically or from lignin methoxyl groups.
  Shuai L, Amiri MT, Questell-Santiago YM, Héroguel F, Li Y, Kim H, Meilan R, Chapple C, Ralph J, Luterbacher JS (2016) Formaldehyde stabilization facilitates lignin monomer production during biomass depolymerization. Science **354:** 329-333.
  http://science.sciencemag.org/content/354/6310/329
- **Cooperative electrocatalytic alcohol oxidation with electron-proton transfer mediators.** We examined the electrochemical oxidation of alcohols and identified a cooperative catalyst system with 2 components, an organic nitroxyl TEMPO and Cu(bpy). The co-catalyst system represents a unique class of electrocatalysts for alcohol oxidation,

which can offer much faster electrocatalytic rates and lower overpotentials, both of which are crucial in energy-conversion applications.
Badalyan A, Stahl SS (2016) Cooperative electrocatalytic alcohol oxidation with electron-proton-transfer mediators. Nature **535:** 406-410.
http://www.nature.com/nature/journal/v535/n7612/full/nature18008.html

- **Evolution of cellulolytic activity in Streptomyces.** We compared the phylogenetic diversity of over 1,100 strains of Streptomyces, and were able to identify that while plant biomass degrading enzymes (CAZy) are widespread in the genus, key enzyme families were obtained by horizontal gene transfer, and were retained in the most highly cellulolytic strains. This research gave insight into how specialized interactions between microbes and insects has given rise to increased microbial capability to deconstruct plant biomass, and identified the key genes, regulatory circuits, and enzymes used in this process.
Book AJ, Lewin GR, McDonald BR, Takasuka TE, Wendt-Pienkowski E, Doering DT, Suh S, Raffa KF, Fox BG, Currie CR (2016) Evolution of high cellulolytic activity in symbiotic *Streptomyces* through selection of expanded gene content and coordinated gene expression. PLOS Biology **14:** e1002475.
http://dx.doi.org/10.1371%2Fjournal.pbio.1002475
- **Saccharification of thermochemically pretreated cellulosic biomass using native and engineered cellulosomal enzymes.** We compared the hydrolytic activity of the most abundant cellulosomal enzymes from *C. thermocellum* and investigated the importance of enzyme complexation using a model engineered protein scaffold – rosettasome. Our results indicate that the type of pretreatment can significantly impact the saccharification efficiency of cellulosomal enzymes for various consolidated bioprocessing (CBP) scenarios: pretreatments that remove both lignin and hemicellulose can help improve the specific activity of cellulosomal enzymes.
Chundawat SPS, Paavola CD, Raman B, Nouailler M, Chan SL, Mielenz JR, Receveur-Brechot V, Trent JD, Dale BE (2016) Saccharification of thermochemically pretreated cellulosic biomass using native and engineered cellulosomal enzyme systems. Reaction Chemistry & Engineering **1:** 616-628.
http://dx.doi.org/10.1039/C6RE00172F
- **Next generation ammonia pretreatment enhances cellulosic biofuel production and separate lignin streams.** We developed a new liquid ammonia pretreatment methodology called Extractive Ammonia (EA) to simultaneously convert native crystalline cellulose I to a highly digestible cellulose III allomorph and selectively extract up to 45% of the lignin from lignocellulosic biomass with near-quantitative retention of all polysaccharides. EA pretreated corn stover yielded a higher fermentable sugar yield compared to AFEX while using 60% lower enzyme loading. It preserves extracted lignin functionalities, offering the potential to co-produce lignin-derived fuel and chemicals in the biorefinery.
da Costa Sousa L, Jin M, Chundawat SPS, Bokade V, Tang X, Azarpira A, Lu F, Avci U, Humpula J, Uppugundla N, Gunawan C, Pattathil S, Cheh AM, Kothari N, Kumar R, Ralph J, Hahn MG, Wyman CE, Seema S, Simmons BA, Dale BE, Balan V (2016) Next-generation ammonia pretreatment enhances cellulosic biofuel production. Energy & Environmental Science **9:** 1215-1223.
http://pubs.rsc.org/en/content/articlelanding/2016/ee/c5ee03051j - !divAbstract
da Costa Sousa L, Foston M, Bokade V, Azarpira A, Lu F, Ragauskas AJ, Ralph J, Dale B, Balan V (2016) Isolation and characterization of new lignin streams derived from extractive-ammonia (EA) pretreatment. Green Chemistry **18:** 4205-4215.
http://pubs.rsc.org/en/content/articlelanding/2016/gc/c6gc00298f - !divAbstract
- **Nanoscale structure of biomass.** Using *in situ* imaging at nanoscale resolution and real-time changes during biomass deconstruction process, we were able to summarize the

general structure of the plant cell wall in different plant tissues and plant species, as well as the physicochemical properties of biomass that affect the efficiency of thermochemical pretreatment and enzymatic hydrolysis.
Ding S-Y (2016) Nanoscale structure of biomass. *In* Marcel Schlaf, Z. Conrad Zhang, eds, Reaction Pathways and Mechanisms in Thermocatalytic Biomass Conversion I, Green Chemistry and Sustainable Technology. Springer Singapore, Singapore, pp 1-14.
http://link.springer.com/chapter/10.1007%2F978-981-287-688-1_1

- **Structural and biochemical characterization of enzymes in the lignin β-aryl ether cleavage pathway from *Sphingobium* sp SYK-6.** Collaborative studies by GLBRC, JBEI, and others structurally and biochemically characterized enzymes in the lignin β-aryl ether cleavage pathway from *Sphingobium* sp SYK-6. With lignin as the most abundant aromatic polymer in nature, these results inform broader lignin valorization efforts that will ultimately enable the development of efficient pathways for the conversion of lignin into renewable aromatics with applications in advanced biofuels and chemicals.
  Helmich KE, Pereira JH, Gall DL, Heins RA, McAndrew RP, Bingman C, Deng K, Holland KC, Noguera DR, Simmons BA, Sale KL, Ralph J, Donohue TJ, Adams PD, Phillips GN, Jr. (2016) Structural basis of stereospecificity in the bacterial enzymatic cleavage of β-aryl ether bonds in lignin. Journal of Biological Chemistry **291:** 5234-5246.
  http://www.jbc.org/content/291/10/5234.full
  Pereira JH, Heins RA, Gall DL, McAndrew RP, Deng K, Holland KC, Donohue TJ, Noguera DR, Simmons BA, Sale KL, Ralph J, Adams PD (2016) Structural and biochemical characterization of the early and late enzymes in the lignin β-aryl ether cleavage pathway from *Sphingobium* sp SYK-6. The Journal of Biological Chemistry **291:** 10228-10238
  http://www.jbc.org/content/291/19/10228
- **Development of OptSSeq, a synthetic biology tool to identify optimal gene expression elements for ethanol production.** Designing synthetic biofuel pathways with optimized and balanced enzyme levels can be challenging. Using OptSSeq we identified optimal gene expression elements for heterologous ethanol production from a combinatorial library of gene expression signals. OptSSeq is a tool that can be used to tune pathway enzyme levels whose function can be linked to cell growth or survival.
  Ghosh, I. N., and Landick, R. (2016) OptSSeq: high-throughput sequencing readout of growth enrichment defines optimal gene expression elements for homoethanologenesis. *ACS synthetic biology* **5**, 1519-1534.
  http://pubs.acs.org/doi/abs/10.1021/acssynbio.6b00121
- **Identification of the cellular target of ionic liquid toxicity and engineering of a yeast tolerant strain.** Chemical genomics was used to identify yeast gene deletions that confer sensitivity or resistance to imidazolium-based ionic liquids (IIL). Yeast were subsequently successfully engineered for improved IIL tolerance while demonstrating increased sugar to biofuel conversion relative to non-engineered strains. This paper demonstrates the utility of chemical genomics-guided biodesign for development of biocatalysts.
  Dickinson, Q., Bottoms, S., Hinchman, L., McIlwain, S., Li, S., Myers, C. L., Boone, C., Coon, J. J., Hebert, A., Sato, T. K., Landick, R., and Piotrowski, J. S. (2016) Mechanism of imidazolium ionic liquids toxicity in *Saccharomyces cerevisiae* and rational engineering of a tolerant, xylose-fermenting strain. *Microbial Cell Factories* **15**, 17.
  https://microbialcellfactories.biomedcentral.com/articles/10.1186/s12934-016-0417-7
- **Drought-stressed switchgrass produces compounds inhibitory to microbes.** This study examined how interannual variability in precipitation impacts feedstock deconstruction and biofuel production by microbial catalysts. The results indicate that environmental variation can have significant effects on biomass properties, which can then impact

downstream processes. Understanding how feedstock variability impacts the bioconversion pipeline may lead to the development of predictive models based on known inputs.
Ong, R. G., Higbee, A., Bottoms, S., Dickinson, Q., Xie, D., Smith, S. A., Serate, J., Pohlmann, E., Jones, A. D., Coon, J. J., Sato, T. K., Sanford, G. R., Eilert, D., Oates, L. G., Piotrowski, J. S., Bates, D. M., Cavalier, D., and Zhang, Y. (2016) Inhibition of microbial biofuel production in drought-stressed switchgrass hydrolysate. *Biotechnology for Biofuels* **9**, 237.
https://biotechnologyforbiofuels.biomedcentral.com/articles/10.1186/s13068-016-0657-0

- **Yeast evolved for enhanced xylose utilization reveal unexpected interactions between cell signaling and Fe-S cluster biogenesis.** Rapid xylose utilization in yeast was found to be dependent upon genetic interactions among four genes, uncovering a surprising genetic interaction that facilitates aerobic and anaerobic utilization of xylose. Understanding how yeast cells adapt to non-preferential carbon sources uncovers potential genetic engineering strategies that can improve efficiency of biofuel production.
  Sato, T. K., Tremaine, M., Parreiras, L. S., Herbert, A. S., Myers, K. S., Higbee, A. J., Sardi, M., McIlwain, S. J., Ong, I. M., Breuer, R. J., Narasimhan, R. A., McGee, M. A., Dickinson, Q., La Reau, A., Xie, D., Tian, M., Piotrowski, J. S., Reed, J. L., Zhang, Y., Coon, J. J., Hittinger, C. T., Gasch, A. P., and Landick, R. (2016) Directed evolution reveals unexpected epistatic interactions that alter metabolic regulation and enable anaerobic xylose use by *Saccharomyces cerevisiae*. *PLoS genetics* **12**, e1006372.
  http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1006372
- **Ecosystem water-use efficiency of annual corn and perennial grasslands.** To examine the interacting influence of dominant plant functional groups (C_3 and C_4) and land-use history on water-use efficiencies WUEs of annual corn and perennial (restored prairie, switchgrass and smooth brome grass) grasslands in the US Midwest, we determined ecosystem-level (*e*WUE) and intrinsic (*i*WUE) WUEs using eddy covariance and plant carbon isotope ratios, respectively. We conclude that ecosystem water-use efficiency (*e*WUE) of planted perennial grasslands is determined to a great extent by the relative abundance of C_3 and C_4 plant species within a given season. These results inform models of the interaction between carbon and water cycles in grassland ecosystems under current and future climate and management scenarios.
  Abraha M, Gelfand I, Hamilton SK, Shao C, Su Y-J, Robertson GP, Chen J (2016) Ecosystem water-use efficiency of annual corn and perennial grasslands: contributions from land-use history and species composition. Ecosystems **19:** 1001-1012.
  https://link.springer.com/article/10.1007/s10021-016-9981-2
- **Nitrogen fertilization effects on productivity and nitrogen loss in perennial bioenergy cropping systems.** In this study, we explore how nitrogen (N) fertilization impacts N loss pathways and plant productivity in three biomass production systems based on grasses and forbs native to North America; we studied a switchgrass monoculture, a mixture of five grasses, and a mixture of 18 prairie species. We observed a cropping systems-level tradeoff between biomass production and loss of environmentally harmful forms of N, with the native grasses and prairie species mixtures having lower N_2O emissions, NO_3^- leaching, and aboveground productivity; our findings hold significant implications for the selection and management of perennial bioenergy cropping systems. Our results show, with respect to nitrogen processing, polycultural biomass production systems can be resilient in the face of annual weather fluctuations, which indicates the environmental and management benefits of these systems should not be overlooked.

Duran BEL, Duncan DS, Oates LG, Kucharik CJ, Jackson RD (2016) Nitrogen fertilization effects on productivity and nitrogen loss in three grass-based perennial bioenergy cropping systems. PLOS ONE **11:** e0151919.
http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0151919

- **Cover crops and pest suppression in annual maize bioenergy cropping systems.** The overall goal of our two-year, two-state study was to determine the effects of a winter cover crop system designed to enhance the agronomic performance of a bioenergy cropping system on predatory invertebrate communities and biocontrol services. Our specific objectives were 1) to determine if winter cover crops altered the abundance and diversity of predator communities, and 2) to assess the impact of the resulting predator communities on rates of predation in the subsequent crop. Our results show that planting a rye/pea cover crop in continuous maize systems grown for grain and stover did not alter biocontrol services under the conditions we studied; while we found no significant positive or negative impacts of this cover crop system on biocontrol services, bioenergy cover cropping systems could be managed to increase multiple ecosystem services by altering cover crop identity, or timing of planting and harvest.
  Fox AF, Kim TN, Bahlai CA, Woltz JM, Gratton C, Landis DA (2016) Cover crops have neutral effects on predator communities and biological control services in annual cellulosic bioenergy cropping systems. Agriculture, Ecosystems & Environment **232:** 101-109.
  http://www.sciencedirect.com/science/article/pii/S0167880916303711
- **Effect of switchgrass rhizospheres on agricultural soils of the upper Midwest.** Rhizosphere microbial communities play an essential role in determining plant productivity, particularly in agriculturally marginal environments. We compared microbial communities in switchgrass rhizospheres and their associated bulk soils in two regions of the U.S. upper Midwest (Michigan and Wisconsin) with contrasting soil types, and at two site types with differing switchgrass establishment ages and management intensities. Overall, our findings suggest switchgrass rhizospheres systematically stimulate microbial growth and microbial residue turnover.
  Liang C, da C. Jesus E, Duncan DS, Quensen JF, Jackson RD, Balser TC, Tiedje JM (2016) Switchgrass rhizospheres stimulate microbial biomass but deplete microbial necromass in agricultural soils of the upper Midwest, USA. Soil Biology and Biochemistry **94:** 173-180.
  http://www.sciencedirect.com/science/article/pii/S0038071715004137
- **Importance of minimizing nitrogen fertilizer use in the biofuel industry.** To evaluate possible climate benefits of cellulosic biofuel crops, we measured soil N_2O emissions and nitrate leaching along a switchgrass high resolution N-fertilizer gradient for three years post-establishment. Results revealed an exponential increase in annual N_2O emissions that each year became stronger; concomitantly, switchgrass yields became less responsive each year to N fertilizer. Minimizing N fertilizer use will be an important strategy for fully realizing the climate benefits of cellulosic biofuel production.
  Ruan L, Bhardwaj AK, Hamilton SK, Robertson GP (2016) Nitrogen fertilization challenges the climate benefit of cellulosic biofuels. Environmental Research Letters **11:** 064007.
  http://iopscience.iop.org/article/10.1088/1748-9326/11/6/064007/meta

Year 10 (Dec. 1, 2016 - Nov. 1, 2017)

- **Altering carbon allocation in hybrid poplar impacts cell wall growth and development.** In this study we test the hypothesis that cell wall attributes and plant development can be altered by augmenting the available pools of soluble sucrose; to do so, we overexpressed *Arabidopsis* galactinol synthase (*AtGolS3*) in hybrid poplar. These

transgenic lines possessed altered cell wall chemistries and fiber properties, traits characteristic of specialized tension wood (lower total lignin content, higher cellulose content, xylem that often contains small vessels and fibers with a unique inner cell wall layer made primarily of cellulose). This transgenic approach, which yields increased cellulose content, altered hemicellulose composition, and reduced lignin content, is an ideal strategy for poplar and other lignocellulosic-derived feedstocks for improved industrial processing, especially for bioenergy applications.
Unda F, Kim H, Hefer C, Ralph J, Mansfield SD (2017) Altering carbon allocation in hybrid poplar (*Populus alba × grandidentata*) impacts cell wall growth and development. Plant Biotechnology Journal **15:** 865-878.
http://onlinelibrary.wiley.com/doi/10.1111/pbi.12682/abstract

- **Suppression of *CCR* increases the level of "zips" incorporated into maize lignins.** In this study, we examined the features of a lignin biosynthetic mutant in maize that we hypothesized could result in an increase in the levels of more readily cleavable ester bonds in the lignin backbone ("zip-lignin"). Analysis of a maize *ccr1* insertion mutant, in comparison to wild-type, shows reduced total lignin levels, normal growth and development, increased zip-lignin levels, and increased digestibility as measured by glucose and xylose release. The increased monolignol ferulate incorporation into lignins (*i.e.,* higher zip-lignin levels) in *ccr1* mutant maize plants suggests that downregulation of *CCR* may be a viable biosynthetic strategy for increasing zip levels in other biofuel crops as well.
Smith RA, Cass CL, Mazaheri M, Sekhon RS, Heckwolf M, Kaeppler H, de Leon N, Mansfield SD, Kaeppler SM, Sedbrook JC, Karlen SD, Ralph J (2017) Suppression of *CINNAMOYL-CoA REDUCTASE* increases the level of monolignol ferulates incorporated into maize lignins. Biotechnology for Biofuels **10:** 109.
https://biotechnologyforbiofuels.biomedcentral.com/articles/10.1186/s13068-017-0793-1
- **Establishment of a vernalization requirement in *Brachypodium distachyon* requires *REPRESSOR OF VERNALIZATION1*.** In order to further the molecular-level understanding of the flowering regulatory network to enable manipulation of flowering time and biomass yield, we screened for *Brachypodium* mutants that flower rapidly without vernalization. We identified a new gene, *REPRESSOR OF VERNALIZATION1* (*RVR1*), required for the repression of the *VRN1* gene prior to cold; thus *RVR1* plays a role in establishing a vernalization requirement in *Brachypodium* and is likely to play the same role in other vernalization-requiring pooid grasses.
Woods DP, Ream TS, Bouché F, Lee J, Thrower N, Wilkerson C, Amasino RM (2017) Establishment of a vernalization requirement in *Brachypodium distachyon* requires *REPRESSOR OF VERNALIZATION1*. Proceedings of the National Academy of Sciences of the United States of America **114:** 6623-6628.
http://www.pnas.org/content/114/25/6623
- **Characterization of vegetative sorghum stem internode development.** Here we conducted a detailed characterization of the development of vegetative sorghum stem internodes to provide a baseline of information on stem anatomy and gene expression that may be useful for improving biomass yield and composition. Transcriptome profiling indicates that dynamic variation in the levels and action of hormones GA, CK, IAA, BR, ethylene, ABA, and JA modulate gene expression and growth during internode growth and development. This study provides detailed microscopic and transcriptomic data useful for identifying genes and molecular pathways regulating internode elongation in response to various developmental and environmental signals.

Kebrom TH, McKinley B, Mullet JE (2017) Dynamics of gene expression during development and expansion of vegetative stem internodes of bioenergy sorghum. Biotechnology for Biofuels **10:** 159. https://biotechnologyforbiofuels.biomedcentral.com/articles/10.1186/s13068-017-0848-3

- **Identification of new lignin monomers in palm lignins.** Recent studies indicate that lignification is a flexible mechanism and that plants are capable of using a variety of phenolic compounds for the formation of lignin polymers. In two studies this year, we report the occurrence of new classes of polyphenolic compounds in the lignins of palm species. The incorporation of nonconventional monomers, not usually present in the lignins of other plants, can open up new ways to design and engineer the lignin structure to produce polymers and plant-based biomaterials with altered properties.
  del Río JC, Rencoret J, Gutiérrez A, Kim H, Ralph J (2017) Hydroxystilbenes are monomers in palm fruit endocarp lignins. Plant Physiology **174:** 2072-2082. http://www.plantphysiol.org/content/early/2017/06/06/pp.17.00362
  Karlen SD, Smith RA, Kim H, Padmakshan D, Bartuce A, Mobley JK, Free HCA, Smith BG, Harris PJ, Ralph J (2017) Highly decorated lignins in leaf tissues of the Canary Island date palm *Phoenix canariensis*. Plant Physiology [DOI: 10/1104/pp.17.011172]. http://www.plantphysiol.org/content/early/2017/09/11/pp.17.01172
- **Transcriptional analysis of flowering time in switchgrass.** Our objective was to identify flowering time gene candidates that could be employed to manipulate flowering time in upland, cold-tolerant switchgrass cultivars, in order to increase total biomass yield for these northern accessions. Orthologs of known flowering time genes had either ecotype- or flowering time-specific patterns, allowing for the possible separation of flowering time traits from other traits used in breeding or transgenic manipulation efforts. The candidate genes presented here may be used to guide switchgrass improvement through marker-assisted breeding and/or transgenic or gene editing approaches.
  Tornqvist C-E, Vaillancourt B, Kim J, Buell CR, Kaeppler SM, Casler MD (2017) Transcriptional analysis of flowering time in switchgrass. BioEnergy Research **10:** 700-713. https://link.springer.com/article/10.1007/s12155-017-9832-9
- **Development of rapid bioconversion with integrated recycle technology for ethanol production using Extractive Ammonia**. As was done previously with AFEX, we applied the rapid bioconversion with integrated recycle technology (RaBIT) process on the Extractive Ammonia (EA) pretreatment for conversion of corn stover (CS) to ethanol at high solids loading, recycling enzymes via recycling of the unhydrolyzed solids, and shortening the enzymatic hydrolysis and fermentation times to 24 h. We found that ethanol productivity was enhanced 2-fold and the enzyme loading was reduced by 30%, suggesting that the integration of RaBIT with EA enables a very substantial decrease in enzyme loading.
  Jin M, Liu Y, da Costa Sousa L, Dale BE, Balan V (2017) Development of rapid bioconversion with integrated recycle technology for ethanol production from extractive ammonia pretreated corn stover. Biotechnology and Bioengineering **114:** 1713-1720. http://onlinelibrary.wiley.com/doi/10.1002/bit.26302/full
- **Lignocellulosic pretreatment in a fungus-cultivating termite.** In our study to characterize the natural lignocellulosic degradation system in fungus-cultivating termites, we demonstrate that lignin depolymerization takes place during the rapid passage through the pH-neutral gut of young termite workers in a process that is striking in its speed and efficiency at destroying the traditionally-considered most recalcitrant C–C bonded lignin structural units. This process releases the plant polysaccharide component, thereby facilitating degradation of the substrate by processes subsequently occurring via the fungus-comb microbiome. Thus, natural systems for lignin degradation/pretreatment are

far beyond what was previously recognized and are potential sources of novel ligninolytic agents, enabling more efficient plant cell wall utilization.
Li H, Yelle DJ, Li C, Yang M, Ke J, Zhang R, Liu Y, Zhu N, Liang S, Mo X, Ralph J, Currie CR, Mo J (2017) Lignocellulosic pretreatment in a fungus-cultivating termite. Proceedings of the National Academy of Sciences of the United States of America **114:** 4709-4714.
http://www.pnas.org/content/114/18/4709.full

- **Fine-tuned identification of glycoside hydrolase specificity on plant cell walls.** We used glycome profiling and NIMS to characterize cell-wall enzymatic hydrolysis in non-pretreated and AFEX-pretreated corn stover and switchgrass using three *Ruminiclostridium thermocellum* enzymes. The three enzymes fall into three classes of glycosyl hydrolysases, and results showed that the GH5 and GH11 enzymes had a broader specificity than G10. In addition to fine-tuned, quantitative analysis of enzyme specificities, these methods can help functionally annotate carbohydrate-active enzyme databases that are organized according to genomic data.
  Walker JA, Pattathil S, Bergeman LF, Beebe ET, Deng K, Mirzai M, Northen TR, Hahn MG, Fox BG (2017) Determination of glycoside hydrolase specificities during hydrolysis of plant cell walls using glycome profiling. Biotechnology for Biofuels **10:** 31.
  http://dx.doi.org/10.1186/s13068-017-0703-6
- **Discovery of mutations that increase bacterial lipid production.** Microbial lipids are a potential replacement for petroleum-based fuels but achieving high yields is challenging. High-lipid (HL) production bacterial mutants were isolated and shown to have increased lipid accumulation with alterations to the bacterial cell envelope; two HL mutants were shown to accumluate ~60% of the lipids extracellularly, potentially aided in recovery of product. Knowledge of the mechanisms that govern microbial lipid production can reveal new strategies to increase lipid yield and increase the economic viability of alternatives to fuels or chemicals currently derived from petroleum.
  Lemmer, K. C., Zhang, W., Langer, S. J., Dohnalkova, A. C., Hu, D., Lemke, R. A., Piotrowski, J. S., Orr, G., Noguera, D. R., and Donohue, T. J. (2017) Mutations that alter the bacterial cell envelope increase lipid production. *mBio* **8**, e00513-00517.
  http://mbio.asm.org/content/8/3/e00513-17
- **GVL-based deconstruction strategy triples the fraction of biomass converted to high-value products.** This study sought to determine the yield of high-value products from the primary components of lignocellulosic biomass to assess the economic viability of an integrated biorefinery. Results show that up to 80% of the biomass was obtained as high-value products from the three major components of lignocellulosic biomass (cellulose, hemicellulose, and lignin). Technoeconomic analysis indicates that the technology can be cost-competitive with a current petroleum refinery.
  Alonso, D. M., Hakim, S., Zhou, S., Won, W., Hosseinaei, O., Tao, J., Garcia-Negron, V., Motagamwala, A. H., Mellmer, M. A., Huang, K., Houtman, C. J., Labbe, N., Harper, D. P., Maravelias, C., Runge, T., and Dumesic, J. A. (2017) Increasing the revenue from lignocellulosic biomass: maximizing feedstock utilization. *Science Advances* **3**, e1603301.
  http://advances.sciencemag.org/content/3/5/e1603301
- **Increased ability to identify and predict essential genes from bacterial Tn-seq libraries.** Here we developed a computational tool to identify essential genes under a range of conditions, based on the frequency of random transposon insertions across the genome. Results show that the tool was able to accurately predict the essentiality of many known genes and identified genes not previously considered to be essential. Combining genome-scale experimental and computational methods can provide insight into enzymes and pathways involved in synthesis of biofuels and biochemicals.

Burger, B. T., Imam, S., Scarborough, M. J., Noguera, D. R., and Donohue, T. J. (2017) Combining genome-scale experimental and computational methods to identify essential genes in *Rhodobacter sphaeroides*. *mSystems* **2**, e00015-00017.
http://msystems.asm.org/content/2/3/e00015-17

- **GVL plus co-solvent system for biomass deconstruction is economically feasible and cost-competitive.** The GVL method is a promising biomass-agnostic, renewable technology for biomass deconstruction. Technoeconomic analysis of the use of a system containing GVL, water, and organic co-solvent showed that recovery of high-yielding sugar streams and lignin is comparable to other methods. The estimated cost of GVL-derived ethanol had an ~10-12% decrease in minimum selling price per gasoline equivalent compared to other benchmarked processes.
  Won, W., Motagamwala, A. H., Dumesic, J. A., and Maravelias, C. T. (2017) A co-solvent hydrolysis strategy for the production of biofuels: process synthesis and technoeconomic analysis. *Reaction Chemistry and Engineering* **2**, 397-405.
  http://pubs.rsc.org/en/content/articlelanding/2017/re/c6re00227g - !divAbstract
- **Yeast hybridization and adaptive evolution leverages traits relevant to biofuel production.** Interspecies yeast hybrids were generated and adaptively evolved for enhanced biofuel production from biomass. Traits such as enhanced xylose utilization and hydrolysate toxin tolerance contributed to more robust performance in the hybrids relative to natural isolates. This study demonstrates the role and relevance of studying natural isolates to identify useful biofuel traits for biocatalyst design. **Peris D, Moriarty RV, Alexander WG, Baker E, Sylvester K, Sardi M, Langdon QK, Libkind D, Wang Q-M, Bai F-Y, Leducq J-B, Charron G, Landry CR, Sampaio JP, Goncalves P, Hyma KE, Fay JC, Sato TK, Hittinger CT** (2017) Hybridization and adaptive evolution of diverse *Saccharomyces* species for cellulosic biofuel production. Biotechnology for Biofuels **10:** 78.
  https://biotechnologyforbiofuels.biomedcentral.com/articles/10.1186/s13068-017-0763-7
- **Hotspots of soil N_20 emission enhanced through water absorption by plant residue.** Here we quantify physical and hydrological soil characteristics that lead to strikingly accelerated N_2O emissions in plant residue-induced hotspots. Results reveal a mechanism for microscale N_2O emissions: water absorption by plant residue that creates unique micro-environmental conditions, markedly different from those of the bulk soil (moisture levels within plant residue exceeded those of bulk soil by 4–10-fold and led to accelerated N_2O production via microbial denitrification). Understanding and modeling hotspot microscale physical and hydrologic characteristics is a promising route to predict N_2O emissions and thus to develop effective mitigation strategies and estimate global fluxes in a changing environment.
  Kravchenko AN, Toosi ER, Guber AK, Ostrom NE, Yu J, Azeem K, Rivers ML, Robertson GP (2017) Hotspots of soil N_2O emission enhanced through water absorption by plant residue. Nature Geoscience **10:** 496-500.
  http://www.nature.com/ngeo/journal/v10/n7/full/ngeo2963.html
- **Cover crop root contributions to soil C in a no-till corn bioenergy cropping system.** Here, we examine the relative contributions of cover crop root and shoot to soil carbon (C) in order to determine whether belowground cover crop C could help offset the deleterious effects of residue removal in a no-till continuous corn bioenergy cropping system. We labeled cereal rye (*Secale cereale)*, a common winter cover crop, *in situ* with $^{13}CO_2$, tracked inputs from rhizodeposits during the growing season, and tracked root and shoot inputs into different soil C pools over the following 2 years. Our results suggest that including winter cover crops in annual rotation could increase biofuel feedstocks directly and indirectly; aboveground cover crop residues could contribute to biofuel feedstocks and

belowground cover crop inputs could offset the C removal associated with the use of main crop stover as a biofuel feedstock.
Austin EE, Wickings K, McDaniel MD, Robertson GP, Grandy AS (2017) Cover crop root contributions to soil carbon in a no-till corn bioenergy cropping system. Global Change Biology – Bioenergy **9:** 1252-1263.
http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12428/full

- **Cellulosic biofuel contributions to a sustainable energy future: choices and outcomes.** Understanding the effects of management choices is key for realizing the climate and other environmental benefits provided by cellulosic bioenergy crops. Here, we synthesize recent empirical research that targets sustainability concerns to identify potential solutions for managing the land use–related trade-offs of cellulosic biofuels. We organize our conclusions to articulate seven emerging principles that are relevant globally to the sustainability of cellulosic biofuel crop production.
  Robertson GP, Hamilton SK, Barham BL, Dale BE, Izaurralde RC, Jackson RD, Landis DA, Swinton SM, Thelen KD, Tiedje JM (2017) Cellulosic biofuel contributions to a sustainable energy future: choices and outcomes. Science **356:** pii: eaal2324.
  http://science.sciencemag.org/content/356/6345/eaal2324
- **Plant community composition influences fine root production and biomass allocation in perennial bioenergy cropping systems of the upper Midwest, USA.** Fine roots play a key role in the global carbon (C) cycle because much of the C accumulating in soil is the result of fine root production and turnover. Here we explore the effect of plant community composition and diversity on fine root production in surface soils and plant biomass allocation to fine roots in six perennial cropping systems in composition and diversity planted as biofuel feedstocks. Findings demonstrate a greater potential for diverse biofuel cropping systems to allocate C belowground to fine roots as compared to monocultures, with potential implications for soil C sequestration.
  Sprunger CD, G. OL, Jackson RD, Robertson GP (2017) Plant community composition influences fine root production and biomass allocation in perennial bioenergy cropping systems of the upper Midwest, USA. Biomass and Bioenergy **105:** 248-258.
  http://www.sciencedirect.com/science/article/pii/S0961953417302283
- **Soil depth and crop determinants of bacterial communities under ten biofuel cropping systems.** Biofuel-cropping systems, projected for large land areas, can potentially change their soil microbiome and the ecosystem services they catalyze. We determined the bacterial community composition and relevant soil properties for samples collected after six crop years at 0–10 cm, 10–25 cm, 25–50 cm, and 50–100 cm under corn, switchgrass, *Miscanthus*, and restored prairie, as well as 0–10 cm under six additional candidate biofuel crops in replicate side-by side plots. We found that soil depth, as a proxy for changes in soil biogeochemical, edaphic, and structural properties, was a strong factor in shaping bacterial community structure under a wide range of cropping systems; crop type was a secondary driver and was significant at soil depths above 50 cm after 6 years, with switchgrass' effects deeper.
  Zhang B, Penton CR, Xue C, Quensen JF, Roley SS, Guo J, Garoutte A, Zheng T, Tiedje JM (2017) Soil depth and crop determinants of bacterial communities under ten biofuel cropping systems. Soil Biology and Biochemistry **112:** 140-152.
  http://www.sciencedirect.com/science/article/pii/S0038071716303236

PUBLICATIONS ATTRIBUTED TO GLBRC GRANT NUMBER DE-FC02-07ER64494

2008

1. **Babcock BA** (2008) Breaking the link between food and biofuels. *In* Center for Agricultural and Rural Development Briefing Paper 08-BP 53. Iowa State University, Ames, IA.
2. **Benning C, Pichersky E** (2008) Harnessing plant biomass for biofuels and biomaterials. The Plant Journal **54:** 533-535
3. **Cavalier DM, Lerouxel O, Neumetzler L, Yamauchi K, Reinecke A, Freshour G, Zabotina OA, Hahn MG, Burgert I, Pauly M, Raikhel NV, Keegstra K** (2008) Disrupting two *Arabidopsis thaliana* xylosyltransferase genes results in plants deficient in xyloglucan, a major primary cell wall component. The Plant Cell **20:** 1519-1537
4. **Durrett TP, Benning C, Ohlrogge JB** (2008) Plant triacylglycerols as feedstocks for the production of biofuels. The Plant Journal **54:** 593-607
5. **Feng H, Babcock BA** (2008) Impacts of ethanol on planted acreage in market equilibrium (Iowa State Report). *In* Center for Agricultural and Rural Development, Iowa State University. Center for Agricultural and Rural Development, Iowa State University, Ames, IA.
6. **Landis DA, Gardiner MM, van der Werf W, Swinton SM** (2008) Increasing corn for biofuel production reduces biocontrol services in agricultural landscapes. Proceedings of the National Academy of Sciences of the United States of America **105:** 20552-20557
7. **Liang C, Balser TC** (2008) Preferential sequestration of microbial carbon in subsoils of a glacial-landscape toposequence, Dane County, WI, USA. Geoderma **148:** 113-119
8. **Pauly M, Keegstra K** (2008) Cell-wall carbohydrates and their modification as a resource for biofuels. The Plant Journal **54:** 559-568
9. **Pauly M, Keegstra K** (2008) Physiology and metabolism ‘Tear down this wall’. Current Opinion in Plant Biology **11:** 233-235
10. **Pollard M, Beisson F, Li Y, Ohlrogge JB** (2008) Building lipid barriers: biosynthesis of cutin and suberin. Trends in Plant Science **13:** 236-246
11. **Robertson GP, Dale VH, Doering OC, Hamburg SP, Melillo JM, Wander MM, Parton WJ, Adler PR, Barney JN, Cruse RM, Duke CS, Fearnside PM, Follett RF, Gibbs HK, Goldemberg J, Mladenoff DJ, Ojima D, Palmer MW, Sharpley A, Wallace L, Weathers KC, Wiens JA, Wilhelm WW** (2008) Sustainable biofuels redux. Science **322:** 49-50
12. **Suen G, Currie CR** (2008) Ancient fungal farmers of the insect world. Microbiology Today **35:** 172-175
13. **Tiedje J, Donohue T** (2008) Microbes in the energy grid. Science **320:** 985
14. **Zabotina OA, van de Ven WT, Freshour G, Drakakaki G, Cavalier DM, Mouille G, Hahn MG, Keegstra K, Raikhel NV** (2008) Arabidopsis *XXT5* gene encodes a putative α-1,6-xylosyltransferase that is involved in xyloglucan biosynthesis. The Plant Journal **56:** 101-115

2009

1. **Allen DK, Libourel IGL, Shachar-Hill Y** (2009) Metabolic flux analysis in plants: coping with complexity. Plant, Cell & Environment **32:** 1241-1257
2. **Allen DK, Ohlrogge JB, Shachar-Hill Y** (2009) The role of light in soybean seed filling metabolism. The Plant Journal **58:** 220-234
3. **Awai K, Lechno-Yossef S, Wolk CP** (2009) Heterocyst envelope glycolipids. *In* Hajime Wada, Norio Murata, eds, Lipids in Photosynthesis. Springer Netherlands, pp 179-202
4. **Balan V, Bals B, Chundawat SPS, Marshall D, Dale BE** (2009) Lignocellulosic biomass pretreatment using AFEX. *In* Jonathan R. Mielenz, ed, Biofuels: Methods and Protocols, Methods in Molecular Biology, Vol 581. Humana Press, pp 61-77

5. **Balan V, da Costa Sousa L, Chundawat SPS, Marshall D, Sharma LN, Chambliss CK, Dale BE** (2009) Enzymatic digestibility and pretreatment degradation products of AFEX-treated hardwoods (*Populus nigra*). Biotechnology Progress **25:** 365-375
6. **Bates PD, Durrett TP, Ohlrogge JB, Pollard M** (2009) Analysis of acyl fluxes through multiple pathways of triacylglycerol synthesis in developing soybean embryos. Plant Physiology **150:** 55-72
7. **Binder JB, Raines RT** (2009) Simple chemical transformation of lignocellulosic biomass into furans for fuels and chemicals. Journal of the American Chemical Society **131:** 1979-1985
8. **Caldera EJ, Poulsen M, Suen G, Currie CR** (2009) Insect symbioses: a case study of past, present, and future fungus-growing ant research. Environmental Entomology **38:** 78-92
9. **Casler MD, Mitchell R, Richardson J, Zalesny RS** (2009) Biofuels, bioenergy, and bioproducts from sustainable agricultural and forest crops. BioEnergy Research **2:** 77-78
10. **Cole JR, Wang Q, Cardenas E, Fish J, Chai B, Farris RJ, Kulam-Syed-Mohideen AS, McGarrell DM, Marsh T, Garrity GM, Tiedje JM** (2009) The Ribosomal Database Project: improved alignments and new tools for rRNA analysis. Nucleic Acids Research **37:** D141-145
11. **da Costa Sousa L, Chundawat SPS, Balan V, Dale BE** (2009) Cradle-to-grave assessment of existing lignocellulose pretreatment technologies. Current Opinion in Biotechnology **20:** 339-347
12. **Dale BE, Allen MS, Laser M, Lynd LR** (2009) Protein feeds coproduction in biomass conversion to fuels and chemicals. Biofuels, Bioproducts and Biorefining **3:** 219-230
13. **DeLisa MP, Conrado RJ** (2009) Synthetic metabolic pipelines: controlling the spatial organization of sequential metabolic enzymes may provide a general strategy for increasing the production of valuable compounds. Nature Biotechnology **27:** 728-729
14. **Gao J, Hao X, Thelen KD, Robertson GP** (2009) Agronomic management system and precipitation effects on soybean oil and fatty acid profiles. Crop Science **49:** 1049-1057
15. **Garlock R, Chundawat SPS, Balan V, Dale BE** (2009) Optimizing harvest of corn stover fractions based on overall sugar yields following ammonia fiber expansion pretreatment and enzymatic hydrolysis. Biotechnology for Biofuels **2:** 29
16. **Hedenstrom M, Wiklund-Lindstrom S, Oman T, Lu F, Gerber L, Schatz P, Sundberg B, Ralph J** (2009) Identification of lignin and polysaccharide modifications in *Populus* wood by chemometric analysis of 2D NMR spectra from dissolved cell walls. Molecular Plant **2:** 933-942
17. **Huber GW, Dale BE** (2009) Grassoline at the pump. *In* Scientific American, Vol 301, pp 52-59
18. **Isaacs R, Tuell JK, Fiedler A, Gardiner MA, Landis DA** (2009) Maximizing arthropod-mediated ecosystem services in agricultural landscapes: The role of native plants. Frontiers in Ecology and the Environment **7:** 196-203
19. **James LK, Swinton SM, Pennington D** (2009) Profitability of converting to biofuel crops. *In* Extension Bulletin, Vol E-3084. Michigan State University Extension, East Lansing, MI
20. **Jeffries TW, Van Vleet JR** (2009) *Pichia stipitis* genomics, transcriptomics, and gene clusters. FEMS Yeast Research **9:** 793-807
21. **Jha M, Babcock BA, Gassman PW, Kling CL** (2009) Economic and environmental impacts of alternative energy crops. International Agricultural Engineering Journal **18:** 15-23
22. **Jiang Y, Swinton SM** (2009) Market interactions, farmers' choices, and the sustainability of growing advanced biofuels: a missing perspective? International Journal of Sustainable Development & World Ecology **16:** 438 - 450
23. **Jiang Y, Swinton SM** (2009) Market interactions, farmer choices, and the sustainability of growing advanced biofuels. *In* Michigan State University, Department of Agricultural, Food, and Resource Economics. Michigan State University, East Lansing
24. **Kim H, Kim S, Dale BE** (2009) Biofuels, land use change, and greenhouse gas emissions: some unexplored variables. Environmental Science & Technology **43:** 961-967

25. **Kim S, Dale B** (2009) Regional variations in greenhouse gas emissions of biobased products in the United States—corn-based ethanol and soybean oil. The International Journal of Life Cycle Assessment **14:** 540-546
26. **Ko J-H, Kim W-C, Han K-H** (2009) Ectopic expression of MYB46 identifies transcriptional regulatory genes involved in secondary wall biosynthesis in Arabidopsis. The Plant Journal **60:** 649-665
27. **Kumar M, Thammannagowda S, Bulone V, Chiang V, Han K-H, Joshi CP, Mansfield SD, Mellerowicz E, Sundberg Br, Teeri T, Ellis BE** (2009) An update on the nomenclature for the cellulose synthase genes in *Populus*. Trends in Plant Science **14:** 248-254
28. **Kumar R, Mago G, Balan V, Wyman CE** (2009) Physical and chemical characterizations of corn stover and poplar solids resulting from leading pretreatment technologies. Bioresource Technology **100:** 3948-3962
29. **Kunkes EL, Gürbüz EI, Dumesic JA** (2009) Vapor-phase C-C coupling reactions of biomass-derived oxygenates over Pd/$CeZrO_x$ catalysts. Journal of Catalysis **266:** 236-249
30. **Landis DA** (2009) Sustainability of biofuels: Future research opportunities; Report from the October 2008 workshop, DOE/SC-0114. *In*,
31. **Laser M, Jin H, Jayawardhana K, Dale BE, Lynd LR** (2009) Projected mature technology scenarios for conversion of cellulosic biomass to ethanol with coproduction thermo-chemical fuels, power, and/or animal feed protein. Biofuels, Bioproducts and Biorefining **3:** 231-246
32. **Laser M, Larson E, Dale BE, Wang M, Greene N, Lynd LR** (2009) Comparative analysis of efficiency, environmental impact, and process economics for mature biomass refining scenarios. Biofuels, Bioproducts and Biorefining **3:** 247-270
33. **Lau M, Gunawan C, Dale B** (2009) The impacts of pretreatment on the fermentability of pretreated lignocellulosic biomass: a comparative evaluation between ammonia fiber expansion and dilute acid pretreatment. Biotechnology for Biofuels **2:** 30
34. **Lau MW, Dale BE** (2009) Cellulosic ethanol production from AFEX-treated corn stover using *Saccharomyces cerevisiae* 424A(LNH-ST). Proceedings of the National Academy of Sciences of the United States of America **106:** 1368-1373
35. **Liang C, Pedersen JA, Balser TC** (2009) Aminoglycoside antibiotics may interfere with microbial amino sugar analysis. Journal of Chromatography A **1216:** 5296-5301
36. **Lorenz AJ, Anex RP, Isci A, Coors JG, de Leon N, Weimer PJ** (2009) Forage quality and composition measurements as predictors of ethanol yield from maize (*Zea mays* L.) stover. Biotechnology for Biofuels **2:** 5
37. **Lorenz AJ, Coors JG, de Leon N, Wolfrum EJ, Hames BR, Sluiter AD, Weimer PJ** (2009) Characterization, genetic variation, and combining ability of maize traits relevant to the production of cellulosic ethanol. Crop Science **49:** 85-98
38. **Lynd LR, Larson E, Greene N, Laser M, Sheehan J, Dale BE, McLaughlin S, Wang M** (2009) The role of biomass in America's energy future: framing the analysis. Biofuels, Bioproducts and Biorefining **3:** 113-123
39. **Marner WD, 2nd** (2009) Practical application of synthetic biology principles. Biotechnology Journal **4:** 1406-1419
40. **Nagendran S, Hallen-Adams HE, Paper JM, Aslam N, Walton JD** (2009) Reduced genomic potential for secreted plant cell-wall-degrading enzymes in the ectomycorrhizal fungus *Amanita bisporigera*, based on the secretome of *Trichoderma reesei*. Fungal Genetics and Biology **46:** 427-435
41. **Ohlrogge J, Allen D, Berguson B, DellaPenna D, Shachar-Hill Y, Stymne S** (2009) Driving on biomass. Science **324:** 1019-1020
42. **Phillips GN** (2009) Describing protein conformational ensembles: beyond static snapshots. F1000 Biology Reports **1:** 38-41

43. **Pinto-Tomas AA, Anderson MA, Suen G, Stevenson DM, Chu FST, Cleland WW, Weimer PJ, Currie CR** (2009) Symbiotic nitrogen fixation in the fungus gardens of leaf-cutter ants. Science **326:** 1120-1123
44. **Ralph J, Schatz PF, Lu F, Kim H, Akiyama T, Nelsen SF** (2009) Quinone methides in lignification. *In* Quinone Methides. John Wiley & Sons, Inc., pp 385-420
45. **Román-Leshkov Y, Dumesic J** (2009) Solvent effects on fructose dehydration to 5-hydroxymethylfurfural in biphasic systems saturated with inorganic salts. Topics in Catalysis **52:** 297-303
46. **Searchinger TD, Hamburg SP, Melillo J, Chameides W, Havlik P, Kammen DM, Likens GE, Lubowski RN, Obersteiner M, Oppenheimer M, Robertson GP, Schlesinger WH, Tilman GD** (2009) Climate change. Fixing a critical climate accounting error. Science **326:** 527-528
47. **Sendich ED, Dale BE** (2009) Environmental and economic analysis of the fully integrated biorefinery. Global Change Biology – Bioenergy **1:** 331-345
48. **Song F, Zhao J, Swinton SM** (2009) Switching to perennial energy crops under uncertainty and costly reversibility (MSU Report). *In* Department of Agricultural, Food, and Resource Economics. Staff Paper No. 2009-14, Michigan State University
49. **Speers AM, Cologgi DL, Reguera G** (2009) Anaerobic cell culture. *In* Current Protoccols in Microbiology, Appendix 4F
50. **Stewart JJ, Akiyama T, Chapple C, Ralph J, Mansfield SD** (2009) The effects on lignin structure of overexpression of ferulate 5-hydroxylase in hybrid poplar. Plant Physiology **150:** 621-635
51. **Terashima N, Akiyama T, Ralph SA, Evtuguin D, Pascoal Neto C, Parkås J, Paulsson M, Westermark U, Ralph J** (2009) 2D-NMR (HSQC) difference spectra between specifically ^{13}C-enriched and unenriched protolignin of *Ginkgo biloba* obtained in the solution state of whole cell wall material. Holzforschung: International Journal of the Biology, Chemistry, Physics, and Technology of Wood **63:** 379-384
52. **Van Vleet JH, Jeffries TW** (2009) Yeast metabolic engineering for hemicellulosic ethanol production. Current Opinion in Biotechnology **20:** 300-306
53. **Wagner A, Donaldson L, Kim H, Phillips L, Flint H, Steward D, Torr K, Koch G, Schmitt U, Ralph J** (2009) Suppression of 4-coumarate-CoA ligase in the coniferous gymnosperm *Pinus radiata*. Plant Physiology **149:** 370-383
54. **Warrington DN, Mamedov AI, Bhardwaj AK, Levy GJ** (2009) Primary particle size distribution of eroded material affected by degree of aggregate slaking and seal development. European Journal of Soil Science **60:** 84-93
55. **Wise M, Calvin K, Thomson A, Clarke L, Bond-Lamberty B, Sands R, Smith SJ, Janetos A, Edmonds J** (2009) Implications of limiting CO_2 concentrations for land use and energy. Science **324:** 1183-1186
56. **Wolfrum EJ, Lorenz AJ, deLeon N** (2009) Correlating detergent fiber analysis and dietary fiber analysis data for corn stover collected by NIRS. Cellulose **16:** 577-585
57. **Yang Z, Ohlrogge JB** (2009) Turnover of fatty acids during natural senescence of Arabidopsis, *Brachypodium*, and switchgrass and in Arabidopsis β-oxidation mutants. Plant Physiology **150:** 1981-1989
58. **Yelle DJ, Jakes JE, Ralph J, Frihart CR** (2009) Characterizing polymeric methylene diphenyl diisocyanate reactions with wood: 1. High-resolution solution-state NMR spectroscopy. *In* Charles R. Frihart, Chiristopher G. Hunt, Robert J. Moon, eds, International Conference on Wood Adhesives. Forest Products Society, Lake Tahoe, Nevada, pp 338-342
59. **Zhang A, Lu F, Sun R, Ralph J** (2009) Ferulate-coniferyl alcohol cross-coupled products formed by radical coupling reactions. Planta **229:** 1099-1108
60. **Zhang M, Fan J, Taylor DC, Ohlrogge JB** (2009) *DGAT1* and *PDAT1* acyltransferases have overlapping functions in *Arabidopsis* triacylglycerol biosynthesis and are essential for normal pollen and seed development. The Plant Cell **21:** 3885-3901
61. **Zhang Y-HP, Berson E, Sarkanen S, Dale BE** (2009) Sessions 3 and 8: Pretreatment and biomass recalcitrance: fundamentals and progress. Applied Biochemistry and Biotechnology **153:** 80-83

62. **Zhong C, Lau MW, Balan V, Dale BE, Yuan Y-J** (2009) Optimization of enzymatic hydrolysis and ethanol fermentation from AFEX-treated rice straw. Applied Microbiology and Biotechnology **84:** 667-676

2010

1. **Alonso AP, Dale VL, Shachar-Hill Y** (2010) Understanding fatty acid synthesis in developing maize embryos using metabolic flux analysis. Metabolic Engineering **12:** 488-497
2. **Alonso AP, Piasecki RJ, Wang Y, LaClair RW, Shachar-Hill Y** (2010) Quantifying the labeling and the levels of plant cell wall precursors using ion chromatography tandem mass spectrometry. Plant Physiology **153:** 915-924
3. **Bals B, Rogers C, Jin M, Balan V, Dale BE** (2010) Evaluation of ammonia fiber expansion (AFEX) pretreatment for enzymatic hydrolysis of switchgrass harvested in different seasons and locations. Biotechnology for Biofuels **3:** 11
4. **Banerjee G, Car S, Scott-Craig J, Borrusch M, Walton J** (2010) Rapid optimization of enzyme mixtures for deconstruction of diverse pretreatment/biomass feedstock combinations. Biotechnology for Biofuels **3:** 22
5. **Banerjee G, Car S, Scott-Craig JS, Borrusch MS, Aslam N, Walton JD** (2010) Synthetic enzyme mixtures for biomass deconstruction: production and optimization of a core set. Biotechnology and Bioengineering **106:** 707-720
6. **Banerjee G, Car S, Scott-Craig JS, Borrusch MS, Bongers M, Walton JD** (2010) Synthetic multi-component enzyme mixtures for deconstruction of lignocellulosic biomass. Bioresource Technology **101:** 9097-9105
7. **Banerjee G, Scott-Craig JS, Walton JD** (2010) Improving enzymes for biomass conversion: a basic research perspective. BioEnergy Research **3:** 82-92
8. **Barua D, Kim J, Reed JL** (2010) An automated phenotype-driven approach (*Gene*Force) for refining metabolic and regulatory models. PLOS Computational Biology **6:** e1000970
9. **Binder JB, Blank JJ, Cefali AV, Raines RT** (2010) Synthesis of furfural from xylose and xylan. ChemSusChem **3:** 1268-1272
10. **Binder JB, Cefali AV, Blank JJ, Raines RT** (2010) Mechanistic insights on the conversion of sugars into 5-hydroxymethylfurfural. Energy and Environmental Science **3:** 765-771
11. **Binder JB, Raines RT** (2010) Fermentable sugars by chemical hydrolysis of biomass. Proceedings of the National Academy of Sciences of the United States of America **107:** 4516-4521
12. **Bond JQ, Alonso DM, Wang D, West RM, Dumesic JA** (2010) Integrated catalytic conversion of *γ*-valerolactone to liquid alkenes for transportation fuels. Science **327:** 1110-1114
13. **Casler MD** (2010) Changes in mean and genetic variance during two cycles of within-family selection in switchgrass. BioEnergy Research **3:** 47-54
14. **Casler MD** (2010) DOE Bioenergy Center Special Issue: The Great Lakes Bioenergy Research Center (GLBRC). BioEnergy Research **3:** 1-2
15. **Çetinkol ÖP, Dibble DC, Cheng G, Kent MS, Knierim B, Auer M, Wemmer DE, Pelton JG, Melnichenko YB, Ralph J, Simmons BA, Holmes BM** (2010) Understanding the impact of ionic liquid pretreatment on eucalyptus. Biofuels **1:** 33-46
16. **Chundawat SPS, Balan V, da Costa Sousa L, Dale BE** (2010) Thermochemical pretreatment of lignocellulosic biomass. *In* Jeith Waldron, ed, Bioalcohol Production-Biochemical Conversion of Lignocellulosic Biomass, Vol 3. Woodhead Publishing Ltd., (CRC Press), Cambridge, pp 24-72
17. **Chundawat SPS, Vismeh R, Sharma LN, Humpula JF, daCosta Sousa L, Chambliss CK, Jones AD, Balan V, Dale BE** (2010) Multifaceted characterization of cell wall decomposition products formed during ammonia fiber expansion (AFEX) and dilute-acid based pretreatments. Bioresource Technology **101:** 8429-8438

18. **da C. Jesus E, Susilawati E, Smith SL, Wang Q, Chai B, Farris R, Rodrigues JLM, Thelen KD, Tiedje JM** (2010) Bacterial communities in the rhizosphere of biofuel crops grown on marginal lands as evaluated by 16S rRNA gene pyrosequences. BioEnergy Research **3:** 20-27
19. **Dale BE, Bals BD, Kim S, Eranki P** (2010) Biofuels done right: land efficient animal feeds enable large environmental and energy benefits. Environmental Science & Technology **44:** 8385-8389
20. **Dale VH, Lowrance R, Mulholland P, Robertson GP** (2010) Bioenergy sustainability at the regional scale. Ecology and Society **15:** 23-28
21. **Davis J, Brandizzi F, Liepman A, Keegstra K** (2010) Arabidopsis mannan synthase CSLA9 and glucan synthase CSLC4 have opposite orientations in the Golgi membrane. The Plant Journal **64:** 1028-1037
22. **Durrett TP, McClosky DD, Tumaney AW, Elzinga DA, Ohlrogge J, Pollard M** (2010) A distinct DGAT with *sn*-3 acetyltransferase activity that synthesizes unusual, reduced-viscosity oils in *Euonymus* and transgenic seeds. Proceedings of the National Academy of Sciences of the United States of America **107:** 9464-9469
23. **Egbendewe-Mondzozo A, Swinton SM, Izaurralde RC, Manowitz DH, Zhang X** (2010) Biomass supply from alternative cellulosic crops and crop residues: a preliminary spatial bioeconomic modeling approach. *In* Department of Agricultural, Food, and Resource Economics. Staff Paper No. 2010-07. Michigan State University
24. **Fortenbery TR, Donohue TJ** (2010) Opportunities and challenges for next generation biofuels. *In* Jason Delborne, Daniel Lee Kleinman, Karen A. Cloud-Hansen, Jo Handelsman, eds, Controversies in Science and Technology: From Evolution to Energy, Vol 3: From Evolution to Energy. Mary Ann Liebert, Inc., pp 203-213
25. **Foster CE, Martin TM, Pauly M** (2010) Comprehensive compositional analysis of plant cell walls (lignocellulosic biomass) part I: Lignin. Journal of Visualized Experiments**:** e1745
26. **Foster CE, Martin TM, Pauly M** (2010) Comprehensive compositional analysis of plant cell walls (lignocellulosic biomass) part II: Carbohydrates. Journal of Visualized Experiments**:** e1837
27. **Gao D, Chundawat SPS, Krishnan C, Balan V, Dale BE** (2010) Mixture optimization of six core glycosyl hydrolases for maximizing saccharification of ammonia fiber expansion (AFEX) pretreated corn stover. Bioresource Technology **101:** 2770-2781
28. **Gao D, Chundawat SPS, Liu T, Hermanson S, Gowda K, Brumm P, Dale BE, Balan V** (2010) Strategy for identification of novel fungal and bacterial glycosyl hydrolase hybrid mixtures that can efficiently saccharify pretreated lignocellulosic biomass. BioEnergy Research **3:** 67-81
29. **Gardiner MA, Tuell JK, Isaacs R, Gibbs J, Ascher JS, Landis DA** (2010) Implications of three biofuel crops for beneficial arthropods in agricultural landscapes. BioEnergy Research **3:** 6-19
30. **Gardner JG, Keating DH** (2010) Requirement of the type II secretion system for utilization of cellulosic substrates by *Cellvibrio japonicus*. Applied and Environmental Microbiology **76:** 5079-5087
31. **Gelfand I, Snapp SS, Robertson GP** (2010) Energy efficiency of conventional, organic, and alternative cropping systems for food and fuel at a site in the U.S. Midwest. Environmental Science & Technology **44:** 4006-4011
32. **Gregg JS, Izaurralde RC** (2010) Effect of crop residue harvest on long-term crop yield, soil erosion and nutrient balance: trade-offs for a sustainable bioenergy feedstock. Biofuels **1:** 69-83
33. **Gürbüz EI, Kunkes EL, Dumesic JA** (2010) Dual-bed catalyst system for C–C coupling of biomass-derived oxygenated hydrocarbons to fuel-grade compounds. Green Chemistry **12:** 223-227
34. **Gürbüz EI, Kunkes EL, Dumesic JA** (2010) Integration of C-C coupling reactions of biomass-derived oxygenates to fuel-grade compounds. Applied Catalysis B: Environmental **94:** 134-141
35. **Hansey CN, Lorenz AJ, de Leon N** (2010) Erratum to: Cell wall composition and ruminant digestibility of various maize tissues across development. BioEnergy Research **3:** 28-37
36. **Hao X, Thelen KD, Gao J** (2010) Effects of soil and topographic properties on spatial variability of corn grain ethanol yield. Agronomy Journal **102:** 998-1006

37. **Hao X, Thelen KD, Gao J** (2010) Earlier-maturing hybrids improve corn grain profitability in the Northern Corn Belt. Crop Management **9:** 1
38. **Horvath G, Blaho M, Egri Á, Kriska G, Seres I, Robertson B** (2010) Reducing the maladaptive attractiveness of solar panels to polarotactic insects. Conservation Biology **24:** 1644-1653
39. **Jakubowski AR, Casler MD, Jackson RD** (2010) The benefits of harvesting wetland invaders for cellulosic biofuel: an ecosystem services perspective. Restoration Ecology **18:** 789-795
40. **James LK, Swinton SM, Thelen KD** (2010) Profitability analysis of cellulosic energy crops compared with corn. Agronomy Journal **102:** 675-687
41. **Jin M, Lau M, Balan V, Dale BE** (2010) Two-step SSCF to convert AFEX-treated switchgrass to ethanol using commercial enzymes and *Saccharomyces cerevisiae* 424A (LNH-ST). Bioresource Technology **101:** 8171-8178
42. **Kaufman AS, Meier PM, Sinistore JC, Reinemann DJ** (2010) Applying life-cycle assessment to low carbon fuel standards: How allocation choices influence carbon intensity for renewable transportation fuels. Energy Policy **38:** 5229-5241
43. **Keegstra K** (2010) Plant cell walls. Plant Physiology **154:** 483-486
44. **Kiley PJ, Donohue TJ** (2010) Global responses of bacteria to oxygen deprivation. *In* Gisela Storz, Regine Hengge, eds, Bacterial Stress Responses, Vol 2. ASM Press, pp 175-189
45. **Kim H, Ralph J** (2010) Solution-state 2D NMR of ball-milled plant cell wall gels in DMSO-d_6/pyridine-d_5. Organic & Biomolecular Chemistry **8:** 576-591
46. **Kim J, Reed J** (2010) OptORF: optimal metabolic and regulatory perturbations for metabolic engineering of microbial strains. BMC Systems Biology **4:** 53
47. **Krauskopf S** (2010) A life-cycle assessment of biofuels: tracing energy and carbon through a fuel-production system. The Science Teacher **77:** 35-40
48. **Krishnan C, da Costa Sousa L, Jin M, Chang L, Dale BE, Balan V** (2010) Alkali-based AFEX pretreatment for the conversion of sugarcane bagasse and cane leaf residues to ethanol. Biotechnology and Bioengineering **107:** 441-450.
49. **Landis DA, Werling BP** (2010) Arthropods and biofuel production systems in North America. Insect Science **17:** 1-17
50. **Lau M, Dale BE** (2010) Effect of primary degradation-reaction products from ammonia fiber expansion (AFEX)-treated corn stover on the growth and fermentation of *Escherichia coli* KO11. Bioresource Technology **101:** 7849-7855
51. **Lau MJ, Lau MW, Gunawan C, Dale BE** (2010) Ammonia fiber expansion (AFEX) pretreatment, enzymatic hydrolysis, and fermentation on empty palm fruit bunch fiber (EPFBF) for cellulosic ethanol production. Applied Biochemistry and Biotechnology **162:** 1847-1857
52. **Lau MW, Gunawan C, Balan V, Dale BE** (2010) Comparing the fermentation performance of *Escherichia coli* KO11, *Saccharomyces cerevisiae* 424A(LNH-ST) and *Zymomonas mobilis* AX101 for cellulosic ethanol production. Biotechnology for Biofuels **3:** 10
53. **Lennen RM, Braden DJ, West RM, Dumesic JA, Pfleger BF** (2010) A process for microbial hydrocarbon synthesis: overproduction of fatty acids in *Escherichia coli* and catalytic conversion to alkanes. Biotechnology and Bioengineering **106:** 193-202
54. **Lewis IA, Karsten RH, Norton ME, Tonelli M, Westler WM, Markley JL** (2010) NMR method for measuring carbon-13 isotopic enrichment of metabolites in complex solutions. Analytical Chemistry **82:** 4558-4563
55. **Lewis JA, Elkon IM, McGee MA, Higbee AJ, Gasch AP** (2010) Exploiting natural variation in *Saccharomyces cerevisiae* to identify genes for increased ethanol resistance. Genetics **186:** 1197-1205
56. **Li B-Z, Balan V, Yuan Y-J, Dale BE** (2010) Process optimization to convert forage and sweet sorghum bagasse to ethanol based on ammonia fiber expansion (AFEX) pretreatment. Bioresource Technology **101:** 1285-1292

57. **Liang C, Balser TC** (2010) Mass spectrometric characterization of amino sugar aldononitrile acetate derivatives used for isotope enrichment assessment of microbial residues. Soil Biology and Biochemistry **42:** 904-909
58. **Liang C, Cheng G, Wixon D, Balser T** (2010) An Absorbing Markov Chain approach to understanding the microbial role in soil carbon stabilization. Biogeochemistry **106:** 303-309
59. **Liko D, Conway MK, Grunwald DS, Heideman W** (2010) Stb3 plays a role in the glucose-induced transition from quiescence to growth in *Saccharomyces cerevisiae*. Genetics **185:** 797-810
60. **Lorenz AJ, Coors JG, Hansey CN, Kaeppler SM, de Leon N** (2010) Genetic analysis of cell wall traits relevant to cellulosic ethanol production in maize (*Zea mays* L.). Crop Science **50:** 842-852
61. **Lorenz AJ, Gustafson TJ, Coors JG, de Leon N** (2010) Breeding maize for a bioeconomy: a literature survey examining harvest index and stover yield and their relationship to grain yield. Crop Science **50:** 1-12
62. **Lu F, Marita JM, Lapierre C, Jouanin L, Morreel K, Boerjan W, Ralph J** (2010) Sequencing around 5-hydroxyconiferyl alcohol-derived units in caffeic acid *O*-methyltransferase-deficient poplar lignins. Plant Physiology **153:** 569-579
63. **Masukawa H, Inoue K, Sakurai H, Wolk CP, Hausinger RP** (2010) Site-directed mutagenesis of *Anabaena sp*. strain PCC 7120 nitrogenase active site to increase photobiological hydrogen production. Applied and Environmental Microbiology **76:** 6741-6750
64. **McSwiney C, Bohm S, Grace PR, Robertson GP** (2010) Greenhouse gas emissions calculator for grain and biofuel farming systems. Journal of Natural Resources and Life Sciences Education **39:** 125-131
65. **Meehan TD, Hurlbert AH, Gratton C** (2010) Bird communities in future bioenergy landscapes of the Upper Midwest. Proceedings of the National Academy of Sciences of the United States of America **107:** 18533-18538
66. **Morreel K, Dima O, Kim H, Lu F, Niculaes C, Vanholme R, Dauwe R, Goeminne G, Inzé D, Messens E, Ralph J, Boerjan W** (2010) Mass spectrometry-based sequencing of lignin oligomers. Plant Physiology **153:** 1464-1478
67. **Morreel K, Kim H, Lu F, Dima O, Akiyama T, Vanholme R, Niculaes C, Goeminne G, Inzé D, Messens E, Ralph J, Boerjan W** (2010) Mass spectrometry-based fragmentation as an identification tool in lignomics. Analytical Chemistry **82:** 8095-8105
68. **Pauly M, Keegstra K** (2010) Plant cell wall polymers as precursors for biofuels. Current Opinion in Plant Biology **13:** 305-312
69. **Ralph J** (2010) Hydroxycinnamates in lignification. Phytochemistry Reviews **9:** 65-83
70. **Ralph J, Landucci LL** (2010) NMR of lignins. *In* C. Heitner, D. R. Dimmel, John A. Schmidt, eds, Lignin and Lignans; Advances in Chemistry. CRC Press (Taylor & Francis Group), Boca Raton, FL, pp 137-234
71. **Rancour DM, Backues SK, Bednarek SY** (2010) Protein antigen expression in *Escherichia coli* for antibody production. *In* S.D Schwartzbach, T. Osafune, eds, Methods in Molecular Biology, Ed 2010/07/06 Vol 657, pp 3-20
72. **Santoro N, Cantu SL, Tornqvist C-E, Falbel TG, Bolivar JL, Patterson SE, Pauly M, Walton JD** (2010) A high-throughput platform for screening milligram quantities of plant biomass for lignocellulose digestibility. BioEnergy Research **3:** 93-102
73. **Schwartz CJ, Doyle MR, Manzaneda AJ, Rey PJ, Mitchell-Olds T, Amasino RM** (2010) Natural variation of flowering time and vernalization responsiveness in *Brachypodium distachyon*. BioEnergy Research **3:** 38-46
74. **Scott JJ, Budsberg KJ, Suen G, Wixon D, Balser TC, Currie CR** (2010) Microbial community structure of leaf-cutter ant fungus gardens and refuse dumps. PLOS ONE **5:** e9922
75. **Serrano-Ruiz JC, Braden DJ, West RM, Dumesic JA** (2010) Conversion of cellulose to hydrocarbon fuels by progressive removal of oxygen. Applied Catalysis B: Environmental **100:** 184-189

76. **Shao Q, Chundawat SPS, Krishnan C, Bals B, da Costa Sousa L, Thelen KD, Dale BE, Balan V** (2010) Enzymatic digestibility and ethanol fermentability of AFEX treated starch-rich lignocellulosics like corn silage and whole corn plant. Biotechnology for Biofuels **3:** 12
77. **Simmons BA, Loqué D, Ralph J** (2010) Advances in modifying lignin for enhanced biofuel production. Current Opinion in Plant Biology **13:** 313-320
78. **Slater S, Keegstra K, Donohue TJ** (2010) The US Department of Energy Great Lakes Bioenergy Research Center: Midwestern biomass as a resource for renewable fuels. BioEnergy Research **3:** 3-5
79. **Song F, Zhao J, Swinton SM** (2010) Alternative land use policies: real options with costly reversibility. *In* Agricultural & Applied Economics Association 2010 AAEA. Agricultural and Applied Economics Association, Denver, Colorado
80. **Srinivasan R, Zhang X, Arnold JG** (2010) SWAT ungauged: hydrological budget and crop yield predictions in the Upper Mississippi River Basin. Transactions of the ASABE **53:** 1533-1546
81. **Suen G, Aylward FO, Slater SC, Goldman BS** (2010) From genetics to genomics. *In* S. Maloy, K.T. Hughes, J. Casadesus, eds, The lure of bacterial genetics: a tribute to John Roth. American Society for Microbiology Press, Washington, D.C., pp 257-266
82. **Suen G, Scott JJ, Aylward FO, Adams SM, Tringe SG, Pinto-Tomás AA, Foster CE, Pauly M, Weimer PJ, Barry KW, Goodwin LA, Bouffard P, Li L, Osterberger J, Harkins TT, Slater SC, Donohue TJ, Currie CR** (2010) An insect herbivore microbiome with high plant biomass-degrading capacity. PLOS Genetics **6:** e1001129
83. **Thelen KD, Fronning BE, Kravchenko SA, Min D-H, Robertson GP** (2010) Integrating livestock manure with corn-soybean bioenergy cropping systems improves short-term carbon sequestration rates and net global warming potential. Biomass and Bioenergy **34:** 960-966
84. **van Parijs FRD, Morreel K, Ralph J, Boerjan W, Merks RMH** (2010) Modeling lignin polymerization. I. Simulation model of dehydrogenation polymers. Plant Physiology **153:** 1332-1344
85. **Vanholme R, Morreel K, Ralph J, Boerjan W** (2010) Lignin biosynthesis and structure. Plant Physiology **153:** 895-905
86. **Vanholme R, Ralph J, Akiyama T, Lu F, Rencoret Pazo J, Kim H, Christensen JH, Van Reusel B, Storme Vr, De Rycke R, Rohdel A, Morreel K, Boerjan W** (2010) Engineering traditional monolignols out of lignin by concomitant up-regulation of *F5H1* and down-regulation of *COMT* in Arabidopsis. The Plant Journal **64:** 885-897
87. **Vaughn LM, Baldwin KL, Jia G, Verdonk JC, Strohm AK, Masson PH** (2010) The cytoskeleton and root growth behavior. *In* Bo Liu, ed, The Plant Cytoskeleton. Advances in Plant Biology 2, Ed 1st Vol 1. Springer Verlag, pp 307-326
88. **Weng J-K, Akiyama T, Bonawitz ND, Li X, Ralph J, Chapple C** (2010) Convergent evolution of syringyl lignin biosynthesis via distinct pathways in the lycophyte *Selaginella* and flowering plants. The Plant Cell **22:** 1033-1045
89. **Werling BP, Meehan TD, Robertson B, Tuell JK** (2010) 2009 Landowner Report: Plants, birds, and insects in three potential biofuel crops. *In* GLBRC White Paper, pp 1-10
90. **Wymelenberg AV, Gaskell J, Mozuch M, Sabat G, Ralph J, Skyba O, Mansfield SD, Blanchette RA, Martinez D, Grigoriev I, Kersten PJ, Cullen D** (2010) Comparative transcriptome and secretome analysis of wood decay fungi *Postia placenta* and *Phanerochaete chrysosporium*. Applied and Environmental Microbiology **76:** 3599-3610
91. **Yilmaz LS, Kontur WS, Sanders AP, Sohmen U, Donohue TJ, Noguera DR** (2010) Electron partitioning during light- and nutrient-powered hydrogen production by *Rhodobacter sphaeroides*. BioEnergy Research **3:** 55-66
92. **Zhang A, Lu F, Liu C, Sun R-C** (2010) Isolation and characterization of lignins from *Eucalyptus tereticornis* (12ABL). Journal of Agriculture and Food Chemistry **58:** 11287-11293

93. **Zhang X, Izaurralde RC, Manowitz D, West TO, Post WM, Thomson AM, Bandaru VP, Nichols J, Williams JR** (2010) An integrative modeling framework to evaluate the productivity and sustainability of biofuel crop production systems. Global Change Biology – Bioenergy **2:** 258-277
94. **Zhang X, Srinivasan R** (2010) GIS-based spatial precipitation estimation using next generation radar and raingauge data. Environmental Modelling & Software **25:** 1781-1788

2011

1. **Adams AS, Jordan MS, Adams SM, Suen G, Goodwin LA, Davenport KW, Currie CR, Raffa KF** (2011) Cellulose-degrading bacteria associated with the invasive woodwasp *Sirex noctilio*. The International Society for Microbial Ecology Journal **5:** 1323-1331
2. **Alonso AP, Dale VL, Shachar-Hill Y** (2011) Central metabolic fluxes in the endosperm of developing maize seeds and their implications for metabolic engineering. Metabolic Engineering **13:** 96-107
3. **Alonso DM, Wettstein SG, Bond JQ, Root TW, Dumesic JA** (2011) Production of biofuels from cellulose and corn stover using alkylphenol solvents. ChemSusChem **4:** 1078-1081
4. **Azarpira A, Lu F, Ralph J** (2011) Reactions of dehydrodiferulates with ammonia. Organic & Biomolecular Chemistry **9:** 6779-6787
5. **Babcock BA, Marette S, Tréguer D** (2011) Opportunity for profitable investments in cellulosic biofuels. Energy Policy **39:** 714-719
6. **Balan V, Bals B, daCosta Sousa L, Garlock R, Dale BE** (2011) A short review on ammonia based lignocellulosic biomass pretreatment. *In* Blake Simmons, ed, Chemical and Biochemical Catalysis for Next Generation Biofuels. Royal Soceity of Chemistry, pp 89-114
7. **Bals B, Dale BE** (2011) Economic comparison of multiple techniques for recovering leaf protein in biomass processing. Biotechnology and Bioengineering **108:** 530-537
8. **Bals B, Wedding C, Balan V, Sendich E, Dale B** (2011) Evaluating the impact of ammonia fiber expansion (AFEX) pretreatment conditions on the cost of ethanol production. Bioresource Technology **102:** 1277-1283
9. **Banerjee G, Car S, Scott-Craig J, Hodge DB, Walton JD** (2011) Alkaline peroxide pretreatment of corn stover: effects of biomass, peroxide, and enzyme loading and composition on yields of glucose and xylose. Biotechnology for Biofuels **4:** 16
10. **Bellesia G, Chundawat SPS, Langan P, Dale BE, Gnanakaran S** (2011) Probing the early events associated with liquid ammonia pretreatment of native crystalline cellulose. The Journal of Physical Chemistry B **115:** 9782-9788
11. **Bhardwaj AK, Jasrotia P, Hamilton SK, Robertson GP** (2011) Ecological management of intensively cropped agro-ecosystems improves soil quality with sustained productivity. Agriculture, Ecosystems and Environment **140:** 419-429
12. **Bhardwaj AK, Zenone T, Jasrotia P, Robertson GP, Chen J, Hamilton SK** (2011) Water and energy footprints of bioenergy crop production on marginal lands. Global Change Biology – Bioenergy **3:** 208-222
13. **Bianchetti CM, Elsen NL, Fox BG, Phillips GN, Jr.** (2011) Structure of cellobiose phosphorylase from *Clostridium thermocellum* in complex with phosphate. Acta Crystallographica. Section F, Structural biology and crystallization communications **67:** 1345-1349
14. **Bourgis F, Kilaru A, Cao X, Ngando-Ebongue G-F, Drira N, Ohlrogge JB, Arondel V** (2011) Comparative transcriptome and metabolite analysis of oil palm and date palm mesocarp that differ dramatically in carbon partitioning. Proceedings of the National Academy of Sciences of the United States of America **108:** 12527-12532
15. **Braden DJ, Henao CA, Heltzel J, Maravelias CC, Dumesic JA** (2011) Production of liquid hydrocarbon fuels by catalytic conversion of biomass-derived levulinic acid. Green Chemistry **13:** 1755-1765

16. **Brown CT, Tiedje JM** (2011) Metagenomics: the paths forward. *In* Frans J. de Bruijn, ed, Handbook of Molecular Microbial Ecology II: Metagenomics in Different Habitats. Wiley-Blackwell, pp 581-588
17. **Brumm P, Hermanson S, Hochstein B, Boyum J, Hermersmann N, Gowda K, Mead D** (2011) Mining *Dictyoglomus turgidum* for enzymatically active carbohydrases. Applied Biochemistry and Biotechnology **163:** 205-214
18. **Brumm P, Mead D, Boyum J, Drinkwater C, Gowda K, Stevenson D, Weimer PJ** (2011) Functional annotation of *Fibrobacter succinogenes* S85 carbohydrate active enzymes. Applied Biochemistry and Biotechnology **163:** 649-657
19. **Brumm PJ, Hermanson S, Luedtke J, Mead DA** (2011) Identification, cloning and characterization of *Dictyoglomus turgidum* CelA, an endoglucanase with cellulase and mannanase activity. Journal of Life Sciences **5:** 488-496
20. **Caes BR, Binder JB, Blank JJ, Raines RT** (2011) Separable fluorous ionic liquids for the dissolution and saccharification of cellulose. Green Chemistry **13:** 2719-2722
21. **Caes BR, Raines RT** (2011) Conversion of fructose into 5-(hydroxymethyl)furfural in sulfolane. ChemSusChem **4:** 353-356
22. **Chapman KD, Ohlrogge JB** (2011) Compartmentation of triacylglycerol accumulation in plants. Journal of Biological Chemistry **287:** 2288-2294
23. **Chen J, Stefano G, Brandizzi F, Zheng H** (2011) *Arabidopsis* RHD3 mediates the generation of the tubular ER network and is required for Golgi distribution and motility in plant cells. Journal of Cell Science **124:** 2241-2252
24. **Chen X, Alonso AP, Allen DK, Reed JL, Shachar-Hill Y** (2011) Synergy between ^{13}C-metabolic flux analysis and flux balance analysis for understanding metabolic adaption to anaerobiosis in *E. coli*. Metabolic Engineering **13:** 38-48
25. **Chundawat SPS, Beckham GT, Himmel ME, Dale BE** (2011) Deconstruction of lignocellulosic biomass to fuels and chemicals. Annual Review of Chemical and Biomolecular Engineering **2:** 121-145
26. **Chundawat SPS, Bellesia G, Uppugundla N, da Costa Sousa L, Gao D, Cheh AM, Agarwal UP, Bianchetti CM, Phillips GN, Langan P, Balan V, Gnanakaran S, Dale BE** (2011) Restructuring the crystalline cellulose hydrogen bond network enhances its depolymerization rate. Journal of the American Chemical Society **133:** 11163-11174
27. **Chundawat SPS, Donohoe BS, da Costa Sousa L, Elder T, Agarwai UP, Lu F, Ralph J, Himmel M, Balan V, Dale BE** (2011) Multi-scale visualization and characterization of plant cell wall deconstruction during thermochemical pretreatment. Energy and Environmental Science **4:** 973-984
28. **Chundawat SPS, Lipton MS, Purvine SO, Uppugundla N, Gao D, Balan V, Dale BE** (2011) Proteomics-based compositional analysis of complex cellulase–hemicellulase mixtures. Journal of Proteome Research **10:** 4365-4372
29. **Chylla RA, Hu K, Ellinger JJ, Markley JL** (2011) Deconvolution of two-dimensional NMR spectra by fast maximum likelihood reconstruction: application to quantitative metabolomics. Analytical Chemistry **83:** 4871-4880
30. **Cole JR, Wang Q, Chai B, Tiedje JM** (2011) The Ribosomal Database Project: sequences and software for high-throughput rRNA analysis. *In* Frans J. de Bruijn, ed, Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches. Wiley-Blackwell, pp 313-324
31. **Cornish AJ, Gärtner K, Yang H, Peters JW, Hegg EL** (2011) Mechanism of proton transfer in [FeFe]-hydrogenase from *Clostridium pasteurianum*. The Journal of Biological Chemistry **286:** 38341-33847
32. **Davidson RM, Hansey CN, Gowda M, Childs KL, Lin H, Vailancourt B, Sekhon RS, de Leon N, Kaeppler SM, Jiang N, Buell CR** (2011) Utility of RNA sequencing for analysis of maize reproductive transcriptomes. The Plant Genome **4:** 191-203

33. **Donath MJ, 2nd, Dominguez MA, Withers ST, 3rd** (2011) Development of an automated platform for high-throughput P1-phage transduction of *Escherichia coli*. Journal of Laboratory Automation **16:** 141-147
34. **Donohue T** (2011) Great Lakes Bioenergy Research Center. Industrial Biotechnology **7:** 255-256
35. **Egbendewe-Mondzozo A, Swinton SM, Bals BD, Dale BE** (2011) Can dispersed biomass processing protect the environment and cover the bottom line for biofuel? (MSU Report). *In* Michigan State University Staff Paper 2011-15. Michigan State University
36. **Egbendewe-Mondzozo A, Swinton SM, Izaurralde RC, Manowitz DH, Zhang X** (2011) Biomass supply from alternative cellulosic crops and crop residues: a spatially explicit bioeconomic modeling approach. Biomass and Bioenergy **35:** 4636-4647
37. **Eranki P, Bals BD, Dale BE** (2011) Advanced regional biomass processing depots: a key to the logistical challenges of the cellulosic biofuel industry. Biofuels, Bioproducts and Biorefining **5:** 621-630
38. **Eranki PL, Dale BE** (2011) Comparative life cycle assessment of centralized and distributed biomass processing systems combined with mixed feedstock landscapes. Global Change Biology – Bioenergy **3:** 427-438
39. **Fisher AC, Haitjema CH, Guarino C, Celik E, Endicott CE, Reading CA, Merritt JH, Ptak AC, Zhang S, DeLisa MP** (2011) Production of secretory and extracellular N-linked glycoproteins in *Escherichia coli*. Applied and Environmental Microbiology **77:** 871-881
40. **Fletcher RJ, Robertson BA, Evans J, Doran PJ, Alavalapati JRR, Schemske DJ** (2011) Biodiversity conservation in the era of biofuels: risks and opportunities. Frontiers in Ecology and the Environment **9:** 161-168
41. **Gao D, Chundawat SPS, Uppugundla N, Balan V, Dale BE** (2011) Binding characteristics of *Trichoderma reesei* cellulases on untreated, ammonia fiber expansion (AFEX), and dilute-acid pretreated lignocellulosic biomass. Biotechnology and Bioengineering **108:** 1788-1800
42. **Gao D, Uppaguntala N, Chundawat SPS, Liu T, Hermanson S, Gowda K, Brumm P, Balan V, Dale BE** (2011) Hemicellulases and auxiliary enzymes for improved conversion of lignocellulosic biomass to monosaccharides. Biotechnology for Biofuels **4:** 5
43. **Gao J, Qian L, Thelen KD, Hao X, da Costa Sousa L, Balan V, Dale BE** (2011) Corn harvest strategies for combined starch and cellulosic bioprocessing to ethanol. Agronomy Journal **103:** 844-850
44. **Gardner JG, Zeitler LA, Wigstrom WJS, Engel KC, Keating DH** (2011) A high-throughput solid phase screening method for identification of lignocellulose-degrading bacteria from environmental isolates. Biotechnology Letters **34:** 81-89
45. **Garlock RJ, Wong YS, Balan V, Dale BE** (2011) AFEX pretreatment and enzymatic conversion of black locust (*Robinia pseudoacacia* L.) to soluble sugars. BioEnergy Research **5:** 306-318
46. **Gelfand I, Zenone T, Jasrotia P, Chen J, Hamilton SK, Robertson GP** (2011) Carbon debt of Conservation Reserve Program (CRP) grasslands converted to bioenergy production. Proceedings of the National Academy of Sciences of the United States of America **108:** 13864-13869
47. **Gille S, de Souza A, Xiong G, Benz M, Cheng K, Schultink A, Reca I-B, Pauly M** (2011) *O*-Acetylation of *Arabidopsis* hemicellulose xyloglucan requires AXY4 or AXY4L, proteins with a TBL and DUF231 domain. The Plant Cell **23:** 4041-4053
48. **Gonzales-Vigil E, Bianchetti CM, Phillips GN, Howe GA** (2011) Adaptive evolution of threonine deaminase in plant defense against insect herbivores. Proceedings of the National Academy of Sciences of the United States of America **108:** 5897-5902
49. **Grubbs KJ, Biedermann PHW, Suen G, Adams SM, Moeller JA, Klassen JL, Goodwin LA, Woyke T, Munk AC, Bruce D, Detter C, Tapia R, Han CS, Currie CR** (2011) Genome sequence of *Streptomyces griseus* strain (XyelbKG-1), an ambrosia beetle-associated actinomycete. Journal of Bacteriology **193:** 2890-2891
50. **Gürbüz EI, Alonso DM, Bond JQ, Dumesic JA** (2011) Reactive extraction of levulinate esters and conversion to γ-valerolactone for production of liquid fuels. ChemSusChem **4:** 357-361

51. **Gürbüz EI, Braden D, Dumesic JA** (2011) Aqueous phase catalytic processing in biomass valorization to H_2 and liquid fuels. *In* Paolo Fornasiero, Mauro Graziani, eds, Renewable Resources and Renewal Energy: A Global Challenge, Ed Second. CRC Press, Boca Raton, pp 37-66

52. **Hansey CN, de Leon N** (2011) Biomass yield and cell wall composition of corn with alternative morphologies planted at variable densities. Crop Science **51:** 1005-1015

53. **Hansey CN, Johnson JM, Kaeppler SM, de Leon N** (2011) Genetic diversity of a maize association population with restricted phenology. Crop Science **51:** 704-715

54. **Held MA, Be E, Zemelis S, Withers S, Wilkerson C, Brandizzi F** (2011) CGR3: a golgi-localized protein influencing homogalacturonan methylesterification. Molecular Plant **4:** 832-844

55. **Hoover SW, Marner WD, 2nd, Brownson AK, Lennen RM, Wittkopp TM, Yoshitani u, Zulkifly S, Graham LE, Chaston SD, McMahon KD, Pfleger BF** (2011) Bacterial production of free fatty acids from freshwater macroalgal cellulose. Applied Microbiology and Biotechnology **91:** 435-446

56. **Hu K, Ellinger JJ, Chylla RA, Markley JL** (2011) Measurement of absolute concentrations of individual compounds in metabolite mixtures by gradient-selective time-zero ^1H-^{13}C HSQC with two concentration references and fast maximum likelihood reconstruction analysis. Analytical Chemistry **83:** 9352-9360

57. **Hu K, Westler WM, Markley JL** (2011) Simultaneous quantification and identification of individual chemicals in metabolite mixtures by two-dimensional extrapolated time-zero ^1H-^{13}C HSQC ($HSQC_0$). Journal of the American Chemical Society **133:** 1662-1665

58. **Hu K, Westler WM, Markley JL** (2011) Two-dimensional concurrent HMQC-COSY as an approach for small molecule chemical shift assignment and compound identification. Journal of Biomolecular NMR **49:** 291-296

59. **Hulcr J, Adams AS, Raffa K, Hofstetter RW, Klepzig KD, Currie CR** (2011) Presence and diversity of *Streptomyces* in *Dendroctonus* and sympatric bark beetle galleries across North America. Microbial Ecology **61:** 759-768

60. **Hull S, Arntzen J, Bleser C, Crossley A, Jackson R, Lobner E, Paine L, Radloff G, Ribic C, Sample D, Vanderbrook J, Ventura S, Walling S, Widholm J, Williams C** (2011) Wisconsin sustainable planting and harvest guidelines for nonforest biomass. *In* Report to the Wisconsin Bioenergy Council, Madison, pp 1-88

61. **Humpula JF, Chundawat SPS, Vismeh R, Jones AD, Balan V, Dale BE** (2011) Rapid quantification of major reaction products formed during thermochemical pretreatment of lignocellulosic biomass using GC-MS. Journal of Chromatography B **879:** 1018-1022

62. **Imam S, Yilmaz S, Sohmen U, Gorzalski AS, Reed JL, Noguera DR, Donohue TJ** (2011) iRsp1095: a genome-scale reconstruction of the *Rhodobacter sphaeroides* metabolic network. BMC Systems Biology **5:** 116

63. **Iwai S, Chai B, da C. Jesus E, Penton CR, Lee TK, Cole JR, Tiedje JM** (2011) Gene-targeted-metagenomics (GT-metagenomics) to explore the extensive diversity of genes of interest in microbial communities. *In* Frans J. de Bruijn, ed, Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches. Wiley-Blackwell, pp 235-244

64. **Jakubowski AR, Casler MD, Jackson RD** (2011) Has selection for improved agronomic traits made reed canarygrass invasive? PLOS ONE **6:** e25757

65. **Jakubowski AR, Jackson RD, Johnson RC, Hu J, Casler MD** (2011) Genetic diversity and population structure of Eurasian populations of reed canarygrass: cytotypes, cultivars, and interspecific hybrids. Crop and Pasture Science **62:** 982-991

66. **Jensen JK, Kim H, Cocuron J-C, Orler R, Ralph J, Wilkerson CG** (2011) The DUF579 domain containing proteins IRX15 and IRX15-L affect xylan synthesis in Arabidopsis. The Plant Journal **66:** 387-400

67. **Jin M, Balan V, Gunawan C, Dale BE** (2011) Consolidated bioprocessing (CBP) performance of *Clostridium phytofermentans* on AFEX-treated corn stover for ethanol production. Biotechnology and Bioengineering **108:** 1290-1297

68. **Kallenbach C, Grandy AS** (2011) Controls over soil microbial biomass responses to carbon amendments in agricultural systems: a meta-analysis. Agriculture, Ecosystems, and Environment **144:** 241-252

69. **Kim J, Reed JL, Maravelias CT** (2011) Large-scale bi-level strain design approaches and mixed-integer programming solution techniques. PLOS ONE **6:** e24162

70. **Kim S, Dale BE** (2011) Indirect land use change for biofuels: testing predictions and improving analytical methodologies. Biomass and Bioenergy **35:** 3235-3240

71. **Klassen JL, Adams SM, Bramhacharya S, Giles SS, Goodwin LA, Woyke T, Currie CR** (2011) Draft genome sequence of *Streptomyces* sp. strain Wigar10, isolated from a surface-sterilized garlic bulb. Journal of Bacteriology **193:** 6999-7000

72. **Ko J-H, Kim H-T, Han K-H** (2011) Biotechnological improvement of lignocellulosic feedstock for enhanced biofuel productivity and processing. Plant Biotechnology Reports **5:** 1-7

73. **Ko J-H, Prassinos C, Keathley D, Han K-H** (2011) Novel aspects of transcriptional regulation in the winter survival and maintenance mechanism of poplar. Tree Physiology **31:** 208-255

74. **Kontur WS, Ziegelhoffer EC, Spero MS, Imam S, Noguera DR, Donohue TJ** (2011) Pathways involved in reductant distribution during photobiological H_2 production by *Rhodobacter sphaeroides*. Applied and Environmental Microbiology **77:** 7425-7429

75. **Kravchenko AN, Robertson GP** (2011) Whole-profile soil carbon stocks: the danger of assuming too much from analyses of too little. Soil Science Society of America Journal **75:** 235-240

76. **Lennen RM, Kruziki MA, Kumar K, Zinkel RA, Burnum KE, Lipton MS, Hoover SW, Ranatunga DR, Wittkopp TM, Marner WD, 2nd, Pfleger BF** (2011) Membrane stresses induced by overproduction of free fatty acids in *Escherichia coli*. Applied and Environmental Microbiology **77:** 8114-8128

77. **Levine UY, Teal TK, Robertson GP, Schmidt TM** (2011) Agriculture's impact on microbial diversity and associated fluxes of carbon dioxide and methane. The International Society for Microbial Ecology Journal **5:** 1683-1691

78. **Li C, Cheng G, Balan V, Kent MS, Ong M, Chundawat SPS, daCosta Sousa L, Melnichenko YB, Dale BE, Simmons BA, Singh S** (2011) Influence of physico-chemical changes on enzymatic digestibility of ionic liquid and AFEX pretreated corn stover. Bioresource Technology **102:** 6928-6936

79. **Li L-L, Taghavi S, McCorkle S, Zhang Y-B, Blewitt M, Brunecky R, Adney W, Himmel M, Brumm P, Drinkwater C, Mead D, Tringe S, van der Lelie D** (2011) Bioprospecting metagenomics of decaying wood: mining for new glycoside hydrolases. Biotechnology for Biofuels **4:** 23

80. **Liang C, Balser TC** (2011) Microbial production of recalcitrant organic matter in global soils: implications for productivity and climate policy. Nature Reviews Microbiology **9:** 75

81. **Liang C, Sanford GR, Jackson RD, Balser TC** (2011) Potential legacy effects of biofuel cropping systems on soil microbial communities in southern Wisconsin. Agricultural Sciences **2:** 131-137

82. **Liang C, Zhang X, Wei L, He H, Higbee AJ, Balser TC** (2011) Investigation of the molecular ion structure for aldononitrile acetate derivatized muramic acid. Journal of Microbiological Methods **86:** 224-230

83. **Liu J, Wolk CP** (2011) Mutations in genes *patA* and *patL* of *Anabaena* sp strain PCC 7120 result in similar phenotypes, and the proteins encoded by those genes may interact. Journal of Bacteriology **193:** 6070-6074

84. **Lu F, Ralph J** (2011) Solution-state NMR of lignocellulosic biomass. Journal of Biobased Materials and Bioenergy **5:** 169-180

85. **Malmstrom CM, Melcher U, Bosque-Pérez NA** (2011) The expanding field of plant virus ecology: historical foundations, knowledge gaps, and research directions. Virus Research **159:** 84-94

86. **Meehan TD, Werling BP, Landis DA, Gratton C** (2011) Agricultural landscape simplification and insecticide use in the Midwestern United States. Proceedings of the National Academy of Sciences of the United States of America **108:** 11500-11505

87. **Mendez-Perez D, Begemann MB, Pfleger BF** (2011) Modular synthase-encoding gene involved in α-olefin biosynthesis in *Synechococcus* sp. strain PCC 7002. Applied and Environmental Microbiology **77:** 4264-4267

88. **Miesel JR, Renz MJ, Doll JE, Jackson RD** (2011) Effectiveness of weed management methods in establishment of switchgrass and a native species mixture for biofuels in Wisconsin. Biomass and Bioenergy **36:** 121-131

89. **Miller DA, Suen G, Bruce D, Copeland A, Cheng J-F, Detter C, Goodwin LA, Han CS, Hauser LJ, Land ML, Lapidus A, Lucas S, Meincke L, Pitluck S, Tapia R, Teshima H, Woyke T, Fox BG, Angert ER, Currie CR** (2011) Complete genome sequence of the cellulose-degrading bacterium *Cellulosilyticum lentocellum*. Journal of Bacteriology **193:** 2357-2358

90. **Mukherjee A, Ané J-M** (2011) Plant hormones and initiation of legume nodulation and arbuscular mycorrhization. *In* J C. Polacco, C. D. Todd, eds, Ecological Aspects of Nitrogen Metabolism in Plants. Wiley Blackwell Press, Hoboken, NJ, pp 354-396

91. **Mukherjee A, Ané J-M** (2011) Germinating spore exudates from arbuscular mycorrhizal fungi: molecular and developmental responses in plants and their regulation by ethylene. Molecular Plant-Microbe Interactions **24:** 260-270

92. **Muñoz JD, Kravchenko A** (2011) Soil carbon mapping using on-the-go near infrared spectroscopy, topography and aerial photographs. Geoderma **166:** 102-110

93. **Nichols J, Kang S, Post WM, Wang D, Bandaru VP, Manowitz D, Zhang X, Izaurralde RC** (2011) HPC-EPIC for high resolution simulations of environmental and sustainability assessment. Computers and Electronics in Agriculture **79:** 112-115

94. **Ohlrogge JB, Chapman K** (2011) The seeds of green energy: Expanding the contribution of plant oils as biofuels. The Biochemist **33:** 34-38

95. **Parthasarathi R, Bellesia G, Chundawat SP, Dale BE, Langan P, Gnanakaran S** (2011) Insights into hydrogen bonding and stacking interactions in cellulose. Journal of Physical Chemistry A **115:** 14191-14202

96. **Peckham SD, Gower ST** (2011) Simulated long-term effects of harvest and biomass residue removal on soil carbon and nitrogen content and productivity for two Upper Great Lakes forest ecosystems. Global Change Biology – Bioenergy **3:** 135-147

97. **Rencoret J, Gutierrez A, Nieto L, Jimenez-Barbero J, Faulds CB, Kim H, Ralph J, Martinez AT, del Rio JC** (2011) Lignin composition and structure in young versus adult *Eucalyptus globulus* plants. Plant Physiology **155:** 667-682

98. **Riederer A, Takasuka TE, Makino S-i, Stevenson DM, Bukhman YV, Elsen NL, Fox BG** (2011) Global gene expression patterns in *Clostridium thermocellum* from microarray analysis of chemostat culture on cellulose or cellobiose. Applied and Environmental Microbiology **77:** 1243-1253

99. **Robertson BA, Doran PJ, Loomis ER, Robertson JR, Schemske DW** (2011) Avian use of perennial biomass feedstocks as post-breeding and migratory stopover habitat. PLOS ONE **6:** e16941

100. **Robertson BA, Doran PJ, Loomis LR, Robertson JR, Schemske DW** (2011) Perennial biomass feedstocks enhance avian diversity. Global Change Biology – Bioenergy **3:** 235-246

101. **Robertson GP, Hamilton SK, Del Grosso SJ, Parton WJ** (2011) The biogeochemistry of bioenergy landscapes: carbon, nitrogen, and water considerations. Ecological Applications **21:** 1055-1067

102. **Sanjaya, Durrett TP, Weise SE, Benning C** (2011) Increasing the energy density of vegetative tissues by diverting carbon from starch to oil biosynthesis in transgenic Arabidopsis. Plant Biotechnology Journal **9:** 874-883

103. **Schrotenboer AC, Allen MS, Malmstrom CM** (2011) Modification of native grasses for biofuel production may increase virus susceptibility. Global Change Biology – Bioenergy **3:** 360-374

104. **Scott-Craig JS, Borrusch M, Banerjee G, Harvey CM, Walton JD** (2011) Biochemical and molecular characterization of secreted α-xylosidase from *Aspergillus niger*. The Journal of Biological Chemistry **286:** 12848-42854

105. **Sekhon RS, Lin H, Childs KL, Hansey CN, Buell CR, de Leon N, Kaeppler SM** (2011) Genome-wide atlas of transcription during maize development. The Plant Journal **66:** 553-563

106. **Serrano-Ruiz JC, Dumesic JA** (2011) Catalytic routes for the conversion of biomass into liquid hydrocarbon transportation fuels. Energy & Environmental Science **4:** 83-99

107. **Song F, Zhao J, Swinton SM** (2011) Switching to perennial energy crops under uncertainty and costly reversibility. American Journal of Agricultural Economics **93:** 768-783

108. **Sørensen I, Pettolino FA, Bacic A, Ralph J, Lu F, O'Neill MA, Fei Z, Rose JK, Domozych DS, Willats WGT** (2011) The charophycean green algae provide insights into the early origins of plant cell walls. The Plant Journal **68:** 201-211

109. **Suen G, Scott JJ, Aylward FO, Currie CR** (2011) The microbiome of leaf-cutter ant fungus gardens. *In* F.J. de Bruin, ed, Handbook of Molecular Microbial Ecology, Vol 2. Wiley-Blackwell, Hoboken, N.J., pp 367-379

110. **Suen G, Stevenson DM, Bruce DC, Chertkov O, Copeland A, Cheng J-F, Detter C, Detter JC, Goodwin LA, Han CS, Hauser LJ, Ivanova NN, Kyrpides NC, Land ML, Lapidus A, Lucas S, Ovchinnikova G, Pitluck S, Tapia R, Woyke T, Boyum J, Mead D, Weimer PJ** (2011) Complete genome of the cellulolytic ruminal bacterium *Ruminococcus albus* 7. Journal of Bacteriology **193:** 5574-5575

111. **Suen G, Teiling C, Li L, Holt C, Abouheif E, Bornberg-Bauer E, Bouffard P, Caldera EJ, Cash E, Cavanaugh A, Denas O, Elhaik E, Favé M-J, Gadau J, Gibson JD, Graur D, Grubbs KJ, Hagen DE, Helmkampf M, Hu H, Johnson BR, Kim J, Marsh SE, Moeller JA, Muñoz-Torres MC, Murphy MC, Naughton MC, Nigam S, Overson R, Rajakumar R, Reese JT, Scott JJ, Smith CR, Tao S, Tsutsui ND, Viljakainen L, Wissler L, Yandell MD, Zimmer F, Harkins TT, Taylor J, Slater SC, Clifton SW, Warren WC, Elsik CG, Smith CD, Weinstock GM, Gerardo NM, Currie CR** (2011) The genome sequence of the leaf-cutter ant *Atta cephalotes* reveals insights into its obligate symbiotic lifestyle. PLOS Genetics **7:** e1002007

112. **Suen G, Weimer PJ, Stevenson DM, Aylward FO, Boyum J, Deneke J, Drinkwater C, Ivanova NN, Mikhailova N, Chertkov O, Goodwin LA, Currie CR, Mead D, Brumm PJ** (2011) The complete genome sequence of *Fibrobacter succinogenes* S85 reveals a cellulolytic and metabolic specialist. PLOS ONE **6:** e18814

113. **Swinton SM, Babcock BA, James LK, Bandaru V** (2011) Higher US crop prices trigger little area expansion so marginal land for biofuel crops is limited. Energy Policy **39:** 5254-5258

114. **Syswerda SP, Corbin AT, Mokma DL, Kravchenko AN, Robertson GP** (2011) Agricultural management and soil carbon storage in surface vs. deep layers. Soil Science Society of America Journal **75:** 92

115. **Tobimatsu Y, Davidson CL, Grabber JH, Ralph J** (2011) Fluorescence-tagged monolignols: synthesis, and application to studying in vitro lignification. Biomacromolecules **12:** 1752-1761

116. **Troncoso-Ponce M, Kilaru A, Cao X, Durrett T, Fan J, Jensen J, Thrower N, Pauly M, Wilkerson C, Ohlrogge J** (2011) Comparative deep transcriptional profiling of four developing oilseeds. The Plant Journal **68:** 1014-1027

117. **Van Acker R, Storme V, Goeminne G, Ivens B, Custers R, Aerts D, Soetaert W, Ralph J, Santoro N, Leple J-C, Pilate G, Boerjan W** (2011) Science, society and biosafety of a field trial with transgenic biofuel poplars. BMC Proceedings **5:** 123

118. **Varbanova M, Porter K, Lu F, Ralph J, Hammerschmidt R, Jones AD, Day B** (2011) Molecular and biochemical basis for stress-induced accumulation of free and bound *p*-coumaraldehyde in cucumber. Plant Physiology **157:** 1056-1066

119. **Wagner A, Tobimatsu Y, Phillips L, Flint H, Torr K, Donaldson L, Pears L, Ralph J** (2011) *CCoAOMT* suppression modifies lignin composition in *Pinus radiata*. The Plant Journal **67:** 119-129

120. **Walton J, Banerjee G, Car S** (2011) GENPLAT: an automated platform for biomass enzyme discovery and cocktail optimization. Journal of Visualized Experiments**:** e3314

121. **Weise SE, van Wijk KJ, Sharkey TD** (2011) The role of transitory starch in C$_3$, CAM, and C$_4$ metabolism and opportunities for engineering leaf starch accumulation. Journal of Experimental Botany **62:** 3109-3118

122. **Weng J-K, Akiyama T, Ralph J, Chapple C** (2011) Independent recruitment of an *O*-methyltransferase for syringyl lignin biosynthesis in *Selaginella moellendorffii*. The Plant Cell **23:** 2708-2724

123. **Werling BP, Meehan TD, Gratton C, Landis DA** (2011) Influence of habitat and landscape perenniality on insect natural enemies in three candidate biofuel crops. Biological Control **59:** 304-312

124. **Werling BP, Meehan TD, Robertson BA, Gratton C, Landis DA** (2011) Biocontrol potential varies with biofuel-crop plant community and landscape perenniality. Global Change Biology – Bioenergy **3:** 347-359

125. **Wohlbach DJ, Kuo A, Sato TK, Potts KM, Salamov AA, LaButti KM, Sun H, Clum A, Pangilinan JL, Lindquist EA, Lucas S, Lapidus A, Jin M, Gunawan C, Balan V, Dale BE, Jeffries TW, Zinkel R, Barry KW, Grigoriev IV, Gasch AP** (2011) Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. Proceedings of the National Academy of Sciences of the United States of America **108:** 13212-13217

126. **Wymelenberg AV, Gaskell J, Mozuch M, Splinter Bondurant S, Sabat G, Ralph J, Skyba O, Mansfield SD, Blanchette RA, Grigoriev IV, Kersten PJ, Cullen D** (2011) Significant alteration of gene expression in wood decay fungi *Postia placenta* and *Phanerochaete chrysosporium* by plant species. Applied and Environmental Microbiology **77:** 4499-4507

127. **Xia J, Jones AD, Lau MW, Yuan Y-J, Dale BE, Balan V** (2011) Comparative lipidomic profiling of xylose-metabolizing *S. cerevisiae* and its parental strain in different media reveals correlations between membrane lipids and fermentation capacity. Biotechnology and Bioengineering **108:** 12-21

128. **Xu C, Liang C, Wullschleger S, Wilson C, McDowell N** (2011) Importance of feedback loops between soil inorganic nitrogen and microbial communities in the heterotrophic soil respiration response to global warming. Nature Reviews Microbiology **9:** 222-222

129. **Yelle DJ, Ralph J, Frihart CR** (2011) Delineating pMDI-model reactions with loblolly pine via solution-state NMR spectroscopy. Part 1. Catalyzed reactions with wood models and wood polymers. Holzforschung: International Journal of the Biology, Chemistry, Physics, and Technology of Wood **65:** 131-143

130. **Yelle DJ, Ralph J, Frihart CR** (2011) Delineating pMDI-model reactions with loblolly pine via solution-state NMR spectroscopy. Part 2. Non-catalyzed reactions with the wood cell wall. Holzforschung: International Journal of the Biology, Chemistry, Physics, and Technology of Wood **65:** 145-154

131. **Yelle DJ, Wei D, Ralph J, Hammel KE** (2011) Multidimensional NMR analysis reveals truncated lignin structures in wood decayed by the brown rot basidiomycete *Postia placenta*. Environmental Microbiology **13:** 1091-1100

132. **Youngquist JT, Lennen RM, Ranatunga DR, Bothfeld WH, Marner II WD, Pfleger BF** (2011) Kinetic modeling of free fatty acid production in *Escherichia coli* based on continuous cultivation of a plasmid free strain. Biotechnology and Bioengineering **109:** 1518-1527

133. **Zalapa JE, Price DL, Kaeppler SM, Tobias CM, Okada M, Casler MD** (2011) Hierarchical classification of switchgrass genotypes using SSR and chloroplast sequences: ecotypes, ploidies, gene pools, and cultivars. Theoretical and Applied Genetics **122:** 805-817

134. **Zenone T, Chen J, Deal MW, Wilske B, Jasrotia P, Xu J, Bhardwaj AK, Hamilton SK, Philip Robertson G** (2011) CO$_2$ fluxes of transitional bioenergy crops: effect of land conversion during the first year of cultivation. Global Change Biology – Bioenergy **3:** 401-412

135. **Zhang X, Izaurralde RCs, Arnold JG, Sammons NB, Manowitz DH, Thomson AM, Williams JR** (2011) Comment on “Modeling miscanthus in the Soil and Water Assessment Tool (SWAT) to simulate its water quality effects as a bioenergy crop”. Environmental Science & Technology **45:** 6211-6212

136. **Zhang X, Liang F, Yu B, Zong Z** (2011) Explicitly integrating parameter, input and structure uncertainties into Bayesian Neural Networks for probabilistic hydrologic forecasting. Journal of Hydrology **409:** 696-709
137. **Zhang Y, Zalapa J, Jakubowski A, Price D, Acharya A, Wei Y, Brummer E, Kaeppler S, Casler M** (2011) Post-glacial evolution of *Panicum virgatum*: centers of diversity and gene pools revealed by SSR markers and cpDNA sequences. Genetica **139:** 933-948
138. **Zhang Y, Zalapa J, Jakubowski AR, Price DL, Acharya A, Wei Y, Brummer E, Kaeppler SM, Casler MD** (2011) Natural hybrids and gene flow between upland and lowland switchgrass. Crop Science **51:** 2626-2641
139. **Zhu X, Mitchell JC** (2011) KFC2: a knowledge-based hot spot prediction method based on interface solvation, atomic density, and plasticity features. Proteins **79:** 2671-2683
140. **Zhu Y, Ralph J** (2011) Stereoselective synthesis of 1-*O*-β-feruloyl and 1-*O*-β-sinapoyl glucopyranoses. Tetrahedron Letters **52:** 3729-3731

2012

1. **Agnew DE, Stevermer AK, Youngquist JT, Pfleger BF** (2012) Engineering *Escherichia coli* for production of C_{12}-C_{14} polyhydroxyalkanoate from glucose. Metabolic Engineering **14:** 705-713
2. **Allen DK, Laclair RW, Ohlrogge JB, Shachar-Hill Y** (2012) Isotope labelling of Rubisco subunits provides *in vivo* information on subcellular biosynthesis and exchange of amino acids between compartments. Plant, Cell & Environment **35:** 1232-1244
3. **Alonso DM, Wettstein SG, Dumesic JA** (2012) Bimetallic catalysts for upgrading of biomass to fuels and chemicals. Chemical Society Reviews **41:** 8075-8098
4. **Aylward FO, Burnum KE, Scott JJ, Suen G, Tringe SG, Adams SM, Barry KW, Nicora CD, Piehowski PD, Purvine SO, Starrett GJ, Goodwin LA, Smith RD, Lipton MS, Currie CR** (2012) Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. The International Society for Microbial Ecology Journal **6:** 1688-7101
5. **Aylward FO, Currie CR, Suen G** (2012) The evolutionary innovation of nutritional symbioses in leaf-cutter ants. Insects **3:** 41-61
6. **Azadi P, Carrasquillo-Flores R, Pagan-Torres YJ, Gurbuz EI, Farnood R, Dumesic JA** (2012) Catalytic conversion of biomass using solvents derived from lignin. Green Chemistry **14:** 1573-1576
7. **Backhaus J, Rothamer D** (2012) Design methodology for volatility characteristics of bio-derived drop-in gasoline fuels. *In* Spring Technical Meeting of the Central States Section of the Combustion Institute, Vol 1. Curran Associates, Inc., Dayton, Ohio, pp 222-234
8. **Balan V, da Costa Sousa L, Chundawat SPS, Humpula JF, Dale BE** (2012) Overview to ammonia pretreatments for lignocellulosic biorefineries. *In* Microbiology. Dynamic Biochemistry, Process Biotechnology and Molecular Biology, Vol 6 (Special Issue 2), pp 1-11
9. **Balan V, Kumar S, Bals B, Chundawat S, Jin M, Dale B** (2012) Biochemical and thermochemical conversion of switchgrass to biofuels. *In* Andrea Monti, ed, Switchgrass: A Valuable Biomass Crop for Energy, Ed 2012. Springer London, pp 153-185
10. **Bals B, Teymouri F, Campbell T, Jin M, Dale B** (2012) Low temperature and long residence time AFEX pretreatment of corn stover. BioEnergy Research **5:** 372-379
11. **Bals BD, Dale BE** (2012) Developing a model for assessing biomass processing technologies within a local biomass processing depot. Bioresource technology **106:** 161-169
12. **Banerjee G, Car S, Liu T, Williams DL, López Meza S, Walton JD, Hodge DB** (2012) Scale-up and integration of alkaline hydrogen peroxide pretreatment, enzymatic hydrolysis, and ethanolic fermentation. Biotechnology and Bioengineering **109:** 922-931

13. **Bellesia G, Chundawat SPS, Langan P, Redondo A, Dale BE, Gnanakaran S** (2012) Coarse-grained model for the interconversion between native and liquid ammonia-treated crystalline cellulose. The Journal of Physical Chemistry B **116:** 8031-8037
14. **Brennan M, McLean JP, Altaner CM, Ralph J, Harris PJ** (2012) Cellulose microfibril angles and cell-wall polymers in different wood types of *Pinus radiata*. Cellulose **19:** 1385-1404
15. **Broadbent JR, Neeno-Eckwall EC, Stahl B, Tandee K, Cai H, Morovic W, Horvath P, Heidenreich J, Perna NT, Barrangou R, Steele JL** (2012) Analysis of the *Lactobacillus casei* supragenome and its influence in species evolution and lifestyle adaptation. BMC Genomics **13:** 533
16. **Chen F, Tobimatsu Y, Havkin-Frenkel D, Dixon RA, Ralph J** (2012) A polymer of caffeyl alcohol in plant seeds. Proceedings of the National Academy of Sciences of the United States of America **109:** 1772-1777
17. **Chen X, Shachar-Hill Y** (2012) Insights into metabolic efficiency from flux analysis. Journal of Experimental Botany **63:** 2343-2351
18. **Chia J-M, Song C, Bradbury PJ, Costich D, de Leon N, Doebley J, Elshire RJ, Gaut B, Geller L, Glaubitz JC, Gore M, Guill KE, Holland J, Hufford MB, Lai J, Li M, Liu X, Lu Y, McCombie R, Nelson R, Poland J, Prasanna BM, Pyhajarvi T, Rong T, Sekhon RS, Sun Q, Tenaillon MI, Tian F, Wang J, Xu X, Zhang Z, Kaeppler SM, Ross-Ibarra J, McMullen MD, Buckler ES, Zhang G, Xu Y, Ware D** (2012) Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics **44:** 803-807
19. **Chundawat SPS, Chang L, Gunawan C, Balan V, McMahan C, Dale BE** (2012) Guayule as a feedstock for lignocellulosic biorefineries using ammonia fiber expansion (AFEX) pretreatment. Industrial Crops and Products **37:** 486–492
20. **Currie CR** (2012) The tangled banks of ants and microbes. *In* Maloy & Kolter, ed, Microbes and Evolution: The World That Darwin Never Saw. ASM Press, pp 181-190
21. **Dale BE, Ong RG** (2012) Energy, wealth, and human development: why and how biomass pretreatment research must improve. Biotechnology Progress **28:** 893-898
22. **del Río JC, Prinsen P, Rencoret J, Nieto L, Jiménez-Barbero J, Ralph J, Martínez ÁT, Gutiérrez A** (2012) Structural characterization of the lignin in the cortex and pith of elephant grass (*Pennisetum purpureum*) stems. Journal of Agricultural and Food Chemistry **60:** 3619-3634
23. **del Rio JC, Rencoret J, Prinsen P, Martínez ÁT, Ralph J, Gutiérrez A** (2012) Structural characterization of wheat straw lignin as revealed by analytical pyrolysis, 2D-NMR, and reductive cleavage methods. Journal of Agricultural and Food Chemistry **60:** 5922-5935
24. **Dufour YS, Donohue TJ** (2012) Signal correlations in ecological niches can shape the organization and evolution of bacterial gene regulatory networks. *In* Advances in Microbial Physiology, Vol 61, pp 1-36
25. **Egbendewe-Mondzozo A, Swinton SM, Izaurralde RC, Manowitz DH, Zhang X** (2012) Maintaining environmental quality while expanding energy biomass production: policy simulations from Michigan, USA. *In* International Association of Agricultural Economists (IAAE) Triennial Conference, Foz do Iguaçu, Brazil
26. **Ellinger JJ, Miller DC, Lewis IA, Markley JL** (2012) Semiautomated device for batch extraction of metabolites from tissue samples. Analytical Chemistry **84:** 1809-1812
27. **Elumalai S, Tobimatsu Y, Grabber JH, Pan X, Ralph J** (2012) Epigallocatechin gallate incorporation into lignin enhances the alkaline delignification and enzymatic saccharification of cell walls. Biotechnology for Biofuels **5:** 59
28. **Eudes A, George A, Mukerjee P, Kim JS, Pollet B, Benke PI, Yang F, Mitra P, Sun L, Cetinkol OP, Chabout S, Mouille G, Soubigou-Taconnat L, Balzergue S, Singh S, Holmes BM, Mukhopadhyay A, Keasling JD, Simmons BA, Lapierre C, Ralph J, Loque D** (2012) Biosynthesis and incorporation of side-chain-truncated lignin monomers to reduce lignin polymerization and enhance saccharification. Plant Biotechnology Journal **10:** 609-620

29. **Gardner JG, Keating DH** (2012) Genetic and functional genomic approaches for the study of plant cell wall degredation in *Celvibrio japonicus*. *In* Harry J. Gilbert, ed, Methods in Enzymology, Vol 510, pp 331-347
30. **Garlock RJ, Balan V, Dale BE** (2012) Optimization of AFEX™ pretreatment conditions and enzyme mixtures to maximize sugar release from upland and lowland switchgrass. Bioresoure Technology **104:** 757-768
31. **Garlock RJ, Bals B, Jasrotia P, Balan V, Dale BE** (2012) Influence of variable species composition on the saccharification of AFEX™ pretreated biomass from unmanaged fields in comparison to corn stover. Biomass and Bioenergy **37:** 49-59
32. **Gärtner K, Lechno-Yossef S, Cornish AJ, Wolk CP, Hegg EL** (2012) Expression of *Shewanella oneidensis* MR-1 [FeFe]-hydrogenase genes in *Anabaena* sp. strain PCC 7120. Applied and Environmental Microbiology **78:** 8579-8586
33. **Grieshop MJ, Werling BP, Buehrer K, Perrone J, Isaacs R, Landis DA** (2012) Big brother is watching: studying insect predation in the age of digital surveillance. American Entomologist **58:** 172-182
34. **Gunckel K, Mohan L, Covitt BA, Anderson CW** (2012) Addressing challenges in developing learning progressions for environmental science literacy. *In* A. Alonzo, A. Gotwals, eds, Learning progressions in science: Current challenges and future directions. Sense Publishers, Boston, pp 39-75
35. **Gürbüz EI, Wettstein SG, Dumesic JA** (2012) Conversion of hemicellulose to furfural and levulinic acid using biphasic reactors with alkylphenol solvents. ChemSusChem **5:** 383-387
36. **Haft R, Gardner J, Keating D** (2012) Quantitative colorimetric measurement of cellulose degradation under microbial culture conditions. Applied Microbiology and Biotechnology **94:** 223-229
37. **Hansey CN, Vaillancourt B, Sekhon RS, de Leon N, Kaeppler SM, Buell CR** (2012) Maize (*Zea mays* L.) genome diversity as revealed by RNA-sequencing. PLOS ONE **7:** e33071
38. **Hao X, Thelen KD, Gao J** (2012) Prediction of the ethanol yield of dry-grind maize grain using near infrared spectroscopy. Biosystems Engineering **112:** 161-170
39. **Harholt J, Jensen JK, Verhertbruggen Y, Sogaard C, Bernard S, Nafisi M, Poulsen CP, Geshi N, Sakuragi Y, Driouich A, Knox JP, Scheller HV** (2012) ARAD proteins associated with pectic Arabinan biosynthesis form complexes when transiently overexpressed in planta. Planta **236:** 115-128
40. **Hittinger CT** (2012) Endless rots most beautiful. Science **336:** 1649-1650
41. **Hoover SW, Youngquist JT, Angart PA, Withers ST, Lennen RM, Pfleger BF** (2012) Isolation of improved free fatty acid overproducing strains of *Escherichia coli* via Nile red based high-throughput screening. Environmental Progress & Sustainable Energy **31:** 17-23
42. **Howe AC, Pell J, Canino-Koning R, Mackelprang R, Tringe S, Jansson J, Tiedje JM, Brown CT** (2012) Illumina sequencing artifacts revealed by connectivity analysis of metagenomic datasets. arXiv **1212.0159**
43. **Hufford MB, Xu X, van Heerwaarden J, Pyhajarvi T, Chia J-M, Cartwright RA, Elshire RJ, Glaubitz JC, Guill KE, Kaeppler SM, Lai J, Morrell PL, Shannon LM, Song C, Springer NM, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Ware D, Buckler ES, Yang S, Ross-Ibarra J** (2012) Comparative population genomics of maize domestication and improvement. Nature Genetics **44:** 808-811
44. **Izaurralde RC, McGill WB, Williams JR** (2012) Development and application of the EPIC Model for carbon cycle, greenhouse gas mitigation, and biofuel studies. *In* M.A Liebig, A. J. Franzluebbers, R. F. Follett, eds, Managing Agricultural Greenhouse Gases: Coordinated Agricultural Research through GRACEnet to Address our Changing Climate. Academic Press, Amsterdam, pp 293-308
45. **Jensen JK, Schultink A, Keegstra K, Wilkerson CG, Pauly M** (2012) RNA-Seq analysis of developing nasturtium seeds (*Tropaeolum majus*): identification and characterization of an additional galactosyltransferase involved in xyloglucan biosynthesis. Molecular Plant **5:** 984-992

46. **Jin H, Anderson CW** (2012) Developing assessments for a learning progression on carbon-transforming processes in socio-ecological systems. *In* Alicia C. Alonzo, Amelia Wenk Gotwals, eds, Learning progressions in science: Current challenges and future directions. Sense Publishers, Rotterdam, pp 151-181
47. **Jin M, Balan V, Gunawan C, Dale BE** (2012) Quantitatively understanding reduced xylose fermentation performance in AFEX™ treated corn stover hydrolysate using *Saccharomyces cerevisiae* 424A (LNH-ST) and *Escherichia coli* KO11. Bioresource Technology **111:** 294–300
48. **Jin M, Gunawan C, Balan V, Dale BE** (2012) Consolidated bioprocessing (CBP) of AFEX™-pretreated corn stover for ethanol production using *Clostridium phytofermentans* at a high solids loading. Biotechnology and Bioengineering **109:** 1929-1936
49. **Jin M, Gunawan C, Balan V, Lau MW, Dale BE** (2012) Simultaneous saccharification and co-fermentation (SSCF) of AFEX™ pretreated corn stover for ethanol production using commercial enzymes and *Saccharomyces cerevisiae* 424A(LNH-ST). Bioresource Technology **110:** 587–594
50. **Jin M, Gunawan C, Uppugundla N, Balan V, Dale BE** (2012) A novel integrated biological process for cellulosic ethanol production featuring high ethanol productivity, enzyme recycling and yeast cells reuse. Energy & Environmental Science **5:** 7168-7175
51. **Kaeppler S** (2012) Heterosis: many genes, many mechanisms—end the search for an undiscovered unifying theory. ISRN Botany **2012:** Article ID 682824
52. **Kashefi K** (2012) Hyperthermophiles: metabolic diversity and biotechnological applications. *In* Roberto Paul Anitori, ed, Extremophiles: Microbiology and Biotechnology. Caister Academic Press, Oregon, U.S.A., pp 183-232
53. **Kaur H, Shaker K, Heinzel N, Ralph J, Galis I, Baldwin IT** (2012) Environmental stresses of field growth allow cinnamyl alcohol dehydrogenase-deficient *Nicotiana attenuata* plants to compensate for their structural deficiencies. Plant Physiology **159:** 1545-1570
54. **Kim J, Reed JL** (2012) RELATCH: relative optimality in metabolic networks explains robust metabolic and regulatory responses to perturbations. Genome Biology **13:** R78
55. **Kim S, Dale BE, Ong RG** (2012) An alternative approach to indirect land use change: allocating greenhouse gas effects among different uses of land. Biomass and Bioenergy **46:** 447-452
56. **Kim S-J, Brandizzi F** (2012) News and views into the SNARE complexity in *Arabidopsis*. Frontiers in Plant Science **3:** 28
57. **Kim W-C, Ko J-H, Han K-H** (2012) Identification of a *cis*-acting regulatory motif recognized by MYB46, a master transcriptional regulator of secondary wall biosynthesis. Plant Molecular Biology **78:** 489-501
58. **Ko J-H, Kim H-T, Hwang I, Han K-H** (2012) Tissue-type-specific transcriptome analysis identifies developing xylem-specific promoters in poplar. Plant Biotechnology Journal **10:** 587-596
59. **Ko J-H, Kim W-C, Kim J-Y, Ahn S-J, Han K-H** (2012) MYB46-mediated transcriptional regulation of secondary wall biosynthesis. Molecular Plant **5:** 961-963
60. **Kontur WS, Noguera DD, Donohue TJ** (2012) Maximizing reductant flow into microbial H_2 production. Current Opinion in Biotechnology **23:** 382-389
61. **Kontur WS, Shackwitz WS, Ivanova NN, Martin J, LaButti K, Deshpande S, Tice HN, Pennachio C, Sodergren E, Weinstock G, Noguera DR, Donohue TJ** (2012) Revised sequence and annotation of the *Rhodobacter sphaeroides* 2.4.1 genome. Journal of Bacteriology **194:** 7016-7017
62. **Kosma DK, Molina I, Ohlrogge JB, Pollard M** (2012) Identification of an Arabidopsis fatty alcohol: caffeoyl-coenzyme A acyltransferase required for the synthesis of alkyl hydroxycinnamates in root waxes. Plant Physiology **160:** 237-248
63. **Landis DA, Gardiner MM, Tompkins J** (2012) Using native plant species to diversify agriculture. *In* Geoff M. Gurr, Steve D. Wratten, William E. Snyder, Donna M. Y. Read, eds, Biodiversity and Insect Pests: Key Issues for Sustainable Management. John Wiley & Sons, Ltd, Chichester, U.K., pp 276-292

64. **Lau MW, Bals BD, Chundawat SPS, Jin M, Gunawan C, Balan V, Jones AD, Dale BE** (2012) An integrated paradigm for cellulosic biorefineries: utilization of lignocellulosic biomass as self-sufficient feedstocks for fuel, food precursors and saccharolytic enzyme production. Energy & Environmental Science **5:** 7100-7110
65. **Lennen RM, Pfleger BF** (2012) Engineering *Escherichia coli* to synthesize free fatty acids. Trends in Biotechnology **30:** 659-667
66. **Lewis JA, Gasch AP** (2012) Natural variation in the yeast glucose-signaling network reveals a new role for the Mig3p transcription factor. G3: Genes | Genomes | Genetics **2:** 1607-1612
67. **Li M, Foster CE, Pu Y, Holmes D, Saffron C, Ragauskas A, Hodge DB** (2012) Structural characterization of alkaline hydrogen peroxide pretreated grasses exhibiting diverse lignin phenotypes. Biotechnology for Biofuels **5:** 38
68. **Liang C, Duncan DS, Balser TC, Tiedje JM, Jackson RD** (2012) Soil microbial residue storage linked to soil legacy under biofuel cropping systems in southern Wisconsin, USA. Soil Biology and Biochemistry **57:** 939-942
69. **Liang C, Jesus EdC, Duncan DS, Jackson RD, Tiedje JM, Balser TC** (2012) Soil microbial communities under model biofuel cropping systems in southern Wisconsin, USA: impact of crop species and soil properties. Applied Soil Ecology **54:** 24-31
70. **Liang C, Read HW, Balser TC** (2012) GC-based detection of aldononitrile acetate derivatized glucosamine and muramic acid for microbial residue determination in soil. Journal of Visualized Experiments**:** e3767
71. **Liepman AH, Cavalier DM** (2012) The CELLULOSE SYNTHASE-LIKE A and CELLULOSE SYNTHASE-LIKE C families: recent advances and future perspectives. Frontiers in Plant Science **3:** 109
72. **Long TM, Su Y-KK, Headman J, Higbee A, Willis LB, Jeffries TW** (2012) Cofermentation of glucose, xylose, and cellobiose by the beetle-associated yeast, *Spathaspora passalidarum*. Applied and Environmental Microbiology **78:** 5492-54500
73. **Lu F, Wei L, Azarpira A, Ralph J** (2012) Rapid syntheses of dehydrodiferulates via biomimetic radical coupling reactions of ethyl ferulate. Journal of Agricultural and Food Chemistry **60:** 8272-8277
74. **Mansfield SD, Kim H, Lu F, Ralph J** (2012) Whole plant cell wall characterization using solution-state 2D NMR. Nature Protocols **7:** 1579-1589
75. **Masukawa H, Kitashima M, Inoue K, Sakurai H, Hausinger RP** (2012) Genetic engineering of cyanobacteria to enhance biohydrogen production from sunlight and water. Ambio **41:** 169-173
76. **Masukawa H, Mochimaru M, Takaichi S** (2012) Characterization of carotenogenesis genes in the cyanobacterium *Anabaena* sp. PCC 7120. *In* José-Luis Barredo, ed, Methods in Molecular Biology, Ed 2012/05/25 Vol 892. Humana Press, pp 297-306
77. **McLaughlin LS, Haft RJ, Forest KT** (2012) Structural insights into the Type II secretion nanomachine. Current Opinion in Structural Biology **22:** 208-216
78. **Mead D, Lucas S, Copeland A, Lapidus A, Cheng J-F, Bruce DC, Goodwin LA, Pitluck S, Chertkov O, Zhang X, Detter JC, Han CS, Tapia R, Land ML, Hauser LJ, Chang Y-j, Kyrpides NC, Ivanova NN, Ovchinnikova G, Woyke T, Brumm C, Hochstein R, Schoenfeld T, Brumm P** (2012) Complete genome sequence of *Paenibacillus* strain Y4.12MC10, a novel *Paenibacillus lautus* strained isolated from Obsidian Hot Spring in Yellowstone National Park. Standards in Genomic Science **6:** 366-385
79. **Meehan TD, Werling BP, Landis DA, Gratton C** (2012) Pest-suppression potential of Midwestern landscapes under contrasting bioenergy scenarios. PLOS ONE **7:** e41728
80. **Miao R, Hennessy DA, Babcock BA** (2012) Investment in cellulosic biofuel refineries: Do waivable biofuel mandates matter? American Journal of Agricultural Economics **9:** 750-762
81. **Mitchell JC, Rutkoski TJ, Bannen RM, Phillips GNJ** (2012) Combined computational and experimental approaches to sequence-based design of protein thermal stability. *In* Srikanta Sen, Lennart Nilsson, eds, Thermostable Proteins: Structural Stability and Design. CRC Press, pp 105-116

82. **Muttoni G, Johnson JM, Santoro N, Rhiner CJ, Haro von Mogel KJ, Kaeppler SM, de Leon N** (2012) A high-throughput core sampling device for the evaluation of maize stalk composition. Biotechnology for Biofuels **5:** 27
83. **Nadakuduti SS, Pollard M, Kosma DK, Allen C, Ohlrogge JB, Barry CS** (2012) Pleiotropic phenotypes of the sticky peel mutant provide new insight into the role of *CUTIN DEFICIENT2* in epidermal cell function in tomato. Plant Physiology **159:** 945-960
84. **Nikièma P, Rothstein DE, Miller RO** (2012) Initial greenhouse gas emissions and nitrogen leaching losses associated with converting pastureland to short-rotation woody bioenergy crops in northern Michigan, USA. Biomass and Bioenergy **39:** 413-426
85. **O'Neill BJ, Gurbuz EI, Dumesic JA** (2012) Reaction kinetics studies of the conversions of formic acid and butyl formate over carbon-supported palladium in the liquid phase. Journal of Catalysis **290:** 193-201
86. **Pell J, Hintze A, Canino-Koning R, Howe A, Tiedje JM, Brown CT** (2012) Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. Proceedings of the National Academy of Sciences of the United States of America **109:** 13272-13277
87. **Peters JM, Mooney RA, Grass JA, Jessen ED, Tran F, Landick R** (2012) Rho and NusG suppress pervasive antisense transcription in *Escherichia coli*. Genes and Development **26:** 2621-2633
88. **Poskar CH, Huege J, Krach C, Franke M, Shachar-Hill Y, Junker B** (2012) *iMS2Flux* - a high-throughput processing tool for stable isotope labeled mass spectrometric data used for metabolic flux analysis. BMC Bioinformatics **13:** 295
89. **Ralph J, Akiyama T, Coleman DC, Mansfield SD** (2012) Effects on lignin structure of coumarate 3-hydroxylase downregulation in Poplar. BioEnergy Research **5:** 1009-1019
90. **Ream TS, Woods DP, Amasino RM** (2012) The molecular basis of vernalization in different plant groups. *In* Cold Spring Harbor symposia on quantitative biology, Vol 77, pp 105-115
91. **Reed JL** (2012) Shrinking the metabolic solution space using experimental datasets. PLOS Computational Biology **8:** e1002662
92. **Robertson B, Porter C, Landis D, Schemske D** (2012) Agroenergy crops influence the diversity, biomass, and guild structure of terrestrial arthropod communities. BioEnergy Research **5:** 179-188
93. **Robertson BA, Rice RA, Sillet TS, Babcock BA, Landis DA, Ribic CA, Herkert JR, Fletcher RJ, Fontaine JJ, Schemske DJ** (2012) Are agrofuels a threat or opportunity for grassland birds in the United States? The Condor **114:** 679-688
94. **Rothamer DA, Jennings JH** (2012) Study of the knocking propensity of 2,5-dimethylfuran–gasoline and ethanol–gasoline blends. Fuel **98:** 203-212
95. **Ruiz-May E, Kim S-J, Brandizzi F, Rose JK** (2012) The secreted plant *N*-glycoproteome and associated secretory pathways. Frontiers in Plant Science **3:** 117
96. **Sanford GR, Posner JL, Jackson RD, Kucharik CJ, Hedtcke JL, Lin T-L** (2012) Soil carbon lost from Mollisols of the North Central U.S.A. with 20 years of agricultural best management practices. Agriculture, Ecosystems and Environment **162:** 68-76
97. **Schwalbach MS, Keating DH, Tremaine M, Marner WD, 2nd, Zhang YH, Bothfeld WH, Higbee AJ, Grass JA, Cotten C, Reed JL, da Costa Sousa L, Jin M, Balan V, Ellinger JJ, Dale B, Kiley PJ, Landick R** (2012) Complex physiology and compound stress responses during fermentation of alkali-pretreated corn stover hydrolysate by an *Escherichia coli* ethanologen. Applied and Environmental Microbiology **78:** 3442-3457
98. **Sekhon RS, Childs KL, Santoro N, Foster CE, Buell CR, de Leon N, Kaeppler SM** (2012) Transcriptional and metabolic analysis of senescence induced by preventing pollination in maize. Plant Physiology **159:** 1730-1744
99. **Sen M, Alonso DM, Wettstein SG, Gurbuz EI, Henao CA, Dumesic JA, Maravelias CT** (2012) A sulfuric acid management strategy for the production of liquid hydrocarbon fuels via catalytic conversion of biomass-derived levulinic acid. Energy and Environmental Science **5:** 9690-9697

100. **Sen M, Gurbuz EI, Wettstein SG, Alonso DM, Dumesic JA, Maravelias CT** (2012) Production of butene oligomers as transportation fuels using butene for esterification of levulinic acid from lignocellulosic biomass: process synthesis and technoeconomic evaluation. Green Chemistry **14:** 3289-3294
101. **Sen MS, Henao CA, Braden DJ, Dumesic JA, Maravelias CT** (2012) Catalytic conversion of lignocellulosic biomass to fuels: process development and technoeconomic evaluation. Chemical Engineering Science **67:** 57-67
102. **Sen SM, Binder JB, Raines RT, Maravelias CT** (2012) Conversion of biomass to sugars via ionic liquid hydrolysis: process synthesis and economic evaluation. Biofuels, Bioproducts and Biorefining **6:** 444-452
103. **Surendran Nair S, Kang S, Zhang X, Miguez FE, Izaurralde RC, Post WM, Dietze MC, Lynd LR, Wullschleger SD** (2012) Bioenergy crop models: descriptions, data requirements, and future challenges. Global Change Biology – Bioenergy **4:** 620-633
104. **Syswerda SP, Basso B, Hamilton SK, Tausig JB, Robertson GP** (2012) Long-term nitrate loss along an agricultural intensity gradient in the Upper Midwest USA. Agriculture, Ecosystems & Environment **149:** 10-19
105. **Thelen KD, Gao J, Hoben J, Qian L, Saffron C, Withers K** (2012) A spreadsheet-based model for teaching the agronomic, economic, and environmental aspects of bioenergy cropping systems. Computers and Electronics in Agriculture **85:** 157-163
106. **Tjellstrom H, Yang Z, Allen DK, Ohlrogge JB** (2012) Rapid kinetic labeling of Arabidopsis cell suspension cultures: implications for models of lipid export from plastids. Plant Physiology **158:** 601-611
107. **Tobimatsu Y, Elumalai S, Grabber JH, Davidson CL, Pan X, Ralph J** (2012) Hydroxycinnamate conjugates as potential monolignol replacements: in vitro lignification and cell wall studies with rosmarinic acid. ChemSusChem **5:** 676-686
108. **Tscharntke T, Tylianakis JM, Rand TA, Didham RK, Fahrig L, Batáry P, Bengtsson J, Clough Y, Crist TO, Dormann CF, Ewers RM, Fründ J, Holt RD, Holzschuh A, Klein AM, Kleijn D, Kremen C, Landis DA, Laurance W, Lindenmayer D, Scherber C, Sodhi N, Steffan-Dewenter I, Thies C, van der Putten WH, Westphal C** (2012) Landscape moderation of biodiversity patterns and processes - eight hypotheses. Biological Reviews **87:** 661-685
109. **Vanholme R, Morreel K, Darrah C, Oyarce P, Grabber JH, Ralph J, Boerjan W** (2012) Metabolic engineering of novel lignin in biomass crops. New Phytologist **196:** 978-1000
110. **Ventura S, Hull S, Jackson R, Radloff G, Sample D, Walling S, Williams C** (2012) Guidelines for sustainable planting and harvest of nonforest biomass in Wisconsin. Journal of Soil and Water Conservation **67:** 17A-20A
111. **Vieler A, Wu G, Tsai C-H, Bullard B, Cornish AJ, Harvey C, Reca I-B, Thornburg C, Achawanantakun R, Buehl CJ, Campbell MS, Cavalier D, Childs KL, Clark TJ, Deshpande R, Erickson E, Ferguson AA, Handee W, Kong Q, Li X, Liu B, Lundback S, Peng C, Roston R, Sanjaya, Simpson JP, TerBush A, Warakanont J, Zauner S, Farre EM, Hegg EL, Jiang N, Kuo M-H, Lu Y, Niyogi KK, Ohlrogge J, Osteryoung KW, Shachar-Hill Y, Sears BB, Takahashi H, Yandell M, Shui S-H, Benning C** (2012) Genome, functional gene annotation, and nuclear transformation of the heterokont oleaginous alga *Nannochloropsis oceanica* CCMP1779. PLOS Genetics **8:** e1003064
112. **Visser AA, Nobre TM, Currie CR, Aanen DK, Poulsen M** (2012) Exploring the potential for Actinobacteria as defensive symbionts in fungus-growing termites. Microbial Ecology **63:** 975-985
113. **Wagner A, Donaldson L, Ralph J** (2012) Lignification and lignin manipulations in conifers. *In* Lise Jouanin, Catherine Lapierre, eds, Advances in Botanical Research: Lignins, Vol 61. Academic Press, Burlington, pp 37-76
114. **Wang Y, Alonso A, Wilkerson C, Keegstra K** (2012) Deep EST profiling of developing fenugreek endosperm to investigate galactomannan biosynthesis and its regulation. Plant Molecular Biology **79:** 243-258

115. **Weise SE, Aung K, Jarou ZJ, Mehrshahi P, Li Z, Hardy AC, Carr DJ, Sharkey TD** (2012) Engineering starch accumulation by manipulation of phosphate metabolism of starch. Plant Biotechnology Journal **10:** 545-554
116. **Werling BP, Pennington D, Landis DA** (2012) Ecosystem services and bioenergy landscapes. *In* Extension Bulletin E-3164. Michigan State University
117. **Wettstein SG, Alonso DM, Gurbuz EI, Dumesic JA** (2012) A roadmap for conversion of lignocellulosic biomass to chemicals and fuels. Current Opinion in Chemical Engineering **1:** 218-224
118. **Wettstein SG, Alonso DM, Yuxuan C, Dumesic JA** (2012) Production of levulinic acid and gamma-valerolactone (GVL) from cellulose using GVL as a solvent in biphasic systems. Energy & Environmental Science **5:** 8199-8203
119. **Wettstein SG, Bond JQ, Alonso DM, Pham HN, Datye AK, Dumesic JA** (2012) RuSn bimetallic catalysts for selective hydrogenation of levulinic acid to γ-valerolactone. Applied Catalysis B: Environmental **117-118:** 321-329
120. **Withers S, Lu F, Kim H, Zhu Y, Ralph J, Wilkerson CG** (2012) Identification of grass-specific enzyme that acylates monolignols with *p*-coumarate. The Journal of Biological Chemistry **287:** 8347-8355
121. **Woltz JM, Werling BP, Landis DA** (2012) Natural enemies and insect outbreaks in agriculture: a landscape perspective. *In* D. K. Letourneau P. Barbosa, A. Agrawal, ed, Insect Outbreaks. John Wiley & Sons, Ltd, Chichester, U.K., pp 355-370
122. **Yue F, Lu F, Sun R, Ralph J** (2012) Synthesis and characterization of new 5-linked pinoresinol lignin models. Chemistry, A European Journal **18:** 16402-16410
123. **Yue F, Lu F, Sun R-C, Ralph J** (2012) Syntheses of lignin-derived thioacidolysis monomers and their uses as quantitation standards. Journal of Agriculture and Food Chemistry **60:** 922–928
124. **Zabotina OA, Avci U, Cavalier D, Pattathil S, Chou Y-H, Eberhard S, Danhof L, Keegstra K, Hahn MG** (2012) Mutations in multiple *XXT* genes of Arabidopsis reveal the complexity of xyloglucan biosynthesis. Plant Physiology **159:** 1367-1384
125. **Zhang K, Bhuiya M-W, Rencoret J, Pazo Y, Kim H, Ralph J, Liu C-J** (2012) An engineered monolignol 4-*O*-methyltransferase depresses lignin polymerization and confers novel metabolic capability in *Arabidopsis*. The Plant Cell **24:** 3122-3139
126. **Zhu Y, Mohammadi A, Ralph J** (2012) Facile synthesis of 4-hydroxycinnamaldehydes. BioEnergy Research **5:** 407-411

2013

1. **Adams AS, Aylward FO, Adams SM, Erbilgin N, Aukema B, Currie CR, Suen G, Raffa KF** (2013) Mountain pine beetles colonizing historical and naïve host trees are associated with a bacterial community highly enriched in genes contributing to terpene metabolism. Applied and Environmental Microbiology **79:** 3468-3475
2. **Agnew DE, Pfleger BF** (2013) Synthetic biology strategies for synthesizing polyhydroxyalkanoates from unrelated carbon sources. Chemical Engineering Science **103:** 58-67
3. **Alonso DM, Gallo JMR, Mellmer MA, Wettstein SG, Dumesic JA** (2013) Direct conversion of cellulose to levulinic acid and gamma-valerolactone using solid acid catalysts. Catalysis Science and Technology **3:** 927-931
4. **Alonso DM, Wettstein SG, Dumesic JA** (2013) Gamma-valerolactone, a sustainable platform molecule derived from lignocellulosic biomass. Green Chemistry **15:** 584
5. **Alonso DM, Wettstein SG, Mellmer MA, Gurbuz EI, Dumesic JA** (2013) Integrated conversion of hemicellulose and cellulose from lignocellulosic biomass. Energy and Environmental Science **6:** 76-80
6. **Asbjornsen H, Hernandez-Santana V, Liebman M, Bayala J, Chen J, Helmers M, Ong CK, Schulte LA** (2013) Targeting perennial vegetation in agricultural landscapes for enhancing ecosystem services. Renewable Agriculture and Food Systems **29:** 101-125

7. **Aylward FO, Burnum KE, Tringe SG, Teiling C, Tremmel DM, Moeller J, Scott JJ, Barry KW, Nicora CD, Piehowski PD, Malfatti SA, Purvine SO, Goodwin LA, Smith RD, Weinstock GM, Gerardo NM, Suen G, Lipton MS, Currie CR** (2013) *Leucoagaricus gongylophorus* produces diverse enzymes for the degradation of recalcitrant plant polymers in leaf-cutter ant fungus gardens. Applied and Environmental Microbiology **79:** 3770-3778
8. **Aylward FO, McDonald BR, Adams SM, Valenzuela A, Schmidt RA, Goodwin LA, Woyke T, Currie CR, Suen G, Poulsen M** (2013) Comparison of 26 sphingomonad genomes reveals diverse environmental adaptations and biodegradative capabilities. Applied and Environmental Microbiology **79:** 3724-3733
9. **Aylward FO, Tremmel DM, Bruce DC, Chain P, Chen A, Walston Davenport K, Detter C, Han CS, Han J, Huntemann M, Ivanova NN, Kyrpides NC, Markowitz V, Mavrommatis K, Nolan M, Pagani I, Pati A, Pitluck S, Szeto E, Wei C-L, Goodwin L, Woyke T, Currie CR** (2013) Complete genome of *Enterobacteriaceae* bacterium strain FGI 57, a strain associated with leaf-cutter ant fungus gardens. Genome Announcements **1:** e00238-00212
10. **Aylward FO, Tremmel DM, Starrett GJ, Bruce DC, Chain P, Chen A, Davenport KW, Detter C, Han CS, Han J, Huntemann M, Ivanova NN, Kyrpides NC, Markowitz V, Mavrommatis K, Nolan M, Pagani I, Pati A, Pitluck S, Teshima H, Deshpande S, Goodwin L, Woyke T, Currie CR** (2013) Complete genome of *Serratia* sp. strain FGI 94, a strain associated with leaf-cutter ant fungus gardens. Genome Announcements **1:** e00239-00212
11. **Balan V, Chiaramonti D, Kumar S** (2013) Review of US and EU initiatives towards development, demonstration and commercialization of lignocellulosic biofuels. Biofuels, Bioproducts and Biorefining **7:** 732-759
12. **Balan V, Jin M, Culbertson A, Uppugundla N** (2013) The saccharification step: *Trichoderma reesei* cellulase hyper producer strains. *In* Vincenza Faraco, ed, Lignocellulose Conversion: Enzymatic and Microbial Tools for Bioethanol Production. Springer, Heidelberg, pp 65-92
13. **Bals BD, Gunawan C, Moore J, Teymouri F, Dale BE** (2013) Enzymatic hydrolysis of pelletized AFEX™-treated corn stover at high solid loadings. Biotechnology and Bioengineering **111:** 264-271
14. **Bandaru V, Izaurralde RC, Manowitz D, Link R, Zhang X, Post WM** (2013) Soil carbon change and net energy associated with biofuel production on marginal lands: a regional modeling perspective. Journal of Environmental Quality **42:** 1802-1814
15. **Bates PD, Stymne S, Ohlrogge J** (2013) Biochemical pathways in seed oil synthesis. Current Opinion in Plant Biology **16:** 1-7
16. **Beissinger TM, Hirsch CN, Sekhon RS, Foerster JM, Johnson JM, Muttoni G, Vaillancourt B, Buell CR, Kaeppler SM, de Leon N** (2013) Marker density and read-depth for genotyping populations using genotyping-by-sequencing. Genetics **193:** 1073-1081
17. **Bianchetti CM, Brumm P, Smith RW, Dyer K, Hura GL, Rutkoski TJ, Phillips Jr GN** (2013) Structure, dynamics, and specificity of endoglucanase D from *Clostridium cellulovorans*. Journal of Molecular Biology **425:** 4267-4285
18. **Bianchetti CM, Harmann CH, Takasuka TE, Hura GL, Dyer K, Fox BG** (2013) Fusion of dioxygenase and lignin-binding domains in a novel secreted enzyme from cellulolytic *Streptomyces* sp. SirexAA-E. Journal of Biological Chemistry **288:** 18574-18587
19. **Brumm PJ** (2013) Bacterial genomes: what they teach us about cellulose degradation. Biofuels **4:** 669-681
20. **Caes BR, Palte MJ, Raines RT** (2013) Organocatalytic conversion of cellulose into a platform chemical. Chemical Science **4:** 196-199
21. **Caes BR, Van Oosbree TR, Lu F, Ralph J, Maravelias CT, Raines RT** (2013) Simulated moving bed chromatography: separation and recovery of sugars and ionic liquid from biomass hydrolysates. ChemSusChem **6:** 2083-2089

22. **Casler MD** (2013) Switchgrass breeding, genetics, and genomics. *In* Andrea Monti, ed, Switchgrass. Springer-Verlag, London, pp 29-52
23. **Chandrasekaran A, Deng K, Koh C-Y, Takasuka TE, Bergeman LF, Fox BG, Adams PD, Singh AK** (2013) A universal flow cytometry assay for screening carbohydrate-active enzymes using glycan microspheres. Chemical Communications **49:** 5441-5443
24. **Chen F, Tobimatsu Y, Jackson L, Ralph J, Dixon RA** (2013) Novel seed coat lignins in the Cactaceae: structure, distribution and implications for the evolution of lignin diversity. The Plant Journal **73:** 201-211
25. **Chen X, Alonso AP, Shachar-Hill Y** (2013) Dynamic metabolic flux analysis of plant cell wall synthesis. Metabolic Engineering **18:** 78-85
26. **Christopherson MR, Suen G** (2013) Nature's bioreactor: the rumen as a model for biofuel production. Biofuels **4:** 511-521
27. **Christopherson MR, Suen G, Bramhacharya S, Jewell KA, Aylward FO, Mead D, Brumm PJ** (2013) The genome sequences of *Cellulomonas fimi* and "*Cellvibrio gilvus*" reveal the cellulolytic strategies of two facultative anaerobes, transfer of "*Cellvibrio gilvus*" to the genus *Cellulomonas*, and proposal of *Cellulomonas gilvus* sp. nov. PLOS ONE **8:** e53954
28. **Chundawat SPS, Bals B, Campbell T, Sousa L, Gao D, Jin M, Eranki PL, Garlock R, Teymouri F, Balen V, Dale BE** (2013) Primer on ammonia fiber expansion pretreatment. *In* Charles E Wyman, ed, Aqueous Pretreatment of Plant Biomass for Biological and Chemical Conversion to Fuels and Chemicals, Ed First. John Wiley & Sons, Ltd., West Sussex, U.K., pp 173-204
29. **Chung D, Park D, Myers K, Grass J, Kiley P, Landick R, Keleş S** (2013) dPeak: High resolution identification of transcription factor binding sites from PET and SET ChIP-Seq data. PLOS Computational Biology **9:** e1003246
30. **Chylla R, Van Acker R, Kim H, Azarpira A, Mukerjee P, Markley JL, Storme V, Boerjan W, Ralph J** (2013) Plant cell wall profiling by fast maximum likelihood reconstruction (FMLR) and region-of-interest (ROI) segmentation of solution-state 2D ^{1}H–^{13}C NMR spectra. Biotechnology for Biofuels **6:** 1-14
31. **Cotten C, Reed JL** (2013) Mechanistic analysis of multi-omics datasets to generate kinetic parameters for constraint-based metabolic models. BMC Bioinformatics **14:** 32
32. **Cotten C, Reed JL** (2013) Constraint-based strain design using continuous modifications (CosMos) of flux bounds finds new strategies for metabolic engineering. Biotechnology Journal **8:** 595-604
33. **Culbertson A, Jin M, da Costa Sousa L, Dale BE, Balan V** (2013) In-house cellulase production from AFEX™ pretreated corn stover using *Trichoderma reesei* RUT C-30. RSC Advances **3:** 25960-25969
34. **de Leon N, Kaeppler SM, Lauer JG** (2013) Breeding maize for lignocellulosic biofuel production. *In* Malay Saha, Hem S. Bhandhari, Joseph C. Bouton, eds, Bioenergy Feedstocks: Breeding and Genetics. Wiley Blackwell, Malden, MA, pp 151-172
35. **Decanio MS, Landick R, Haft RJ** (2013) The non-pathogenic *Escherichia coli* strain W secretes SslE via the virulence-associated type II secretion system beta. BioMed Central Microbiology **13:** 130
36. **Donohue TJ** (2013) Interview with Professor Timothy Donohue. Biofuels **4:** 255-258
37. **Duran BEL, Kucharik CJ** (2013) Comparison of two chamber methods for measuring soil trace-gas fluxes in bioenergy cropping systems. Soil Science Society of America Journal **77:** 1601-1612
38. **Egbendewe-Mondzozo A, Swinton SM, Bals BD, Dale BE** (2013) Can dispersed biomass processing protect the environment and cover the bottom line for biofuel? Environmental Science & Technology **47:** 1695-1703
39. **Egbendewe-Mondzozo A, Swinton SM, Izaurralde RC, Manowitz DH, Zhang X** (2013) Maintaining environmental quality while expanding biomass production: sub-regional U.S. policy simulations. Energy Policy **58:** 518-531

40. **Eranki PL, Manowitz DH, Bals BD, Izaurralde RC, Kim S, Dale BE** (2013) The watershed-scale optimized and rearranged landscape design (WORLD) model and local biomass processing depots for sustainable biofuel production: integrated life cycle assessments. Biofuels, Bioproducts and Biorefining **7:** 537-550
41. **Fish JA, Chai B, Wang Q, Sun Y, Brown CT, Tiedje JM, Cole JR** (2013) FunGene: the functional gene pipeline and repository. Frontiers in Microbiology **4:** 291
42. **Gall DL, Ralph J, Donohue TJ, Noguera DR** (2013) Benzoyl coenzyme A pathway-mediated metabolism of *meta*-hydroxy-aromatic acids in *Rhodopseudomonas palustris*. Journal of Bacteriology **195:** 4112-4120
43. **Gallo JMR, Alonso DM, Mellmer MA, Yeap JH, Wong HC, Dumesic JA** (2013) Production of furfural from lignocellulosic biomass using Beta Zeolite and biomass-derived solvent. Topics in Catalysis **56:** 1775-1781
44. **Gao D, Chundawat SPS, Sethi A, Balan V, Gnanakaran S, Dale BE** (2013) Increased enzyme binding to substrate is not necessary for more efficient cellulose hydrolysis. Proceedings of the National Academy of Sciences of the United States of America **110:** 10922-10927
45. **Gao J, Thelen KD, Hao X** (2013) Life cycle analyses of corn harvest strategies for bioethanol production. Agronomy Journal **105:** 705-712
46. **Gelfand I, Sahajpal R, Zhang X, Izaurralde RC, Gross KL, Robertson GP** (2013) Sustainable bioenergy production from marginal lands in the US Midwest. Nature **493:** 514-517
47. **Gidda SK, Watt S, Collins-Silva J, Kilaru A, Arondel V, Yurchenko O, Horn PJ, James CN, Shintani D, Ohlrogge JB, Chapman KD, Mullen RT, Dyer JM** (2013) Lipid droplet-associated proteins (LDAPs) are involved in the compartmentalization of lipophilic compounds in plant cells. Plant Signaling & Behavior **8:** e27141
48. **Góngora-Castillo E, Buell CR** (2013) Bioinformatics challenges in *de novo* transcriptome assembly using short read sequences in the absence of a reference genome sequence. Natural Product Reports **30:** 490-500
49. **Gürbüz EI, Gallo JMR, Alonso DM, Wettstein SG, Lim WY, Dumesic JA** (2013) Conversion of hemicellulose into furfural using solid acid catalysts in γ-valerolactone. Angewandte Chemie (International Edition) **53:** 1270-1274
50. **Harun S, Balan V, Takriff MS, Hassan O, Jahim J, Dale BE** (2013) Performance of AFEX™ pretreated rice straw as source of fermentable sugars: the influence of particle size. Biotechnology for Biofuels **6:** 40
51. **Hirsch CN, Buell CR** (2013) Tapping the promise of genomics in species with complex, non-model genomes. Annual Review of Plant Biology **64:** 89-110
52. **Hoagland KC, Ruark MD, Renz MJ, Jackson RD** (2013) Agricultural management of switchgrass for fuel quality and thermal energy yield on highly erodible land in the Driftless Area of southwest Wisconsin. BioEnergy Research **6:** 1012-1021
53. **Horn PJ, James CN, Gidda SK, Kilaru A, Dyer JM, Mullen RT, Ohlrogge JB, Chapman KD** (2013) Identification of a new class of lipid droplet-associated proteins in plants. Plant Physiology **162:** 1926-1936
54. **Imam S, Noguera DR, Donohue TJ** (2013) Global insights into energetic and metabolic networks in *Rhodobacter sphaeroides*. BMC Systems Biology **7:** 1-17
55. **Jabbour D, Borrusch MS, Banerjee G, Walton JD** (2013) Enhancement of fermentable sugar yields by α-xylosidase supplementation of commercial cellulases. Biotechnology for Biofuels **6:** 58
56. **Jensen JK, Johnson N, Wilkerson CG** (2013) Discovery of diversity in xylan biosynthetic genes by transcriptional profiling of a heteroxylan containing mucilaginous tissue. Frontiers in Plant Science **4:** 183
57. **Jin M, Bothfeld W, Austin S, Sato TK, LaReau A, Li H, Foston M, Gunawan C, LeDuc RD, Quensen JF, McGee M, Nuppugundia N, Higbee A, Ranatunga R, Donald CW, Bone G, Raguskas AJ, Tiedje JM, Noguera DR, Dale BE, Zhang Y, Balan V** (2013) Effect of storage conditions on the stability and fermentability of enzymatic lignocellulosic hydrolysate. Bioresource Technology **147:** 212-220

58. **Jin M, Gunawan C, Balan V, Yu X, Dale BE** (2013) Continuous SSCF of AFEX™ pretreated corn stover for enhanced ethanol productivity using commercial enzymes and *Saccharomyces cerevisiae* 424A (LNH-ST). Biotechnology and Bioengineering **110:** 1302-1311
59. **Jin M, Sarks C, Gunawan C, Bice BD, Simonett SP, Narasimhan RA, Willis LB, Dale BE, Balan V, Sato TK** (2013) Phenotypic selection of a wild *Saccharomyces cerevisiae* strain for simultaneous saccharification and co-fermentation of AFEX™ pretreated corn stover. Biotechnology for Biofuels **6:** 108
60. **Jordan N, Schulte LA, Williams C, Pitt D, Slotterback CS, Jackson R, Landis D, Dale B, Becker D, Rickenbach M** (2013) Landlabs: an integrated approach to creating agricultural enterprises that meet the triple botom line. Journal of Higher Education Outreach and Engagement **17:** 175-200
61. **Kang S, Post WM, Nichols JA, Wang D, West TO, Bandaru V, Izaurralde RC** (2013) Marginal lands: concept, assessment and management. Journal of Agricultural Science **5:** 129-139
62. **Kang S, Post WM, Wang D, Nichols J, Bandaru VP** (2013) Hierarchical marginal land assessment for land use planning. Land Use Policy **30:** 106-113
63. **Keegstra K** (2013) Interview with Professor Kenneth Keegstra. Biofuels **4:** 147-150
64. **Kim J, Sen SM, Maravelias CT** (2013) An optimization-based assessment framework for biomass-to-fuel conversion strategies. Energy & Environmental Science **6:** 1093-1104
65. **Kim W-C, Kim J-Y, Ko J-H, Kim J, Han K-H** (2013) Transcription factor MYB46 is an obligate component of the transcriptional regulatory complex for functional expression of secondary wall-associated cellulose synthases in *Arabidopsis thaliana*. Journal of Plant Physiology **170:** 1374-1378
66. **Kim W-C, Ko J-H, Kim J-Y, Kim J-M, Bae H-J, Han K-H** (2013) MYB46 directly regulates the gene expression of secondary wall-associated cellulose synthases in Arabidopsis. The Plant Journal **73:** 26-36
67. **King JS, Ceulemans R, Albaugh JM, Dillen SY, Domec J-C, Fichot R, Fischer M, Leggett Z, Sucre E, Trnka M, Zenone T** (2013) The challenge of lignocellulosic bioenergy in a water-limited world. BioScience **63:** 102-117
68. **Klassen JL, Currie CR** (2013) ORFcor: identifying and accommodating ORF prediction inconsistencies for phylogenetic analysis. PLOS ONE **8:** e58387
69. **Kraatz S, Sinistore JC, Reinemann DJ** (2013) Energy intensity and global warming potential of corn grain ethanol production in Wisconsin (USA). Food and Energy Security **2:** 207-219
70. **Kucharik CJ, VanLoocke A, Lenters JD, Motew MM** (2013) Miscanthus establishment and overwintering in the Midwest USA: a regional modeling study of crop residue management on critical minimum soil temperatures. PLOS ONE **8:** e68847
71. **Lennen RM, Pfleger BF** (2013) Modulating membrane composition alters free fatty acid tolerance in *Escherichia coli*. PLOS ONE **8:** e54031
72. **Lennen RM, Pfleger BF** (2013) Microbial production of fatty acid-derived fuels and chemicals. Current Opinion in Biotechnology **24:** 1044-1053
73. **Lennen RM, Politz MG, Kruziki MA, Pfleger BF** (2013) Identification of transport proteins involved in free fatty acid efflux in *Escherichia coli*. Journal of Bacteriology **195:** 135-144
74. **Li Z, Chen CH, Hegg EL, Hodge DB** (2013) Rapid and effective oxidative pretreatment of woody biomass at mild reaction conditions and low oxidant loadings. Biotechnology for Biofuels **6:** 119
75. **Li Z, Chen CH, Liu T, Mathrubootham V, Hegg EL, Hodge DB** (2013) Catalysis with $\mathrm{Cu^{II}}$(bpy) improves alkaline hydrogen peroxide pretreatment. Biotechnology and Bioengineering **110:** 1078-1086
76. **Lu S, Li Q, Wei H, Chang M-J, Tunlaya-Anukit S, Kim H, Liu J, Song J, Sun Y-H, Yuan L, Yeh T-F, Peszlen I, Ralph J, Sederoff RR, Chiang VL** (2013) Ptr-miR39a is a negative regulator of laccase genes affecting lignin content in *Populus trichocarpa*. Proceedings of the National Academy of Sciences of the United States of America **110:** 10848-10853
77. **Ma W, Kong Q, Arondel V, Kilaru A, Bates PD, Thrower NA, Benning C, Ohlrogge J** (2013) *WRINKLED1*, a ubiquitous regulator in oil accumulating tissues from *Arabidopsis* embryos to oil palm mesocarp. PLOS ONE **8:** e68887

78. **Mead D, Drinkwater C, Brumm PJ** (2013) Genomic and enzymatic results show *Bacillus cellulosilyticus* uses a novel set of LPXTA carbohydrases to hydrolyze polysaccharides. PLOS ONE **8:** e61131
79. **Meehan TD, Glassberg J, Gratton C** (2013) Butterfly community structure and landscape composition in agricultural landscapes of the central United States. Journal of Insect Conservation **17:** 411-419
80. **Meehan TD, Gratton C, Diehl E, Hunt ND, Mooney DF, Ventura SJ, Barham BL, Jackson RD** (2013) Ecosystem-service tradeoffs associated with switching from annual to perennial energy crops in riparian zones of the US Midwest. PLOS ONE **8:** e80093
81. **Minty JJ, Singer ME, Scholz SA, Bae C-H, Ahn J-H, Foster CE, Liao JC, Lin XN** (2013) Design and characterization of synthetic fungal-bacterial consortia for direct production of isobutanol from cellulosic biomass. Proceedings of the National Academy of Sciences of the United States of America **110:** 14592-14597
82. **Muttoni G, Palacios-Rojas N, Galicia L, Rosales A, de Leon N** (2013) Cell wall composition and biomass digestibility diversity in Mexican maize (*Zea mays* L.) landraces and CIMMYT elite inbred lines. Maydica **58:** 21-33
83. **Myers KS, Yan H, Ong IM, Chung D, Liang K, Tran F, Keles S, Landick R, Kiley PJ** (2013) Genome-scale analysis of *Escherichia coli* FNR reveals complex features of transcription factor binding. PLOS Genetics **9:** e1003565
84. **Paper JM, Scott-Craig JS, Cavalier DM, Faik A, Wiemels RE, Borrusch MS, Bongers M, Walton JD** (2013) α-Fucosidases with different substrate specificities from two species of Fusarium. Applied Microbiology and Biotechnology **97:** 5371-5380
85. **Park DM, Akhtar MS, Ansari AZ, Landick R, Kiley PJ** (2013) The bacterial response regulator ArcA uses a diverse binding site architecture to regulate carbon oxidation globally. PLOS Genetics **9:** e1003839
86. **Park J-J, Lechno-Yossef S, Wolk CP, Vieille C** (2013) Cell-specific gene expression in *Anabaena variabilis* grown phototrophically, mixotrophically, and heterotrophically. BMC Genomics **14:** 759
87. **Peckham SD, Gower ST** (2013) Simulating the effects of harvest and biofuel production on the forest system carbon balance of the Midwest, USA. Global Change Biology – Bioenergy **5:** 431-444
88. **Penton CR, Johnson TA, Quensen III JF, Iwai S, Cole JR, Tiedje JM** (2013) Functional genes to assess nitrogen cycling and aromatic hydrocarbon degradation: primers and processing matter. Frontiers in Microbiology **4:** 279
89. **Politz MC, Copeland MF, Pfleger BF** (2013) Artificial repressors for controlling gene expression in bacteria. Chemical Communications **49:** 4325-4327
90. **Rahimi A, Azarpira A, Kim H, Ralph J, Stahl SS** (2013) Chemoselective metal-free aerobic alcohol oxidation in lignin. Journal of the American Chemical Society **135:** 6415-6418
91. **Ream T, Woods D, Schwartz C, Sanabria C, Mahoy J, Walters E, Kaeppler H, Amasino R** (2013) Interaction of photoperiod and vernalization determine flowering time of *Brachypodium distachyon*. Plant Physiology **164:** 694-709
92. **Rencoret J, Ralph J, Marques G, Gutierrez A, Martinez AT, del Rio JC** (2013) Structural characterization of lignin isolated from coconut (*Cocos nucifera*) coir fibers. Journal of Agriculture and Food Chemistry **61:** 2434-2445
93. **Ridley CE, Jager HI, Clark CM, Efroymson RA, Kwit C, Landis DA, Leggett ZH, Miller DA** (2013) Debate: Can bioenergy be produced in a sustainable manner that protects biodiversity and avoids the risk of invaders? Bulletin of the Ecological Society of America **94:** 277-290
94. **Robertson BA, Doran PJ** (2013) Biofuels and biodiversity: the implications of energy sprawl. *In* Simon A Levin, ed, Encyclopedia of Biodiversity, Ed 2nd. Waltham, San Diego, pp 528-539
95. **Robertson BA, Landis DA, Sillett TS, Loomis ER, Rice RA** (2013) Perennial agroenergy feedstocks as en route habitat for spring migratory birds. BioEnergy Research **6:** 311-320
96. **Robertson GP, Bruulsema TW, Gehl R, Kanter D, Mauzerall D, Rotz A, Williams C** (2013) Nitrogen-climate interactions in US agriculture. Biogeochemistry **114:** 41-70

97. **Rothamer DA, Donohue TJ** (2013) Chemistry and combustion of fit-for-purpose biofuels. Current Opinion in Chemical Biology **17:** 522-528

98. **Ruan L, Robertson GP** (2013) Initial nitrous oxide, carbon dioxide, and methane costs of converting conservation reserve program grassland to row crops under no-till vs. conventional tillage. Global Change Biology **19:** 2478-2489

99. **Sanford GR, Kucharik CJ** (2013) Effect of methodological consideration on soil carbon parameter estimates obtained via the acid hydrolysis-incubation method. Soil Biology and Biochemistry **67:** 295-305

100. **Sanjaya, Miller R, Durrett TP, Kosma DK, Lydic TA, Muthan B, Koo AJK, Bukhman YV, Reid GE, Howe GA, Ohlrogge J, Benning C** (2013) Altered lipid composition and enhanced nutritional value of *Arabidopsis* leaves following introduction of an algal diacylglycerol acyltransferase 2. The Plant Cell **25:** 677-693

101. **Sato TK, Liu T, Parreiras LS, Williams DL, Wohlbach DJ, Bice BD, Ong IS, Breuer RJ, Qin L, Busalacchi D, Deshpande S, Daum C, Gash AP, Hodge DB** (2013) Harnessing genetic diversity in *Saccharomyces cerevisiae* for fermentation of xylose in hydrolysates of alkaline hydrogen peroxide-pretreated biomass. Applied and Environmental Microbiology **80:** 540-554

102. **Schwartz C, Amasino R** (2013) Nitrogen recycling and flowering time in perennial bioenergy crops. Frontiers in Plant Science **4:** 76

103. **Sekhon RS, Briskine R, Hirsch CN, Myers CL, Springer NM, Buell CR, de Leon N, Kaeppler SM** (2013) Maize gene atlas developed by RNA sequencing and comparative evaluation of transcriptomes based on RNA sequencing and microarrays. PLOS ONE **8:** e61005

104. **Smith SL, Thelen KD, MacDonald SJ** (2013) Yield and quality analyses of bioenergy crops grown on a regulatory brownfield. Biomass and Bioenergy **49:** 1230-1130

105. **Takasuka TE, Book AJ, Lewin GR, Currie CR, Fox BG** (2013) Aerobic deconstruction of cellulosic biomass by an insect-associated *Streptomyces*. Scientific Reports **3:** 1030

106. **Tjellstrom H, Strawsine M, Silva J, Cahoon EB, Ohlrogge JB** (2013) Disruption of plastid acyl:acyl carrier protein synthetases increases medium chain fatty acid accumulation in seeds of transgenic Arabidopsis. FEBS Letters **587:** 936-942

107. **Tobimatsu Y, Chen F, Nakashima J, Escamilla-Treviño LL, Jackson L, Dixion RA, Ralph J** (2013) Coexistence but independent biosynthesis of catechyl and guaiacyl/syringyl lignins in plant seeds. The Plant Cell **25:** 2587-2600

108. **Tobimatsu Y, Wagner A, Donaldson L, Mitra P, Niculeas C, Dima O, Kim JI, Anderson N, Loque D, Boerjan W, Chapple C, Ralph J** (2013) Visualization of plant cell wall lignification using fluorescence-tagged monolignols. The Plant Journal **76:** 357-366

109. **Troncoso-Ponce MA, Cao X, Yang Z, Ohlrogge JB** (2013) Lipid turnover during senescence. Plant Science **205-206:** 13-19

110. **Vanholme B, Cesarino I, Geert G, Kim H, Marroni F, Van Acker R, Vanholme R, Morreel K, Ivens B, Pinosio S, Ralph J, Bastien C, Boerjan W** (2013) Breeding with rare defective alleles (BRDA): a natural *Populus nigra* HCT mutant with modified lignin as a case study. New Phytologist **198:** 765-776

111. **Vanholme R, Cesarino I, Rataj K, Xiao Y, Sundin L, Goeminne G, Kim H, Cross J, Morreel K, Araujo P, Welsh L, Haustraete J, McCellan C, Vanholme B, Ralph J, Simpson GG, Halpin C, Boerjan W** (2013) Caffeoyl shikimate esterase (CSE) is an enzyme in the lignin biosynthetic pathway in *Arabidopsis*. Science **341:** 1103-1106

112. **Vismeh R, Humpula JF, Chundawat SPS, Balan V, Dale BE, Jones AD** (2013) Profiling of soluble neutral oligosaccharides from treated biomass using solid phase extraction and LC-TOF MS. Carbohydrate Polymers **94:** 791-799

113. **Vismeh R, Lu F, Chundawat SPS, Humpula JF, Azarpira A, Balan V, Dale BE, Ralph J, Jones AD** (2013) Profiling of diferulates (plant cell wall cross-linkers) using ultrahigh-performance liquid chromatography-tandem mass spectrometry. Analyst **138:** 6683-6692

114. **Wagner A, Tobimatsu Y, Goeminne G, Phillips L, Flint H, Steward D, Torr K, Donaldson L, Boerjan W, Ralph J** (2013) Suppression of *CCR* impacts metabolite profile and cell wall composition in *Pinus radiata* tracheary elements. Plant and Molecular Biology **81:** 105-117

115. **Wang D, Hakim SH, Alonso DM, Dumesic JA** (2013) A highly selective route to linear alpha olefins from biomass-derived lactones and unsaturated acids. Chemical Communications **49:** 7040-7042

116. **Wang D, Osmundsen CM, Taarning E, Dumesic JA** (2013) Selective production of aromatics from alkylfurans over solid acid catalysts. ChemCatChem **5:** 2044-2050

117. **Wang Q, Quensen JF, Fish JA, Lee TK, Sun Y, Tiedje JM, Cole JR** (2013) Ecological patterns of *nifH* genes in four terrestrial climatic zones explored with targeted metagenomics using FrameBot, a new informatics tool. mBio **4:** e00592-00513

118. **Wang Y, Mortimer JC, Davis J, Dupree P, Keegstra K** (2013) Identification of an additional protein involved in mannan biosynthesis. The Plant Journal **73:** 105-117

119. **Williams CL, Charland P, Radloff G, Sample D, Jackson RD** (2013) Grass-shed: place and process for catalyzing perennial grass bioeconomies and their potential multiple benefits. Journal of Soil and Water Conservation **68:** 141A-146A

120. **Williams DL, Hodge DB** (2013) Impacts of delignification and hot water pretreatment on the water induced cell wall swelling behavior of grasses and its relation to cellulolytic enzyme hydrolysis and binding. Cellulose **21:** 221-235

121. **Yelle DJ, Kaparaju P, Hunt CG, Hirth K, Kim H, Ralph J, Felby C** (2013) Two-dimensional NMR evidence for cleavage of lignin and xylan substituents in wheat straw through hydrothermal pretreatment and enzymatic hydrolysis. BioEnergy Research **6:** 211-221

122. **Youngquist JT, Rose JP, Pfleger BF** (2013) Free fatty acid production in *Escherichia coli* under phosphate-limited conditions. Applied Microbiology and Biotechnology **97:** 5149-5159

123. **Youngquist JT, Schumacher MH, Rose JP, Raines TC, Politz MC, Copeland MF, Pfleger BF** (2013) Production of medium chain length fatty alcohols from glucose in *Escherichia coli*. Metabolic Engineering **20:** 177-186

124. **Zenone T, Gelfand I, Chen J, Hamilton SK, Robertson GP** (2013) From set-aside grassland to annual and perennial cellulosic biofuel crops: effects of land use change on carbon balance. Agricultural and Forest Meteorology **182-183:** 1-12

125. **Zhang X, Beeson P, Link R, Manowitz D, Izaurralde RC, Sadeghi A, Thomson AM, Sahajpal R, Srinivasan R, Arnold JG** (2013) Efficient multi-objective calibration of a computationally intensive hydrologic model with parallel computing software in Python. Environmental Modelling & Software **46:** 208-218

126. **Zhang X, Izaurralde RC, Arnold JG, Williams JR, Srinivasan R** (2013) Modifying the Soil and Water Assessment Tool to simulate cropland carbon flux: model development and initial evaluation. Science of the Total Environment **463-464:** 810-822

127. **Zhao Q, Tobimatsu Y, Zhou R, Pattathil S, Gallego-Giraldo L, Fu C, Jackson LA, Hahn MG, Kim H, Ralph J, Chen F, Dixon RA** (2013) Loss of function of cinnamyl alcohol dehydrogenase 1 leads to unconventional lignin and a temperature-sensitive growth defect in *Medicago truncatula*. Proceedings of the National Academy of Sciences of the United States of America **110:** 13660-13665

128. **Zhu Y, Regner M, Lu F, Kim H, Mohammadi A, Pearson TJ, Ralph J** (2013) Preparation of monolignol γ-acetate, γ-*p*-hydroxycinnamate, and γ-*p*-hydroxybenzoate conjugates: selective deacylation of phenolic acetates with hydrazine acetate. RSC Advances **3:** 21964-21971

2014

1. **Alexander HM, Mauck KE, Whitfield AE, Garrett KA, Malmstrom CM** (2014) Plant-virus interactions and the agro-ecological interface. European Journal of Plant Pathology **138:** 529-547
2. **Alexander WG, Doering DT, Hittinger CT** (2014) High-efficiency genome editing and allele replacement in prototrophic and wild strains of *Saccharomyces*. Genetics **198:** 859-866
3. **Almeida P, Goncalves C, Teixeira S, Libkind D, Bontrager M, Masneuf-Pomarede I, Albertin W, Durrens P, Sherman DJ, Marullo P, Todd Hittinger C, Goncalves P, Sampaio JP** (2014) A Gondwanan imprint on global diversity and domestication of wine and cider yeast *Saccharomyces uvarum*. Nature Communications **5:** 4044
4. **Aylward FO, Suen G, Biedermann PHW, Adams AS, Scott JJ, Malfatti SA, Glavina del Rio T, Tringe SG, Poulsen M, Raffa KF, Klepzig KD, Currie CR** (2014) Convergent bacterial microbiotas in the fungal agricultural systems of insects. mBio **5:** e02077-02014
5. **Azarpira A, Ralph J, Lu F** (2014) Catalytic alkaline oxidation of lignin and its model compounds: a pathway to aromatic biochemicals. BioEnergy Research **7:** 78-86
6. **Balan V** (2014) Current challenges in commercially producing biofuels from lignocellulosic biomass. ISRN Biotechnology **Volume 2014:** Article ID 463074
7. **Bates PD, Johnson SR, Cao X, Li J, Nam J-W, Jaworski JG, Ohlrogge JB, Browse J** (2014) Fatty acid synthesis is inhibited by inefficient utilization of unusual fatty acids for glycerolipid assembly. Proceedings of the National Academy of Sciences of the United States of America **111:** 1204-1209
8. **Beissinger TM, Hirsch CN, Vaillancourt B, Deshpande S, Barry K, Buell CR, Kaeppler SM, Gianola D, de Leon N** (2014) A genome-wide scan for evidence of selection in a maize population under long-term artificial selection for ear number. Genetics **196:** 829-840
9. **Bennett A, Isaacs R** (2014) Landscape composition influences pollinators and pollination services in perennial biofuel plantings. Agriculture, Ecosystems & Environment **193:** 1-8
10. **Bennett AB, Meehan TD, Gratton C, Isaacs R** (2014) Modeling pollinator community response to contrasting bioenergy scenarios. PLOS ONE **9:** e110676
11. **Bhalla A, Bischoff KM, Uppugundla N, Balan V, Sani RK** (2014) Novel thermostable endo-xylanase cloned and expressed from bacterium *Geobacillus* sp. WSUCF1. Bioresource Technology **165:** 314-318
12. **Bonawitz ND, Kim JI, Tobimatsu Y, Ciesielski PN, Anderson NA, Ximenes E, Maeda J, Ralph J, Donohoe BS, Ladisch M, Chapple C** (2014) Disruption of Mediator rescues the stunted growth of a lignin-deficient *Arabidopsis* mutant. Nature **509:** 376-380
13. **Book AJ, Lewin GR, McDonald BR, Takasuka TE, Doering DT, Adams AS, Blodgett JAV, Clardy J, Raffa KF, Fox BG, Currie CR** (2014) Cellulolytic *Streptomyces* strains associated with herbivorous insects share a phylogenetically linked capacity for the degradation of lignocellulose. Applied and Environmental Microbiology **80:** 4692-4701
14. **Book AJ, Yennamalli RM, Takasuka TE, Currie CR, Phillips GN, Fox BG** (2014) Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. Biotechnology for Biofuels **7:** 109
15. **Calvey CH, Willis LB, Jeffries TW** (2014) An optimized transformation protocol for *Lipomyces starkeyi*. Current Genetics **60:** 223-230
16. **Cao H, Walton JD, Brumm P, Phillips GN** (2014) Structure and substrate specificity of a eukaryotic fucosidase from *Fusarium graminearum*. Journal of Biological Chemistry **289:** 25624-25638
17. **Chen J, John R, Sun G, McNulty S, Normets A, Xiao J, Turner MG, Franklin JF** (2014) Chapter 6 - Carbon fluxes and storages in forests and landscapes. *In* J.C. Azevedo, A. Perera, M.A Pinto, eds, Forest Landscapes and Global Change: Challenges for Research and Management, Vol XIII. Springer, Newark, N.J., pp 139-166
18. **Chiaramonti D, Martelli F, Balan V, Kumar S** (2014) Industrial initiatives towards lignocellulosic biofuel deployment: an assessment in US and EU. Chemical Engineering Transactions **37:** 313-318

19. **Childs KL, Nandety A, Hirsch CN, Góngora-Castillo E, Schmutz J, Kaeppler SM, Casler MD, Buell CR** (2014) Generation of transcript assemblies and identification of single nucleotide polymorphisms from seven lowland and upland cultivars of switchgrass. The Plant Genome **7:** 1-13
20. **Cole JR, Tiedje JM** (2014) History and impact of RDP: a legacy from Carl Woese to microbiology. RNA Biology **11:** 239-243
21. **Cole JR, Wang Q, Fish JA, Chai B, McGarrell DM, Sun Y, Brown CT, Porras-Alfaro A, Kuske CR, Tiedje JM** (2014) Ribosomal Database Project: data and tools for high throughput rRNA analysis. Nucleic Acids Research **42:** D633-D642
22. **Collier SM, Ruark MD, Oates LG, Jokela WE, Dell CJ** (2014) Measurement of greenhouse gas flux from agricultural soils using static chambers. Journal of Visualized Experiments **90:** e52110
23. **Dale B** (2014) Sobering numbers. Resource Magazine **November/December 2014:** 25
24. **Dale BE, Anderson JE, Brown RC, Csonka S, Dale VH, Herwick G, Jackson RD, Jordan N, Kaffka S, Kline KL, Lynd LR, Malmstrom CM, Ong RG, Richard TL, Taylor C, Wang MQ** (2014) Take a closer look: biofuels can support environmental, economic and social goals. Environmental Science & Technology **48:** 7200–7203
25. **Dale BE, Kim S** (2014) Can the predictions of consequential life cycle assessment be tested in the real world? Comment on "Using Attributional Life Cycle Assessment to Estimate Climate-Change Mitigation...". Journal of Industrial Ecology **18:** 466-467
26. **Dale BE, Ong RG** (2014) Design, implementation, and evaluation of sustainable bioenergy production systems. Biofuels, Bioproducts and Biorefining **8:** 487-503
27. **Deal MW, Xu J, John R, Zenone T, Chen J, Jasrotia P, Kahmark K, Bossenbroek J, Mayer C** (2014) Net primary production in three bioenergy crop systems following land conversion. Journal of Plant Ecology **7:** 451-460
28. **Deng K, Takasuka TE, Heins R, Cheng X, Bergeman LF, Shi J, Aschenbrener R, Deutsch S, Singh S, Sale KL, Simmons BA, Adams PD, Singh AK, Fox BG, Northen TR** (2014) Rapid kinetic characterization of glycosyl hydrolases based on oxime derivatization and nanostructure-initiator mass spectrometry (NIMS). ACS Chemical Biology **9:** 1470-1479
29. **Diehl BG, Watts HD, Kubicki JD, Regner MR, Ralph J, Brown NR** (2014) Towards lignin-protein crosslinking: amino acid adducts of a lignin model quinone methide. Cellulose **21:** 1395-1407
30. **Evans J, Kim J, Childs KL, Vaillancourt B, Crisovan E, Nadety A, Gerhardt DJ, Richmond TA, Jeddeloh JA, Kaeppler SM, Casler MD, Buell CR** (2014) Nucleotide polymorphism and copy number variant detection using exome capture and next generation sequencing in the polyploidy grass *Panicum virgatum*. The Plant Journal **76:** 993-1008
31. **Gall DL, Kim H, Lu F, Donohue TJ, Noguera DR, Ralph J** (2014) Stereochemical features of glutathione-dependent enzymes in the *Sphingobium* sp. strain SYK-6 β-aryl etherase pathway. Journal of Biological Chemistry **289:** 8656-8667
32. **Gall DL, Ralph J, Donohue TJ, Noguera DR** (2014) A group of sequence-related sphingomonad enzymes catalyzes cleavage of β-aryl ether linkages in lignin β-guaiacyl and β-syringyl ether dimers. Environmental Science & Technology **48:** 12454-12463
33. **Gao D, Haarmeyer C, Balan V, Whitehead TA, Dale BE, Chundawat SPS** (2014) Lignin triggers irreversible cellulase loss during pretreated lignocellulosic biomass saccharification. Biotechnology for Biofuels **7:** 175
34. **Gao X, Kumar R, Singh S, Simmons B, Balan V, Dale B, Wyman CE** (2014) Comparison of enzymatic reactivity of corn stover solids prepared by dilute acid, AFEX™, and ionic liquid pretreatments. Biotechnology for Biofuels **7:** 71
35. **Gardner JG, Crouch L, Labourel A, Forsberg Z, Bukhman YV, Vaaje-Kolstad G, Gilbert HJ, Keating DH** (2014) Systems biology defines the biological significance of redox-active proteins during cellulose degradation in an aerobic bacterium. Molecular Microbiology **94:** 1121-1133

36. **Gaskell J, Marty A, Mozuch M, Kersten PJ, Splinter BonDurant S, Sabat G, Azarpira A, Ralph J, Skyba O, Mansfield SD, Blanchette RA, Cullen D** (2014) Influence of *Populus* genotype on gene expression by the wood decay fungus *Phanerochaete chrysosporium*. Applied and Environmental Microbiology **80:** 5828-5835

37. **Gilmanov TG, Baker JM, Bernacchi CJ, Billesbach DP, Burba GG, Castro S, Chen J, Eugster W, Fischer ML, Gamon JA, Gebremedhin MT, Glenn AJ, Griffis TJ, Hatfield JL, Heuer MW, Howard DM, Leclerc MY, Loescher HW, Marloie O, Meyers TP, Olioso A, Phillips RL, Prueger JH, Skinner RH, Suyker AE, Tenuta M, Wylie BK** (2014) Productivity and carbon dioxide exchange of leguminous crops: estimates from flux tower measurements. Agronomy Journal **106:** 545-559

38. **Green AR, Lewis KM, Barr JT, Jones JP, Lu F, Ralph J, Vermerris W, Sattler SE, Kang C** (2014) Determination of the structure and catalytic mechanism of *Sorghum bicolor* caffeic acid *O*-methyltransferase and the structural impact of three *brown midrib12* mutations. Plant Physiology **165:** 1440-1456

39. **Greenler J, Nye L, Tangen T** (2014) Cellulose breakdown. The Science Teacher **81:** 3-11

40. **Haft RJF, Keating DH, Schwaegler T, Schwalbach MS, Vinokur J, Tremaine M, Peters JM, Kotlajich MV, Pohlmann EL, Ong IM, Grass JA, Kiley PJ, Landick R** (2014) Correcting direct effects of ethanol on translation and transcription machinery confers ethanol tolerance in bacteria. Proceedings of the National Academy of Sciences of the United States of America **111:** E2576-E2585

41. **Haitjema CH, Boock JT, Natarajan A, Dominguez MA, Gardner JG, Keating DH, Withers ST, Delisa MP** (2014) Universal genetic assay for engineering extracellular protein expression. ACS Synthetic Biology **3:** 74-82

42. **Han J, Sen SM, Alonso DM, Dumesic JA, Maravelias CT** (2014) A strategy for the simultaneous catalytic conversion of hemicellulose and cellulose from lignocellulosic biomass to liquid transportation fuels. Green Chemistry **16:** 653-661

43. **He J, Pingali SV, Chundawat SPS, Pack A, Jones AD, Langan P, Davison BH, Urban V, Evans B, O'Neill H** (2014) Controlled incorporation of deuterium into bacterial cellulose. Cellulose **21:** 927-936

44. **Hedtcke JL, Sanford GR, Hadley KE, Thelen KD** (2014) Maximizing land use during switchgrass establishment in the North Central United States. Agronomy Journal **106:** 596-604

45. **Held MA, Danhof L, Brandizzi F** (2014) Identifying protein-protein interactions in *Arabidopsis* by co-immunoprecipitation of GFP-tagged proteins and proteomic detection. *In* Joseph A Rothnagel, ed, Fluorescent Proteins. Humana Press

46. **Herzberger AJ, Duncan DS, Jackson RD** (2014) Bouncing back: plant-associated soil microbes respond rapidly to prairie establishment. PLOS ONE **9:** e115775

47. **Hirsch CD, Evans J, Buell CR, Hirsch CN** (2014) Reduced representation approaches to interrogate genome diversity in large, repetitive plant genomes. Briefings in Functional Genomics **13:** 257-267

48. **Hirsch CN, Foerster JM, Johnson JM, Sekhon RS, Muttoni G, Vaillancourt B, Peñagaricano F, Lindquist E, Pedraza MA, Barry K, de Leon N, Kaeppler SM, Buell CR** (2014) Insights into the maize pan-genome and pan-transcriptome. The Plant Cell **26:** 121-135

49. **Howe AC, Jansson JK, Malfatti SA, Tringe SG, Tiedje JM, Brown CT** (2014) Tackling soil diversity with the assembly of large, complex metagenomes. Proceedings of the National Academy of Sciences of the United States of America **111:** 4904-4909

50. **Huang EL, Aylward FO, Kim Y-M, Webb-Robertson B-JM, Nicora CD, Hu Z, Metz TO, Lipton MS, Smith RD, Currie CR, Burnum-Johnson KE** (2014) The fungus gardens of leaf-cutter ants undergo a distinct physiological transition during biomass degradation. Environmental Microbiology Reports **6:** 389-395

51. **Humpula JF, Uppugundla N, Vismeh R, Sousa L, Chundawat SPS, Jones AD, Balan V, Dale BE, Cheh AM** (2014) Probing the nature of AFEX-pretreated corn stover derived decomposition products that inhibit cellulase activity. Bioresource Technology **152:** 38-45

52. **Imam S, Fitzgerald CM, Cook EM, Donohue TJ, Noguera DR** (2014) Quantifying the effects of light intensity on bioproduction and maintenance energy during photosynthetic growth of *Rhodobacter sphaeroides*. Photosynthesis Research **123:** 167-182
53. **Imam S, Noguera DR, Donohue TJ** (2014) Global analysis of photosynthesis transcriptional regulatory networks. PLOS Genetics **10:** e1004837
54. **Jabbour D, Angelos ER, Mukhopadhyay A, Womboldt A, Borrusch MS, Walton JD** (2014) Factors contributing to recalcitrance of herbaceous dicotyledons (forbs) to enzymatic deconstruction. Biotechnology for Biofuels **7:** 52
55. **Jensen JK, Johnson NR, Wilkerson CG** (2014) *Arabidopsis thaliana* IRX10 and two related proteins from psyllium and *Physcomitrella patens* are xylan xylosyltransferases. The Plant Journal **80:** 207-215
56. **Karkehabadi S, Helmich KE, Kaper T, Hansson H, Mikkelsen NE, Gudmundsson M, Piens K, Fujdala M, Banerjee G, Scott-Craig JS, Walton JD, Phillips GN, Sandgren M** (2014) Biochemical characterization and crystal structures of a fungal family 3 β-glucosidase, Cel3A from *Hypocrea jecorina*. Journal of Biological Chemistry **289:** 31624-31637
57. **Keating DH, Zhang Y, Ong IM, McIlwain S, Morales EH, Grass JA, Tremaine M, Bothfeld W, Higbee A, Ulbrich A, Balloon A, Westphall MS, Aldrich J, Lipton M, Kim J, Moskvin OV, Bukhman YV, Coon J, Kiley PJ, Bates DM, Landick R** (2014) Aromatic inhibitors derived from ammonia-pretreated lignocellulose hinder bacterial ethanologenesis by activating regulatory circuits controlling inhibitor efflux and detoxification. Frontiers in Microbiology **5:** 402
58. **Kelkar S, Li Z, Bovee J, Thelen KD, Kriegel RM, Saffron CM** (2014) Pyrolysis of North-American grass species: effect of feedstock composition and taxonomy on pyrolysis products. Biomass and Bioenergy **64:** 152-161
59. **Kells BJ, Swinton SM** (2014) Profitability of cellulosic biomass production in the northern Great Lakes region. Agronomy Journal **106:** 397-406
60. **Kim H, Ralph J** (2014) A gel-state 2D-NMR method for plant cell wall profiling and analysis: model study with the amorphous cellulose and xylan from ball-milled cotton linters. RSC Advances **4:** 7549-7560
61. **Kim J, Reed JL** (2014) Refining metabolic models and accounting for regulatory effects. Current Opinion in Biotechnology **29C:** 34-38
62. **Kim S, Dale BE, Heijungs R, Azapagic A, Darlington T, Kahlbaum D** (2014) Indirect land use change and biofuels: mathematical analysis reveals a fundamental flaw in the regulatory approach. Biomass and Bioenergy **71:** 408-412
63. **Kim S, Dale BE, Keck P** (2014) Energy requirements and greenhouse gas emissions of maize production in the USA. BioEnergy Research **7:** 763-764
64. **Kim S-J, Brandizzi F** (2014) The plant secretory pathway: an essential factory for building the plant cell. Plant and Cell Physiology **55:** 687-693
65. **Kim W-C, Reca I-B, Kim Y, Park S, Thomashow MF, Keegstra K, Han K-H** (2014) Transcription factors that directly regulate the expression of *CSLA9* encoding mannan synthase in *Arabidopsis thaliana*. Plant Molecular Biology **84:** 577-587
66. **Ko J-H, Jeon H-W, Kim W-C, Kim J-Y, Han K-H** (2014) The MYB46/MYB83-mediated transcriptional regulatory programme is a gatekeeper of secondary wall biosynthesis. Annals of Botany **114:** 1099-1107
67. **Leducq J-B, Charron G, Samani P, Dube AK, Sylvester K, James B, Almeida P, Sampaio JP, Hittinger CT, Bell G, Landry CR** (2014) Local climatic adaptation in a widespread microorganism. Proceedings of the Royal Society B: Biological Sciences **281:** 20132472
68. **Lee ZM, Schmidt TM** (2014) Bacterial growth efficiency varies in soils under different land management practices. Soil Biology and Biochemistry **69:** 282-290
69. **Lemke RAS, Peterson AC, Ziegelhoffer EC, Westphall MS, Tjellström H, Coon JJ, Donohue TJ** (2014) Synthesis and scavenging role of furan fatty acids. Proceedings of the National Academy of Sciences of the United States of America **111:** E3450-E3457

70. **Lennon CW, Lemmer KC, Irons JL, Sellman MI, Donohue TJ, Gourse RL, Ross W** (2014) A *Rhodobacter sphaeroides* protein mechanistically similar to *Escherichia coli* DskA regulates photosynthetic growth. mBio **5:** e01105-01114

71. **Lewis JA, Broman AT, Will J, Gasch AP** (2014) Genetic architecture of ethanol-responsive transcriptome variation in *Saccharomyces cerevisiae* strains. Genetics **198:** 369-382

72. **Li Z, Kelkar S, Raycraft L, Garedew M, Jackson JE, Miller DJ, Saffron CM** (2014) A mild approach for bio-oil stabilization and upgrading: electrocatalytic hydrogenation using ruthenium supported on activated carbon cloth. Green Chemistry **16:** 844-852

73. **Liere H, Kim TN, Werling BP, Meehan TD, Landis DA, Gratton C** (2014) Trophic cascades in agricultural landscapes: indirect effects of landscape composition on crop yield. Ecological Applications **25:** 652-661

74. **Lim S, Chundawat SPS, Fox BG** (2014) Expression, purification and characterization of a functional carbohydrate-binding module from *Streptomyces* sp. SirexAA-E. Protein Expression and Purification **98:** 1-9

75. **Lu F** (2014) Lignin: structural analysis, applications in biomaterials, and ecological significance. Nova Science Publishers, Inc,, Hauppauge, New York, USA

76. **Lu F, Ralph J** (2014) The DFRC (Derivatization Followed by Reductive Cleavage) method and its applications for lignin characterization. *In* Fachuang Lu, ed, Lignin: Structural Analysis, Applications in Biomaterials, and Ecological Significance. Nova Science Publishers, Hauppauge, New York, pp 27-66

77. **Luterbacher JS, Alonso DM, Dumesic JA** (2014) Targeted chemical upgrading of lignocellulosic biomass to platform molecules. Green Chemistry **16:** 4816-4838

78. **Luterbacher JS, Rand JM, Martin Alonso D, Han J, Youngquist JT, Maravelias CT, Pfleger BF, Dumesic JA** (2014) Non-enzymatic sugar production from biomass using biomass-derived γ-valerolactone. Science **343:** 277-280

79. **Mandalika A, Qin L, Sato TK, Runge T** (2014) Integrated biorefinery model based on production of furans using open-ended high yield processes. Green Chemistry **16:** 2480-2489

80. **Martin JA, Johnson NV, Gross SM, Schnable J, Meng X, Wang M, Coleman-Derr D, Lindquist E, Wei C-L, Kaeppler S, Chen F, Wang Z** (2014) A near complete snapshot of the *Zea mays* seedling transcriptome revealed from ultra-deep sequencing. Scientific Reports **4:** 4519

81. **Mellmer MA, Alonso DM, Luterbacher JS, Gallo JMR, Dumesic JA** (2014) Effects of γ-valerolactone in hydrolysis of lignocellulosic biomass to monosaccharides. Green Chemistry **16:** 4659-4662

82. **Mellmer MA, Sener C, Gallo JMR, Luterbacher JS, Alonso DM, Dumesic JA** (2014) Solvent effects in acid-catalyzed biomass conversion reactions. Angewandte Chemie (International Edition) **53:** 11872-11875

83. **Mooney DF, Barham BL, Lian C** (2014) Inelastic and fragmented farm supply response to second-generation bioenergy feedstocks: *ex ante* survey evidence from Wisconsin. Applied Economic Perspectives and Policy **37:** 287-310

84. **Moskvin O, McIlwain S, Ong IM** (2014) CAMDA 2014: Making sense of RNA-Seq data: from low-level processing to functional analysis. Systems Biomedicine **2:** 31-40

85. **Mullet J, Morishige D, McCormick R, Truong S, Hilley J, McKinley B, Anderson R, Olson SN, Rooney W** (2014) Energy Sorghum—a genetic model for the design of C4 grass bioenergy crops. Journal of Experimental Botany **65:** 3479-3489

86. **Niculaes C, Morreel K, Kim H, Lu F, McKee LS, Ivens B, Haustraete J, Vanholme B, Rycke RD, Hertzberg M, Fromm J, Bulone V, Polle A, Ralph J, Boerjan W** (2014) Phenylcoumaran benzylic ether reductase prevents accumulation of compounds formed under oxidative conditions in poplar xylem. The Plant Cell **26:** 3775-3791

87. **Ogle SM, Adler PR, Breidt FJ, Del Grosso S, Derner J, Franzluebbers A, Liebig M, Linquist B, Robertson GP, Schoeneberger M, Six J, van Kessel C, Venterea R, West TO** (2014) Chapter 3: Quantifying greenhouse sources and sinks in cropland and grazing land systems. *In* M. Eve, D. Pape, M. Flugge, R.

Steele, D. Man, M. Riley-Gilbert, S. Biggar, eds, Quantifying Greenhouse Gas Fluxes in Agriculture and Forestry: Methods for Entity-Scale Inventory. Technical Bulletin Number 1939, Vol Technical Bulletin Number 1939. Office of the Chief Economist, U.S. Department of Agriculture, Washington, D.C., pp 1-142

88. **Ong RG, Chundawat SPS, Hodge DB, Keskar S, Dale BE** (2014) Linking plant biology and pretreatment: understanding the structure and organization of the plant cell wall and interactions with cellulosic biofuel production. *In* Maureen C. McCann, Marcos S. Buckeridge, Nicholas S Carpita, eds, Plants and Bioenergy. Springer, New York, pp 231-253
89. **Osterholz WR, Kucharik CJ, Hedtcke JL, Posner JL** (2014) Seasonal nitrous oxide and methane fluxes from grain- and forage-based production systems in Wisconsin, USA. Journal of Environmental Quality **43:** 1833-1843
90. **Palmer MM, Forrester JA, Rothstein DE, Mladenoff DJ** (2014) Conversion of open lands to short-rotation woody biomass crops: site variability affects nitrogen cycling and N_2O fluxes in the US Northern Lake States. Global Change Biology – Bioenergy **6:** 450-464
91. **Parreiras LS, Breuer RJ, Narasimhan RA, Higbee AJ, LaReau A, Tremaine M, Qin L, Willis LB, Bice BD, Bonfert BL, Pinhancos RC, Balloon AJ, Uppugundla N, Liu T, Li C, Tanjore D, Ong IM, Li H, Pohlmann EL, Serate J, Withers ST, Simmons BA, Hodge DB, Westphall MS, Coon JJ, Dale BE, Balan V, Keating DH, Zhang Y, Landick R, Gasch AP, Sato TK** (2014) Engineering and two-stage evolution of a lignocellulosic hydrolysate-tolerant *Saccharomyces cerevisiae* strain for anaerobic fermentation of xylose from AFEX pretreated corn stover. PLOS ONE **9:** e107499
92. **Peris D, Sylvester K, Libkind D, Goncalves P, Sampaio JP, Alexander WG, Hittinger CT** (2014) Population structure and reticulate evolution of *Saccharomyces eubayanus* and its lager-brewing hybrids. Molecular Ecology **23:** 2031-2045
93. **Peterson AC, Hauschild J-PP, Quarmby ST, Krumwiede D, Lange O, Lemke RA, Grosse-Coosmann F, Horning S, Donohue TJ, Westphall MS, Coon JJ, Griep-Raming J** (2014) Development of a GC/Quadrupole-Orbitrap mass spectrometer, Part I: Design and characterization. Analytical Chemistry **86:** 10036-10043
94. **Petrik DL, Karlen SD, Cass CL, Padmakshan D, Lu F, Liu S, Le Bris P, Antelme S, Santoro N, Wilkerson CG, Sibout R, Lapierre C, Ralph J, Sedbrook JC** (2014) *p*-Coumaroyl-CoA:monolignol transferase (PMT) acts specifically in the lignin biosynthetic pathway in *Brachypodium distachyon*. The Plant Journal **77:** 713-726
95. **Piotrowski JS, Zhang Y, Bates DM, Keating DH, Sato TK, Ong IM, Landick R** (2014) Death by a thousand cuts: the challenges and diverse landscape of lignocellulosic hydrolysate inhibitors. Frontiers in Microbiology **5:** 90
96. **Pryor SC, Scavia D, Downer C, Gaden M, Iverson L, Nordstrom R, Patz J, Robertson GP** (2014) Chapter 18: Midwest. *In* J. M. Melillo, Terese (T.C.) Richmond, G. W. Yohe, eds, Climate Change Impacts in the United States: The Third National Climate Assessment. U.S. Global Change Research Program, pp 418-440
97. **Rahimi A, Ulbrich A, Coon JJ, Stahl SS** (2014) Formic-acid-induced depolymerization of oxidized lignin to aromatics. Nature **515:** 249-252
98. **Riley RW, Salamova AA, Brown DW, Nagy LG, Floudas D, Held BW, Levasseur A, Lombard V, Morin E, Otillar R, Lindquist E, Sun H, LaButti K, Schmutz J, Jabbour D, Luo H, Baker SE, Pisabarro AG, Walton JD, Blanchette RA, Henrissat B, Martin F, Culen D, Hibbet DS, Grigoriev IV** (2014) Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white rot/brown rot paradigm for wood decay fungi. Proceedings of the National Academy of Sciences of the United States of America **111:** 9923-9928
99. **Robertson GP** (2014) Soil greenhouse gas emissions and their mitigation. *In* N. K. Van Alfen, ed, The Encyclopedia of Agriculture and Food Systems. Academic Press, San Diego, CA, pp 185-196

100. **Robertson GP, Grace PR, Izaurralde RC, Parton WP, Zhang X** (2014) Correspondence: CO_2 emissions from crop residue-derived biofuels. Nature Climate Change **4:** 933-934
101. **Sahajpal R, Zhang X, Izaurralde RC, Gelfand I, Hurtt GC** (2014) Identifying representative crop rotation patterns and grassland loss in the US Western Corn Belt. Computers and Electronics in Agriculture **108:** 173-182
102. **Sarks C, Jin M, Sato TK, Balen V, Dale BE** (2014) Studying the rapid bioconversion of lignocellulosic sugars into ethanol using high cell density fermentations with cell recycle. Biotechnology for Biofuels **7:** 73
103. **Schuetz M, Benske A, Smith RA, Watanabe Y, Tobimatsu Y, Ralph J, Demura T, Ellis B, Samuels AL** (2014) Laccases direct lignification in the discrete secondary cell wall domains of protoxylem. Plant Physiology **166:** 798-807
104. **Sekhon RS, Hirsch CN, Childs KL, Breitzman MW, Kell P, Duvick S, Spalding EP, Buell CR, de Leon N, Kaeppler S** (2014) Phenotypic and transcriptional analysis of divergently selected maize populations reveals the role of developmental timing in seed size determination. Plant Physiology **165:** 658-669
105. **Shcherbak I, Millar N, Robertson GP** (2014) Global metaanalysis of the nonlinear response of soil nitrous oxide (N_2O) emissions to fertilizer nitrogen. Proceedings of the National Academy of Sciences of the United States of America **111:** 9199-9204
106. **Shcherbak I, Philip Robertson G** (2014) Determining the diffusivity of nitrous oxide in soil using in situ tracers. Soil Science Society of America Journal **78:** 79-88
107. **Singh S, Cheng G, Sathitsuksanoh N, Wu D, Varanasi P, George A, Balan V, Gao X, Kumar R, Dale BE, Wyman C, Simmons B** (2014) Comparison of different biomass pretreatment techniques and their impact on chemistry and structure. Frontiers in Energy Research **2:** 62
108. **Skevas T, Swinton SM, Meehan TD, Kim TN, Gratton C, Egbendewe-Mondzozo A** (2014) Integrating agricultural pest biocontrol into forecasts of energy biomass production. Ecological Economics **106:** 195-203
109. **Sundin L, Vanholme R, Geerinck J, Goeminne G, Hofer R, Kim H, Ralph J, Boerjan W** (2014) Mutation of the inducible *ARABIDOPSIS THALIANA CYTOCHROME P450 REDUCTASE2* alters lignin composition and improves saccharification. Plant Physiology **166:** 1956-1971
110. **Syswerda SP, Robertson GP** (2014) Ecosystem services along a management gradient in Michigan (USA) cropping systems. Agriculture, Ecosystems & Environment **189:** 28-35
111. **Takasuka TE, Acheson JF, Bianchetti CM, Prom BM, Bergeman LF, Book AJ, Currie CR, Fox BG** (2014) Biochemical properties and atomic resolution structure of a proteolytically processed β-mannanase from cellulolytic *Streptomyces* sp. SirexAA-E. PLOS ONE **9:** e94166
112. **Takasuka TE, Bianchetti CM, Tobimatsu Y, Bergeman LF, Ralph J, Fox BG** (2014) Structure-guided analysis of catalytic specificity of the abundantly secreted chitosanase SACTE_5457 from *Streptomyces* sp. SirexAA-E. Proteins **82:** 1245-1257
113. **Takasuka TE, Walker JA, Bergeman LF, Vander Meulen KA, Makino S-i, Elsen NL, Fox BG** (2014) Cell-free translation of biofuels enzymes. *In* Kirill Alexandrov, Wayne A. Johnston, eds, Cell-Free Protein Synthesis: Methods and Protocols, Vol 118. The Humana Press Inc., pp 71-95
114. **Tang X, da Costa Sousa L, Jin M, Chundawat SPS, Chambliss CK, Lau MW, Xiao Z, Dale BE, Balan V** (2014) Designer synthetic media for studying microbial-catalyzed biofuel production. Biotechnology for Biofuels **8:** 1
115. **Tobimatsu Y, Van de Wouwer D, Allen E, Kumpf R, Vanholme B, Boerjan W, Ralph J** (2014) A click chemistry strategy for visualization of plant cell wall lignification. Chemical Communications **50:** 12262-12265
116. **Truong SK, McCormick RF, Morishige DT, Mullet JE** (2014) Resolution of genetic map expansion caused by excess heterozygosity in plant recombinant inbred populations. G3: Genes | Genomes | Genetics **4:** 1963-1969

117. **Ulbrich A, Bailey DJ, Westphall MS, Coon JJ** (2014) Organic acid quantitation by NeuCode methylamidation. Analytical Chemistry **86:** 4402-4408

118. **Uppugundla N, Sousa L, Chundawat SPS, Yu X, Simmons B, Singh S, Gao X, Kumar R, Wyman CE, Dale BE, Balan VA** (2014) A comparative study of ethanol production using dilute acid, ionic liquid and AFEX™ pretreated corn stover. Biotechnology for Biofuels **7:** 72

119. **Van Acker R, Leple J-C, Aerts D, Storme V, Goeminne G, Ivens B, Legee F, Lapierre C, Piens K, Van Montagu MCE, Santoro N, Foster CE, Ralph J, Soetaert W, Pilate G, Boerjan W** (2014) Improved saccharification and ethanol yield from field-grown transgenic poplar deficient in cinnamoyl-CoA reductase. Proceedings of the National Academy of Sciences of the United States of America **111:** 845-850

120. **Vanholme B, Vanholme R, Turumtay H, Goeminne G, Cesarino I, Goubet F, Morreel K, Rencoret J, Bulone V, Hooijmaijers C, De Rycke R, Gheysen G, Ralph J, De Block M, Meulewaeter F, Boerjan W** (2014) Accumulation of *N*-acetylglucosamine oligomers in the plant cell wall affects plant architecture in a dose-dependent and conditional manner. Plant Physiology **165:** 290-308

121. **Vinay-Lara E, Hamilton JJ, Stahl B, Broadbent JR, Reed JL, Steele JL** (2014) Genome-scale reconstruction of metabolic networks of *Lactobacillus casei* ATCC 334 and 12A. PLOS ONE **9:** e110785

122. **Werling BP, Dickson TL, Isaacs R, Gaines H, Gratton C, Gross KL, Liere H, Malmstrom CM, Meehan TD, Ruan L, Robertson BA, Robertson GP, Schmidt TM, Schrotenboer AC, Teal TK, Wilson JK, Landis DA** (2014) Perennial grasslands enhance biodiversity and multiple ecosystem services in bioenergy landscapes. Proceedings of the National Academy of Sciences of the United States of America **111:** 1652-1657

123. **Wieder WR, Grandy AS, Kallenbach CM, Bonan GB** (2014) Integrating microbial physiology and physio-chemical principles in soils with the MIcrobial-MIneral Carbon Stabilization (MIMICS) model. Biogeosciences **11:** 3899-3917

124. **Wilkerson CG, Mansfield SD, Lu F, Withers S, Park J-Y, Karlen SD, Gonzales-Vigil E, Padmakshan D, Unda F, Rencoret J, Ralph J** (2014) Monolignol ferulate transferase introduces chemically labile linkages into the lignin backbone. Science **344:** 90-93

125. **Wohlbach DJ, Rovinskiy N, Lewis JA, Sardi M, Schackwitz WS, Martin JA, Deshpande S, Daum CG, Lipzen A, Sato TK, Gasch AP** (2014) Comparative genomics of *Saccharomyces cerevisiae* natural isolates for bioenergy production. Genome Biology and Evolution **6:** 2557-2566

126. **Woods DP, Ream TS, Amasino RM** (2014) Memory of the vernalized state in plants including the model grass *Brachypodium distachyon*. Frontiers in Plant Science **5:** 99

127. **Woods DP, Ream TS, Minevich G, Hobert O, Amasino RM** (2014) PHYTOCHROME C is an essential light receptor for photoperiodic flowering in the temperate grass, *Brachypodium distachyon*. Genetics **198:** 397-408

128. **Wyche TP, Piotrowski JS, Hou Y, Braun D, Deshpande R, McIlwain S, Ong IM, Myers CL, Guzei IA, Westler WM, Andes DR, Bugni TS** (2014) Forazoline A: marine-derived polyketide with antifungal in vivo efficacy. Angewandte Chemie (International Edition) **126:** 11767-11770

129. **Xiang Z, Anthony R, Tobimatsu Y, Runge T** (2014) Emulsifying properties of an arabinoxylan–protein gum from distillers' grains and the co-production of animal feed. Cellulose **21:** 3623-3635

130. **Xiang Z, Watson J, Tobimatsu Y, Runge T** (2014) Film-forming polymers from distillers' grains: structural and material properties. Industrial Crops and Products **59:** 282-289

131. **Yang LH, Gratton C** (2014) Insects as drivers of ecosystem processes. Current Opinion in Insect Science **2:** 26-32

132. **Ye Z, Zheng Y, Li B, Borrusch MS, Storms R, Walton JD** (2014) Enhancement of synthetic *Trichoderma*-based enzyme mixtures for biomass conversion with an alternative family 5 Glycosyl Hydrolase from *Sporotrichum thermophile*. PLOS ONE **9:** e109885

133. **Yelle DJ, Kapich AN, Houtman CJ, Lu F, Timokhin VI, Fort RCJ, Ralph J, Hammel KE** (2014) A highly diastereoselective oxidant contributes to ligninolysis by the white rot basidiomycete *Ceriporiopsis subvermispora*. Applied and Environmental Microbiology **80:** 7536-7544

134. **Zhang X, Sahajpal R, Manowitz DH, Zhao K, Leduc SD, Xu M, Xiong W, Zhang A, Izaurralde RC, Thomson AM, West TO, Post WM** (2014) Multi-scale geospatial agroecosystem modeling: a case study on the influence of soil data resolution on carbon budget estimates. Science of the Total Environment **479-480:** 138-150

2015

1. **Abraha M, Chen J, Chu H, Zenone T, John R, Su Y-J, Hamilton SK, Robertson GP** (2015) Evapotranspiration of annual and perennial biofuel crops in a variable climate. Global Change Biology – Bioenergy **7:** 1344-1356
2. **Anderson NA, Tobimatsu Y, Ciesielski PN, Ximenes E, Ralph J, Donohoe BS, Ladisch M, Chapple C** (2015) Manipulation of guaiacyl and syringyl monomer biosynthesis in an Arabidopsis cinnamyl alcohol dehydrogenase mutant results in atypical lignin biosynthesis and modified cell wall structure. The Plant Cell **27:** 2195-2209
3. **Araya F, Troncoso E, Mendonca RT, Freer J** (2015) Condensed lignin structures and re-localization achieved at high severities in autohydrolysis of *Eucalyptus globulus* wood and their relationship with cellulose accessibility. Biotechnology and Bioengineering **112:** 1783-1791
4. **Austin S, Kontur WS, Ulbrich A, Oshlag JZ, Zhang W, Higbee A, Zhang Y, Coon JJ, Hodge DB, Donohue TJ, Noguera DR** (2015) Metabolism of multiple aromatic compounds in corn stover hydrolysate by *Rhodopseudomonas palustris*. Environmental Science & Technology **49:** 8914-8922
5. **Aylward FO, Khadempour L, Tremmel DM, McDonald BR, Nicora CD, Wu S, Moore RJ, Orton DJ, Monroe ME, Piehowski PD, Purvine SO, Smith RD, Lipton MS, Burnum-Johnson KE, Currie CR** (2015) Enrichment and broad representation of plant biomass-degrading enzymes in the specialized hyphal swellings of *Leucoagaricus gongylophorus*, the fungal symbiont of leaf-cutter ants. PLOS ONE **10:** e0134752
6. **Bahlai CA, vander Werf W, O'Neal M, Hemerik L, Landis DA** (2015) Shifts in dynamic regime of an invasive lady beetle are linked to the invasion and insecticidal management of its prey. Ecological Applications **25:** 1807-1818
7. **Baker E, Wang B, Bellora N, Peris D, Hulfachor AB, Koshalek JA, Adams M, Libkind D, Hittinger CT** (2015) The genome sequence of *Saccharomyces eubayanus* and the domestication of lager-brewing yeasts. Molecular Biology and Evolution **32:** 2818-2831
8. **Bandaru V, Izaurralde RC, Zhao K** (2015) Biomass potential of switchgrass and miscanthus on the USA's marginal lands. *In* A. K. Bhardwaj, T. Zenone, J. Chen, eds, Sustainable Biofuels: An Ecological Assessment of Future Energy. DeGruyter, pp 299-317
9. **Bansal N, Bhalla A, Pattathil S, Adelman SL, Hahn MG, Hodge DB, Hegg EL** (2015) Cell wall-associated transition metals improve alkaline-oxidative pretreatment in diverse hardwoods. Green Chemistry **18:** 1405-1415
10. **Beissinger TM, Rosa GJM, Kaeppler SM, Gianola D, de Leon N** (2015) Defining window-boundaries for genomic analyses using smoothing spline techniques. Genetics Selection Evolution **47:** 30
11. **Bhardwaj AK, Zenone T, Chen J** (2015) Sustainable Biofuels: An Ecological Assessment of Future Energy. DeGruyter
12. **Bianchetti CM, Takasuka TE, Deutsch S, Udell HS, Yik EJ, Bergeman LF, Fox BG** (2015) Active site and laminarin binding in glycoside hydrolase family 55. Journal of Biological Chemistry **290:** 11819-11832
13. **Brumm P, Land ML, Hauser LJ, Jeffries CD, Chang Y-J, Mead DA** (2015) Complete genome sequences of *Geobacillus* sp. Y412MC52, a xylan-degrading strain isolated from obsidian hot spring in Yellowstone National Park. Standards in Genomic Sciences **10:** 81

14. **Brumm P, Land ML, Hauser LJ, Jeffries CD, Chang Y-J, Mead DA** (2015) Complete genome sequence of *Geobacillus* strain Y4.1MC1, a novel CO-utilizing *Geobacillus thermoglucosidasius* strain isolated from Bath Hot Spring in Yellowstone National Park. BioEnergy Research **8:** 1039-1045
15. **Brumm PJ, De Maayer P, Mead DA, Cowan DA** (2015) Genomic analysis of six new *Geobacillus* strains reveals highly conserved carbohydrate degradation architectures and strategies. Frontiers in Microbiology **6:** 430
16. **Brumm PJ, Land ML, Mead DA** (2015) Complete genome sequence of *Geobacillus thermoglucosidasius* C56-YS93, a novel biomass degrader isolated from obsidian hot spring in Yellowstone National Park. Standards in Genomic Sciences **10:** 73
17. **Bukhman YV, DiPiazza NW, Piotrowski J, Shao J, Halstead AGW, Bui MD, Xie E, Sato TK** (2015) Modeling microbial growth curves with GCAT. BioEnergy Research **8:** 1022-1030
18. **Caes BR, Teixeira RE, Knapp KG, Raines RT** (2015) Biomass to furanics: renewable routes to chemicals and fuels. ACS Sustainable Chemistry and Engineering **3:** 2591-2605
19. **Campioli M, Vicca S, Luyssaert S, Bilcke J, Ceschia E, Chapin III FS, Ciais P, Fernández-Martínez M, Malhi Y, Obersteiner M, Olefeldt D, Papale D, Piao SL, Peñuelas J, Sullivan PF, Wang X, Zenone T, Janssens IA** (2015) Biomass production efficiency controlled by management in temperate and boreal ecosystems. Nature Geoscience **8:** 843-846
20. **Carpita NS, Ralph J, McCann M** (2015) The Cell Wall. *In* Wilhelm Gruissem Bob B. Buchanan, Russell L. Jones, ed, Biochemistry and Molecuar Biology of Plants, 2nd Edition. Wiley, pp 45-110
21. **Cass CL, Peraldi A, Dowd PF, Mottiar Y, Santoro N, Karlen SD, Bukhman YV, Foster CE, Thrower N, Bruno LC, Moskvin OV, Johnson ET, Willhoit ME, Phutane M, Ralph J, Mansfield SD, Nicholson P, Sedbrook JC** (2015) Effects of *PHENYLALANINE AMMONIA LYASE (PAL)* knockdown on cell wall composition, biomass digestibility, and biotic and abiotic stress responses in *Brachypodium*. Journal of Experimental Botany **66:** 4317-4335
22. **Clowers KJ, Heilberger J, Piotrowski JS, Will JL, Gasch AP** (2015) Ecological and genetic barriers differentiate natural populations of *Saccharomyces cerevisiae*. Molecular Biology and Evolution **32:** 2317-2327
23. **Clowers KJ, Will JL, Gasch AP** (2015) A unique ecological niche fosters hybridization of oak-tree and vineyard isolates of *Saccharomyces cerevisiae*. Molecular Ecology **24:** 5886-5898
24. **Coelho MA, Almeida JMGCF, Hittinger CT, Goncalves P** (2015) Draft genome sequence of *Sporidiobolus salmonicolor* CBS 6832, a red-pigmented basidiomycetous yeast. Genome Announcements **3:** 300444-300415
25. **Cornish AJ, Green R, Gärtner K, Mason S, Hegg EL** (2015) Charactization of hydrogen metabolism in the multicellular green alga *Volvox carteri*. PLOS ONE **10:** e0125324
26. **Dale BE, Holtzapple M** (2015) SBE Special Section: Lignocellulosic Biofuels – The Need for Biofuels. Chemical Engineering Progress Magazine **81:** 57-69
27. **del Rio JC, Lino AG, Colodette JL, Lima CF, Gutierrez A, Martinez AT, Lu F, Ralph J, Rencoret J** (2015) Differences in the chemical structure of the lignins from sugarcane bagasse and straw. Biomass and Bioenergy **81:** 322-338
28. **Deng K, Guenther JM, Gao J, Bowen BP, Tran H, Reyes-Ortiz V, Cheng X, Sathitsuksanoh N, Heins R, Takasuka TE, Bergeman LF, Geertz-Hansen H, Deutsch S, Loque D, Sale K, Simmons B, Adam PD, Singh AK, Fox BG, Northen TR** (2015) Development of a high throughput platform for screening glycoside hydrolases based on oxime-NIMS. Frontiers in Bioengineering and Biotechnology **3:** 153
29. **Deng K, Takasuka TE, Bianchetti CM, Bergeman LF, Adam PD, Northen TR, Fox BG** (2015) Use of nanostructure initiator mass spectrometry to deduce selectivity of reaction in glycoside hydrolases. Frontiers in Bioengineering and Biotechnology **3:** 165
30. **Dickson TL, Gross KL** (2015) Can the results of biodiversity-ecosystem productivity studies be translated to bioenergy production? PLOS ONE **10:** e0135253

31. **Dima O, Morreel K, Vanholme B, Kim H, Ralph J, Boerjan W** (2015) Small glycosylated lignin oligomers are stored in Arabidopsis leaf vacuoles. The Plant Cell **27:** 695-710
32. **Egbendewe-Mondzozo A, Swinton SM, Kang S, Post WM, Binfield JC, Thompson W** (2015) Bioenergy supply and environmental impacts on cropland: insights from multi-market forecasts in a Great Lakes subregional bioeconomic model. Applied Economic Perspectives and Policy **37:** 602-618
33. **Evans J, Crisovan E, Barry K, Daum C, Jenkins J, Kunde-Ramamoorthy G, Nandety A, Ngan CY, Vaillancourt B, Wei C-L, Schmutz J, Kaeppler SM, Casler MD, Buell CR** (2015) Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. The Plant Journal **84:** 800-815
34. **Foerster JM, Beissinger T, de Leon N, Kaeppler S** (2015) Large effect QTL explain natural phenotypic variation for the developmental timing of vegetative phase change in maize (*Zea mays* L.). Theoretical and Applied Genetics **128:** 529-538
35. **Gelfand I, Cui M, Tang J, Robertson GP** (2015) Short-term drought response of N_2O and CO_2 emissions from mesic agricultural soils in the US Midwest. Agriculture, Ecosystems & Environment **212:** 127-133
36. **Gelfand I, Robertson GP** (2015) Mitigation of greenhouse gases in agricultural ecosystems. *In* Stephen K Hamilton, J.E. Doll, G Philip Robertson, eds, The Ecology of Agricultural Landscapes: Long-Term Research on the Path to Sustainability. Oxford University Press, New York, NY, pp 419-458
37. **Gelfand I, Robertson GP** (2015) A reassessment of the contribution of soybean biological nitrogen fixation to reactive N in the environment. Biogeochemistry **123:** 175-184
38. **Grabber JH, Santoro N, Foster CE, Elumalai S, Ralph J, Pan X** (2015) Incorporation of flavonoid derivatives or pentagalloyl glucose into lignin enhances cell wall saccharification following mild alkaline or acidic pretreatments. BioEnergy Research **8:** 1391-1400
39. **Gratton C, Casler MD, Groves R, Kim TN** (2015) Insecticide applications have minor effects on switchgrass biomass yield. Agronomy Journal **107:** 2031-2037
40. **Groendyk MA, Rothamer DA** (2015) Effects of fuel physical properties on auto-ignition characteristics in a heavy duty compression ignition engine. SAE International Journal of Fuels and Lubricants **8:** 200-213
41. **Guzzo de Carli Poelking V, Giordano A, Ricci-Silva ME, Rhys Williams TC, Alves Pecanha D, Contin Ventrella M, Rencoret J, Ralph J, Pereira Barbosa MH, Loureiro M** (2015) Analysis of a modern hybrid and an ancient sugarcane implicates a complex interplay of factors in affecting recalcitrance to cellulosic ethanol production. PLOS ONE **10:** e0134964
42. **Haase NJ, Bessinger T, Hirsch CN, Vaillancourt B, Deshpande S, Barry K, Buell CR, Kaeppler SM, de Leon N** (2015) Shared genomic regions between derivatives of a large segregating population of maize identified using bulked segregant analysis sequencing and traditional linkage analysis. G3: Genes | Genomes | Genetics **5:** 1593-1602
43. **Hamilton SK, Hussain MZ, Bhardwaj AK, Basso B, Robertson GP** (2015) Comparative water use by maize, perennial crops, restored prairie, and poplar trees in the US Midwest. Environmental Research Letters **10:** 064015
44. **Han J, Luterbacher JS, Alonso DM, Dumesic JA, Maravelias CT** (2015) A lignocellulosic ethanol strategy *via* nonenzymatic sugar production: process synthesis and analysis. BioresourceTechnology **182:** 258-266
45. **Han J, Sen SM, Luterbacher JS, Alonso DM, Dumesic JA, Maravelias CT** (2015) Process systems engineering studies for the synthesis of catalytic biomass-to-fuels strategies. Computers & Chemical Engineering **81:** 57-69
46. **Heckwolf S, Heckwolf M, Kaeppler SM, de Leon N, Spalding EP** (2015) Image analysis of anatomical traits in stalk transections of maize and other grasses. Plant Methods **11:** 26
47. **Hittinger CT, Rokas A, Bai F-Y, Boekhout T, Goncalves P, Jeffries TW, Kominek J, Lachance M-A, Libkind D, Rosa CA, Sampaio JP, Kurtzman CP** (2015) Genomics and the making of yeast biodiversity. Current Opinion in Genetics and Development **35:** 100-109

48. **Hose J, Yong CM, Sardi M, Wang Z, Newton MA, Gasch AP** (2015) Dosage compensation can buffer copy-number variation in wild yeast. eLife **4:** e05462
49. **Imam S, Noguera DR, Donohue TJ** (2015) CceR and AkgR regulate central carbon and energy metabolism in alphaproteobacteria. mBio **6:** e02461-02414
50. **Imam S, Noguera DR, Donohue TJ** (2015) An integrated approach to reconstructing genome-scale transcriptional regulatory networks. PLOS Computational Biology **11:** e1004103
51. **Jach-Smith LC, Jackson RD** (2015) Nitrogen conservation decreases with fertilizer addition in two perennial grass cropping systems for bioenergy. Agriculture, Ecosystems & Environment **204:** 62-71
52. **Kallenbach CM, Grandy AS** (2015) Land-use legacies regulate decomposition dynamics following bioenergy crop conversion. Global Change Biology – Bioenergy **7:** 1232-1244
53. **Kallenbach CM, Grandy AS, Frey SD, Diefendorf AF** (2015) Microbial physiology and necromass regulate agricultural soil carbon accumulation. Soil Biology and Biochemistry **91:** 279-290
54. **Kilaru A, Cao X, Dabbs PB, Sung H-J, Rahman MM, Thrower N, Zynda G, Podicheti R, Ibarra-Laclette E, Herrera-Estrella L, Mockaitis K, Ohlrogge JB** (2015) Oil biosynthesis in a basal angiosperm: transcriptome analysis of *Persea Americana* mesocarp. BMC Plant Biology **15:** 203
55. **Kim S, Dale BE** (2015) Comparing alternative cellulosic biomass biorefining systems: centralized versus distributed processing systems. Biomass and Bioenergy **74:** 135-147
56. **Kim S, Dale BE** (2015) All biomass is local: the cost, volume produced, and global warming impact of cellulosic biofuels depend strongly on logistics and local conditions. Biofuels, Bioproducts and Biorefining **9:** 422-434
57. **Kim S-J, Held MA, Zemelis S, Wilkerson C, Brandizzi F** (2015) CGR2 and CGR3 have critical overlapping roles in pectin methylesterification and plant growth in *Arabidopsis thaliana*. The Plant Journal **82:** 208-220
58. **Kim S-J, Zemelis S, Keegstra K, Brandizzi F** (2015) The cytoplasmic localization of the catalytic site of CSLF6 supports a channeling model for the biosynthesis of mixed-linkage glucan. The Plant Journal **81:** 537-547
59. **Kong Y, Pena MJ, Renna L, Avci U, Pattathil S, Tuomivaara ST, Li X, Reiter W-D, Brandizzi F, Hahn MG, Darvill AG, York WS, O'Neill MA** (2015) Galactose-depleted xyloglucan is dysfunctional and leads to dwarfism in Arabidopsis. Plant Physiology **167:** 1296-1306
60. **Kravchenko AN, Robertson GP** (2015) Statistical challenges in analyses of chamber-based soil CO_2 and N_2O emissions data. Soil Science Society of America Journal **79:** 200-211
61. **Lan W, Lu F, Regner M, Zhu Y, Rencoret J, Ralph SA, Zakai UI, Morreel K, Boerjan W, Ralph J** (2015) Tricin, a flavonoid monomer in monocot lignification. Plant Physiology **167:** 1284-1295
62. **Langner T, Öztürk M, Hartmann S, Cord-Landwehr S, Moerschbacher B, Walton JD, Göhre V** (2015) Chitinases are essential for cell separation in *Ustilago maydis*. Eukaryotic Cell **14:** 846-857
63. **Lemmer KC, Dohnalkova AC, Noguera DR, Donohue TJ** (2015) Oxygen-dependent regulation of bacterial lipid production. Journal of Bacteriology **197:** 1649-1658
64. **Li M, Heckwolf M, Crowe JD, Williams DL, Magee TD, Kaeppler SM, de Leon N, Hodge DB** (2015) Cell-wall properties contributing to improved deconstruction by alkaline pre-treatment and enzymatic hydrolysis in diverse maize (*Zea mays* L.) lines. Journal of Experimental Botany **66:** 4305-4315
65. **Li Z, Bansal N, Azarpira A, Bhalla A, Chen CH, Ralph J, Hegg EL, Hodge DB** (2015) Chemical and structural changes associated with Cu-catalyzed alkaline-oxidative delignification of hybrid poplar. Biotechnology for Biofuels **8:** 123
66. **Lin T-Y, Santos TMA, Kontur WS, Donohue TJ, Weibel DB** (2015) A cardiolipin-deficient mutant of *Rhodobacter sphaeroides* has an altered cell shape and is impaired in biofilm formation. Journal of Bacteriology **197:** 3446-3455
67. **Lin Y, King JY, Karlen SD, Ralph J** (2015) Using 2D NMR spectroscopy to assess effects of UV radiation on cell wall chemistry during litter decomposition. Biogeochemistry **125:** 427-436

68. **Liu J, Rice A, McGlew K, Shaw V, Park H, Clemente T, Pollard M, Ohlrogge J, Durrett TP** (2015) Metabolic engineering of oilseed crops to produce high levels of novel acetyl glyceride oils with reduced viscosity, freezing point and calorific value. Plant Biotechnology Journal **13:** 858-865
69. **Liu J, Tjellström H, McGlew K, Shaw V, Rice A, Simpson J, Kosma D, Ma W, Yang W, Strawsine M, Cahoon E, Durrett TP, Ohlrogge J** (2015) Field production, purification and analysis of high-oleic acetyl-triacylglycerols from transgenic *Camelina sativa*. Industrial Crops and Products **65:** 259-268
70. **Liu Y, Mellmer MA, Alonso DM, Dumesic JA** (2015) Effects of water on the copper-catalyzed conversion of hydroxymethylfurfural in tetrahydrofuran. ChemSusChem **8:** 3983-3986
71. **Long MR, Ong WK, Reed JL** (2015) Computational methods in metabolic engineering for strain design. Current Opinion in Biotechnology **34:** 135-141
72. **Lu F, Karlen SD, Regner M, Kim H, Ralph SA, Sun R-C, Kuroda K-i, Augustin MA, Mawson R, Sabarez H, Singh T, Jimenez-Monteon G, Zakaria S, Hill S, Harris PJ, Boerjan W, Wilkerson CG, Mansfield SD, Ralph J** (2015) Naturally *p*-hydroxybenzoylated lignins in palms. BioEnergy Research **8:** 934-952
73. **Luterbacher JS, Alonso DM, Rand JM, Questell-Santiago YM, Yeap JH, Pfleger BF, Dumesic JA** (2015) Solvent-enabled nonenzymatic sugar production from biomass for chemical and biological upgrading. ChemSusChem **8:** 1317-1322
74. **Luterbacher JS, Azarpira A, Motagamwala AH, Lu F, Ralph J, Dumesic JA** (2015) Lignin monomer production integrated into the γ-valerolactone sugar platform. Energy & Environmental Science **8:** 2657-2663
75. **Ma W, Kong Q, Grix M, Mantyla JJ, Yang Y, Benning C, Ohlrogge JB** (2015) Deletion of a C-terminal intrinsically disordered region of WRINKLED1 affects its stability and enhances oil accumulation in Arabidopsis. The Plant Journal **83:** 864-874
76. **McCormick RF, Truong SK, Mullet JE** (2015) RIG: recalibration and interrelation of genomic sequence data with the GATK. G3: Genes | Genomes | Genetics **5:** 655-665
77. **McGlew K, Shaw V, Zhang M, Kim RJ, Yang W, Shorrosh B, Suh MC, Ohlrogge J** (2015) An annotated database of Arabidopsis mutants of acyl lipid metabolism. Plant Cell Reports **34:** 519-532
78. **Meehan TD, Gratton C** (2015) A consistent positive association between landscape simplification and insecticide use across the Midwestern US from 1997 through 2012. Environmental Research Letters **10:** 114001
79. **Meier PJ, Cronin KR, Frost EA, Runge TM, Dale BE, Reinemann DJ, Detlor J** (2015) Potential for electrified vehicles to contribute to U.S. petroleum and climate goals and implications for advanced biofuels. Environmental Science & Technology **49:** 8277-8286
80. **Mellmer MA, Gallo JMR, Alonso DM, Dumesic JA** (2015) Selective production of levulinic acid from furfuryl alcohol in THF solvent sytems over H-ZSM-5. ACS Catalysis **5:** 3354-3359
81. **Millar N, Robertson GP** (2015) Nitrogen transfers and transformations in row-crop ecosystems. *In* Stephen K Hamilton, J.E. Doll, G Philip Robertson, eds, The Ecology of Agricultural Landscapes: Long-Term Research on the Path to Sustainability. Oxford University Press, New York, NY, pp 289-342
82. **Murfin KE, Lee M-M, Klassen JL, McDonald BR, Larget B, Forst S, Stock SP, Currie CR, Goodrich-Blair H** (2015) *Xenorhabdus bovienii* strain diversity impacts coevolution and symbiotic maintenance with *Steinernema* spp. nematode hosts. mBio **6:** e00076-00015
83. **Myers KS, Park DM, Beauchene NA, Kiley PJ** (2015) Defining bacterial regulons using ChIP-seq. Methods **86:** 80-88
84. **Ohlrogge J, Browse J, Somerville C** (2015) Lipids. *In* Wilhelm Gruissem Bob B. Buchanan, Russell L. Jones, ed, Biochemistry and Molecular Biology of Plants, 2nd Edition, Ed 2nd Edition. Wiley, pp 336-400
85. **Park S-H, Ong RG, Sticklen M** (2015) Strategies for the production of cell wall-deconstructing enzymes in lignocellulosic biomass and their utilization for biofuel production. Plant Biotechnology Journal **14:** 1329-1344

86. **Parker JM, de los Santos EX, Anderson CW** (2015) Learning progressions and climate change. The American Biology Teacher **77:** 232-237
87. **Pattathil S, Hahn MG, Dale BE, Chundawat SPS** (2015) Insights into plant cell wall structure, architecture, and integrity using glycome profiling of native and AFEX™-pre-treated biomass. Journal of Experimental Botany **66:** 4279-4294
88. **Piotrowski JS, Okada H, Lu F, Li SC, Hinchman L, Ranjan A, Smith DL, Higbee AJ, Ulbrich A, Coon JJ, Deshpande R, Bukhman YV, McIlwain S, Ong IM, Myers CL, Boone C, Landick R, Ralph J, Kabbage M, Ohya Y** (2015) Plant-derived antifungal agent poacic acid targets β-1,3-glucan. Proceedings of the National Academy of Sciences of the United States of America **112:** E1490-E1497
89. **Piotrowski JS, Simpkins SW, Li SC, Deshpande R, McIlwain SJ, Ong IM, Myers CL, Boone CB, Andersen RJ** (2015) Chemical genomic profiling via barcode sequencing to predict compound mode of action. *In* Jonathan E Hempel, Charles H Williams, Charles C (Ed) Hong, eds, Chemical Biology - Methods and Protocols, Vol 1263. Springer, New York, pp 299-318
90. **Pisithkul T, Jacobson TB, O'Brien TJ, Stevenson DM, Amador-Noguez D** (2015) Phenolic amides are potent inhibitors of *de novo* nucleotide biosynthesis. Applied and Environmental Microbiology **81:** 5761-5772
91. **Pollard M, Delamarter D, Martin TM, Shachar-Hill Y** (2015) Lipid labeling from acetate or glycerol in cultured embryos of *Camelina sativa* seeds: a tale of two substrates. Phytochemistry **118:** 192-203
92. **Pollard M, Martin TM, Shachar-Hill Y** (2015) Lipid analysis of developing *Camelina sativa* seeds and cultured embryos. Phytochemistry **118:** 23-32
93. **Rachid CTCC, Balieiro FC, Fonseca ES, Peixoto RS, Chaer GM, Tiedje JM, Rosado AS** (2015) Intercropped silviculture systems, a key to achieving soil fungal community management in *Eucalyptus* plantations. PLOS ONE **10:** e0118515
94. **Rafiee M, Miles KC, Stahl SS** (2015) Electrocatalytic alcohol oxidation with TEMPO and bicyclic nitroxyl derivatives: driving force trumps steric effects. Journal of the American Chemical Society **137:** 14751-14757
95. **Ruberti C, Kim S-J, Stefano G, Brandizzi F** (2015) Unfolded protein response in plants: one master, many questions. Current Opinion in Plant Biology **27:** 59-66
96. **Russ RS, Wangen SR, Nye L, Shapiro RB, Strinz W, Ferris M** (2015) Fields of fuel. The Science Teacher **82:** 3-8
97. **Serate J, Xie D, Pohlmann E, Donald Jr. C, Shabani M, Hinchman L, Higbee A, Mcgee M, La Reau A, Klinger GE, Li S, Myers CL, Boone C, Bates DM, Cavalier D, Eilert D, Oates LG, Sanford G, Sato TK, Dale B, Landick R, Piotrowski J, Ong RG, Zhang Y** (2015) Controlling microbial contamination during hydrolysis of AFEX-pretreated corn stover and switchgrass: effects on hydrolysate composition, microbial response and fermentation. Biotechnology for Biofuels **8:** 180
98. **Sinistore JC, Reinemann DJ, Izaurralde RC, Cronin KR, Meier PJ, Runge TM, Zhang X** (2015) Life cycle assessment of switchgrass cellulosic ethanol production in the Wisconsin and Michigan agricultural contexts. BioEnergy Research**:** 897-909
99. **Skevas T, Hayden NJ, Swinton SM, Lupi F** (2015) Landowner willingness to supply marginal land for bioenergy production. Land Use Policy **50:** 507-517
100. **Slater SC, Simmons BA, Rogers TS, Phillips MF, Nordahl K, Davison BH** (2015) The DOE Bioenergy Research Centers: history, operations, and scientific output. BioEnergy Research **8:** 881-896
101. **Slininger PJ, Shea-Andersh MA, Thompson SR, Dien BS, Kurtzman CP, Balan V, da Costa Sousa L, Uppugundla N, Dale BE, Cotta MA** (2015) Evolved strains of *Scheffersomyces stipitis* reaching high ethanol productivity on acid- and base-pretreated biomass hydrolyzate at high solids loading. Biotechnology for Biofuels **8:** 27

102. **Smith RA, Gonzales-Vigil E, Karlen SD, Park J-Y, Lu F, Wilkerson CG, Samuels L, Ralph J, Mansfield SD** (2015) Engineering monolignol *p*-coumarate conjugates into poplar and Arabidopsis lignins. Plant Physiology **169:** 2992-3001
103. **Spero MA, Aylward FO, Currie CR, Donohue TJ** (2015) Phylogenomic analysis and predicted physiological role of the proton-translocating NADH:quinone oxidoreductase (complex I) across bacteria. mBio **6:** e00389-00315
104. **Stelpflug SC, Sekhon RS, Vaillancourt B, Hirsch CN, Buell CR, de Leon N, Kaeppler SM** (2015) An expanded maize gene expression atlas based on RNA sequencing and its use to explore root development. The Plant Genome **9:** 1-16
105. **Su Y-K, Willis LB, Jeffries TW** (2015) Effects of aeration on growth, ethanol and polyol accumulation by *Spathaspora passalidarum* NRRL Y-27907 and *Scheffersomyces stipitis* NRRL Y-7124. Biotechnology and Bioengineering **112:** 457-469
106. **Sylvester K, Wang Q-MM, James B, Mendez R, Hulfachor AB, Hittinger CT** (2015) Temperature and host preferences drive the diversification of *Saccharomyces* and other yeasts: a survey and the discovery of eight new yeast species. FEMS Yeast Research **15:** fov002
107. **Tanger P, Vega-Sánchez ME, Fleming M, Tran K, Singh S, Abrahamson JB, Jahn CE, Santoro N, Naredo EB, Baraoidan M, Danku JMC, Salt DE, McNally KL, Leung H, Ronald PC, Bush DR, McKay JK, Leach JE** (2015) Cell wall composition and bioenergy potential of rice straw tissues are influenced by environment, tissue type, and genotype. BioEnergy Research **8:** 1165-1182
108. **Tiemann LK, Grandy AS** (2015) Mechanisms of soil carbon accrual and storage in bioenergy cropping systems. Global Change Biology – Bioenergy **7:** 161-174
109. **Tiemann LK, Grandy AS, Atkinson EE, Marin-Spiotta E, McDaniel MD** (2015) Crop rotational diversity enhances belowground communities and functions in an agroecosystem. Ecology Letters **18:** 761-771
110. **Tjellström H, Strawsine M, Ohlrogge JB** (2015) Tracking synthesis and turnover of triacylglycerol in leaves. Journal of Experimental Botany **66:** 1453-1461
111. **Truong SK, McCormick RF, Rooney WL, Mullet JE** (2015) Harnessing genetic variation in leaf angle to increase productivity of *Sorghum bicolor*. Genetics **201:** 1229-1238
112. **Tsai C-H, Zienkiewicz K, Amstutz CL, Brink BG, Warakanont J, Roston R, Benning C** (2015) Dynamics of protein and polar lipid recruitment during lipid droplet assembly in *Chlamydomonas reinhardtii*. The Plant Journal **83:** 650-660
113. **Tsuji Y, Vanholme R, Tobimatsu Y, Ishikawa Y, Foster CE, Kamimura N, Hishiyama S, Hashimoto S, Shino A, Hara H, Sato-Izawa K, Oyarce P, Goeminne G, Morreel K, Kikuch iJ, Takano T, Fukuda M, Boerjan W, Ralph J, Masai E, Kajita S** (2015) Introduction of chemically labile substructures into *Arabidopsis* lignin through the use of LigD, the Cα-dehydrogenase from *Sphingobium* sp. strain SYK-6. Plant Biotechnology Journal **13:** 821-832
114. **Underkofler KA, Teixeira RE, Pietsch SA, Knapp KG, Raines RT** (2015) Separation of lignin from corn stover hydrolysate with quantitative recovery of ionic liquid. ACS Sustainable Chemistry and Engineering **3:** 606-613
115. **Wagner A, Tobimatsu Y, Phillips L, Flint H, Geddes B, Lu F, Ralph J** (2015) Syringyl lignin production in conifers: proof of concept in a Pine tracheary element system. Proceedings of the National Academy of Sciences of the United States of America **112:** 6218-6223
116. **Walker JA, Takasuka TE, Deng K, Bianchetti CM, Udell HS, Prom BM, Kim H, Adams PD, Northen TR, Fox BG** (2015) Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. Biotechnology for Biofuels **8:** 220
117. **Wang Q, Fish JA, Gilman M, Sun Y, Brown CT, Tiedje JM, Cole JR** (2015) Xander: employing a novel method for efficient gene-targeted metagenomic assembly. Microbiome **3:** 1-13

118. **Wieder WR, Grandy AS, Kallenbach CM, Taylor PG, Bonan GB** (2015) Representing life in the Earth system with soil microbial functional traits in the MIMICS model. Geoscientific Model Development **8:** 1789-1808
119. **Woods DP, Amasino RM** (2015) Dissecting the control of flowering time in grasses ssing *Brachypodium distachyon*. *In* John P. Vogel, ed, Genetics and Genomics of Brachypodium, Vol 18. Springer International Publishing, pp 259-273
120. **Wyman CE, Dale BE** (2015) Producing biofuels via the sugar platform. Chemical Engineering Progress Magazine **111:** 45-57
121. **Xue S, Uppugundla N, Bowman MJ, Cavalier D, Da Costa Sousa L, Dale BE, Balan V** (2015) Sugar loss and enzyme inhibition due to oligosaccharide accumulation during high solids-loading enzymatic hydrolysis. Biotechnology for Biofuels **8:** 195
122. **Yang Y, Munz J, Cass C, Zienkiewicz A, Kong Q, Ma W, Sanjaya, Sedbrook J, Benning C** (2015) Ectopic expression of *WRINKLED1* affects fatty acid homeostasis in *Brachypodium distachyon* vegetative tissues. Plant Physiology **169:** 1836-1847
123. **Zhang B, Penton CR, Xue C, Wang Q, Zheng T, Tiedje JM** (2015) Evaluation of the Ion Torrent Personal Genome Machine for gene-targeted studies using amplicons of the nitrogenase gene *nifH*. Applied and Environmental Microbiology **81:** 4536-4545
124. **Zhang X, Izaurralde RC, Manowitz DH, Sahajpal R, West TO, Thomson AM, Xu M, Zhao K, LeDuc SD, Williams JR** (2015) Regional scale cropland carbon budgets: evaluating a geospatial agricultural modeling system using inventory data. Environmental Modelling & Software **63:** 199-216

2016

1. **Abraha M, Gelfand I, Hamilton SK, Shao C, Su Y-J, Robertson GP, Chen J** (2016) Ecosystem water-use efficiency of annual corn and perennial grasslands: contributions from land-use history and species composition. Ecosystems **19:** 1001-1012
2. **Adkins A, Thelen K** (2016) Switchgrass ash content response to harvest timing and two harvest/storage methods of a bioenergy cropping system in the Great Lakes Region. American Journal of Biomass and Bioenergy **5:** 98-110
3. **Alexander WG, Peris D, Pfannenstiel BT, Opulente DA, Kuang M, Hittinger CT** (2016) Efficient engineering of marker-free synthetic allotetraploids of *Saccharomyces*. Fungal Genetics and Biology **89:** 10-17
4. **Alexander WG, Wisecaver JH, Rokas A, Hittinger CT** (2016) Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. Proceedings of the National Academy of Sciences of the United States of America **113:** 4116-4121
5. **Badalyan A, Stahl SS** (2016) Cooperative electrocatalytic alcohol oxidation with electron-proton-transfer mediators. Nature **535:** 406-410
6. **Bahlai CA, Landis DA** (2016) Predicting plant attractiveness to pollinators with passive crowdsourcing. Royal Society Open Science **3:** 150677
7. **Barham BL, Mooney DF, Swinton SM** (2016) Inconvenient truths about landowner (Un)willingness to grow dedicated bioenergy crops. Choices **31**
8. **Bellora N, Moline M, David-Palma M, Coelho MA, Hittinger CT, Sampaio JP, Goncalves P, Libkind D** (2016) Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: *Phaffia rhodozyma*. BMC Genomics **17:** 901
9. **Bewg WP, Poovaiah C, Lan W, Ralph J, Coleman HD** (2016) RNAi downregulation of three key lignin genes in sugarcane improves glucose release without reduction in sugar production. Biotechnology for Biofuels **9:** 270
10. **Bhalla A, Bansal N, Stoklosa RJ, Fountain M, Ralph J, Hodge DB, Hegg EL** (2016) Effective alkaline metal-catalyzed oxidative delignification of hybrid poplar. Biotechnology for Biofuels **9:** 34

11. **Blaser MJ, Cardon ZG, Cho MK, Dangl JL, Donohue TJ, Green JL, Knight R, Maxon ME, Northen TR, Pollard KS, Brodie EL** (2016) Toward a predictive understanding of Earth's microbiomes to address 21st century challenges. mBio **7:** e00714-00716
12. **Book AJ, Lewin GR, McDonald BR, Takasuka TE, Wendt-Pienkowski E, Doering DT, Suh S, Raffa KF, Fox BG, Currie CR** (2016) Evolution of high cellulolytic activity in symbiotic *Streptomyces* through selection of expanded gene content and coordinated gene expression. PLOS Biology **14:** e1002475
13. **Brumm PJ, Gowda K, Robb FT, Mead DA** (2016) The complete genome sequence of hyperthermophile *Dictyoglomus turgidum* DSM 6724™ reveals a specialized carbohydrate fermentor. Frontiers in Microbiology **7:** 1979
14. **Cai Y, Zhang K, Kim H, Hou G, Zhang X, Yang H, Feng H, Miller L, Ralph J, Liu C-J** (2016) Enhancing digestibility and ethanol yield of *Populus* wood *via* expression of an engineered monolignol 4-*O*-methyltransferase. Nature Communications **7:** 11989
15. **Cass CL, Lavell AA, Santoro N, Foster CE, Karlen SD, Smith RA, Ralph J, Garvin DF, Sedbrook JC** (2016) Cell wall composition and biomass recalcitrance differences within a genotypically diverse set of *Brachypodium distachyon* inbred lines. Frontiers in Plant Science **7:** 708
16. **Chen S, Kaeppler SM, Vogel KP, Casler MD** (2016) Selection signatures in four lignin genes from switchgrass populations divergently selected for *in vitro* dry matter digestibility. PLOS ONE **11:** e0167005
17. **Chen W, McClelland DJ, Azarpira A, Ralph J, Luo Z, Huber GW** (2016) Low temperature hydrogenation of pyrolytic lignin over Ru/TiO_2: 2D HSQC and ^{13}C NMR study of reactants and products. Green Chemistry **18:** 271-281
18. **Chundawat SPS, Paavola CD, Raman B, Nouailler M, Chan SL, Mielenz JR, Receveur-Brechot V, Trent JD, Dale BE** (2016) Saccharification of thermochemically pretreated cellulosic biomass using native and engineered cellulosomal enzyme systems. Reaction Chemistry & Engineering **1:** 616-628
19. **Collier SM, Dean AP, Oates LG, Ruark MD, Jackson RD** (2016) Does plant biomass manipulation in static chambers affect nitrous oxide emissions from soils? Journal of Environmental Quality **45:** 751-756
20. **Cornish AJ, Ginovska B, Thelen A, da Silva JCS, Soares TA, Raugei S, Dupuis M, Shaw WJ, Hegg EL** (2016) Single-amino acid modifications reveal additional controls on the proton pathway of [FeFe]-hydrogenase. Biochemistry **55:** 3165-3173
21. **Cotten C, Reed JL** (2016) Applications of constraint-based models for biochemical production. *In* Carrie E. Eckert, Cong T. Trinh, eds, Biotechnology for Biofuel Production and Optimization. Elsevier, pp 201-226
22. **da C. Jesus E, Liang C, Quensen JF, Susilawati E, Jackson RD, Balser TC, Tiedje JM** (2016) Influence of corn, switchgrass, and prairie cropping systems on soil microbial communities in the upper Midwest of the United States. Global Change Biology – Bioenergy **8:** 481-494
23. **da Costa Sousa L, Foston M, Bokade V, Azarpira A, Lu F, Ragauskas AJ, Ralph J, Dale B, Balan V** (2016) Isolation and characterization of new lignin streams derived from extractive-ammonia (EA) pretreatment. Green Chemistry **18:** 4205-4215
24. **da Costa Sousa L, Jin M, Chundawat SPS, Bokade V, Tang X, Azarpira A, Lu F, Avci U, Humpula J, Uppugundla N, Gunawan C, Pattathil S, Cheh AM, Kothari N, Kumar R, Ralph J, Hahn MG, Wyman CE, Seema S, Simmons BA, Dale BE, Balan V** (2016) Next-generation ammonia pretreatment enhances cellulosic biofuel production. Energy & Environmental Science **9:** 1215-1223
25. **Dickinson Q, Bottoms S, Hinchman L, McIlwain S, Li S, Myers CL, Boone C, Coon JJ, Hebert A, Sato TK, Landick R, Piotrowski JS** (2016) Mechanism of imidazolium ionic liquids toxicity in *Saccharomyces cerevisiae* and rational engineering of a tolerant, xylose-fermenting strain. Microbial Cell Factories **15:** 17
26. **Ding S-Y** (2016) Nanoscale structure of biomass. *In* Marcel Schlaf, Z. Conrad Zhang, eds, Reaction Pathways and Mechanisms in Thermocatalytic Biomass Conversion I, Green Chemistry and Sustainable Technology. Springer Singapore, Singapore, pp 1-14

27. **Duncan DS, Jewell KA, Suen G, Jackson RD** (2016) Detection of short-term cropping system-induced changes to soil bacterial communities differs among four molecular characterization methods. Soil Biology and Biochemistry **96:** 160-168
28. **Duran BEL, Duncan DS, Oates LG, Kucharik CJ, Jackson RD** (2016) Nitrogen fertilization effects on productivity and nitrogen loss in three grass-based perennial bioenergy cropping systems. PLOS ONE **11:** e0151919
29. **Ferris AM, Rothamer DA** (2016) Methodology for the experimental measurement of vapor-liquid equilibrium distillation curves using a modified ASTM D86 setup. Fuel **182:** 467-479
30. **Fox AF, Kim TN, Bahlai CA, Woltz JM, Gratton C, Landis DA** (2016) Cover crops have neutral effects on predator communities and biological control services in annual cellulosic bioenergy cropping systems. Agriculture, Ecosystems & Environment **232:** 101-109
31. **Garoutte A, Cardenas E, Tiedje J, Howe A** (2016) Methodologies for probing the metatranscriptome of grassland soil. Journal of Microbiological Methods **131:** 122-129
32. **Geertsema W, Rossing WAH, Landis DA, Bianchi FJJA, van Rijn PCJ, Schaminée JHJ, Tscharntke T, van der Werf W** (2016) Actionable knowledge for ecological intensification of agriculture. Frontiers in Ecology and the Environment **14:** 209-216
33. **Gelfand I, Shcherbak I, Millar N, Kravchenko AN, Robertson GP** (2016) Long-term nitrous oxide fluxes in annual and perennial agricultural and unmanaged ecosystems in the upper Midwest USA. Global Change Biology **22:** 3594-3607
34. **Ghosh IN, Landick R** (2016) OptSSeq: high-throughput sequencing readout of growth enrichment defines optimal gene expression elements for homoethanologenesis. ACS Synthetic Biology **5:** 1519-1534
35. **Guo J, Cole JR, Zhang Q, Brown CT, Tiedje JM** (2016) Microbial community analysis with ribosomal gene fragments from shotgun metagenomes. Applied and Environmental Microbiology **82:** 157-166
36. **Ha CM, Escamilla-Trevino L, Serrani Yarce JC, Kim H, Ralph J, Chen F, Dixon RA** (2016) An essential role of caffeoyl shikimate esterase in monolignol biosynthesis in *Medicago truncatula*. The Plant Journal **86:** 363-375
37. **Han J, Chen J, Miao Y, Wan S** (2016) Multiple resource use efficiency (mRUE): a new concept for ecosystem production. Scientific Reports **6:** 37453
38. **Hao X, Thelen K, Gao J** (2016) Spatial variability in biomass yield of switchgrass, native prairie, and corn at field scale. Agronomy Journal **108:** 548-558
39. **Harman-Ware AE, Foster C, Happs RM, Doeppke C, Meunier K, Gehan J, Yue F, Lu F, Davis M** (2016) Quantitative analysis of lignin monomers by a thioacidolysis method tailored for higher-throughput analysis. Biotechnology Journal **11:** 1268-1273
40. **Helmich KE, Pereira JH, Gall DL, Heins RA, McAndrew RP, Bingman C, Deng K, Holland KC, Noguera DR, Simmons BA, Sale KL, Ralph J, Donohue TJ, Adams PD, Phillips GN, Jr.** (2016) Structural basis of stereospecificity in the bacterial enzymatic cleavage of β-aryl ether bonds in lignin. Journal of Biological Chemistry **291:** 5234-5246
41. **Hirsch CN, Hirsch CD, Brohammer AB, Bowman MJ, Soifer I, Barad O, Shem-Tov D, Baruch K, Lu F, Hernandez AG, Fields CJ, Wright CL, Koehler K, Springer NM, Buckler E, Buell CR, de Leon N, Kaeppler SM, Childs KL, Mikel MA** (2016) Draft assembly of elite inbred line PH207 provides insights into genomic and transcriptome diversity in maize. The Plant Cell **28:** 2700-2714
42. **Horn PJ, Benning C** (2016) The plant lipidome in human and environmental health. Science **353:** 1228-1232
43. **Horn PJ, Liu J, Cocuron J-C, McGlew K, Thrower NA, Larson M, Lu C, Alonso AP, Ohlrogge J** (2016) Identification of multiple lipid genes with modifications in expression and sequence associated with the evolution of hydroxy fatty acid accumulation in *Physaria fendleri*. The Plant Journal **86:** 322-348

44. **Jin M, da Costa Sousa L, Schwartz C, He Y, Sarks C, Gunawan C, Balan V, Dale BE** (2016) Toward lower cost cellulosic biofuel production using ammonia based pretreatment technologies. Green Chemistry **18:** 957-966
45. **Kang J-H, Campos ML, Zemelis-Durfee S, Al-Haddad JM, Jones A, Daniel, Telewski FW, Brandizzi F, Howe GA** (2016) Molecular cloning of the tomato Hairless gene implicates actin dynamics in trichome-mediated defense and mechanical properties of stem tissue. Journal of Experimental Botany **67:** 5313-5324
46. **Karlen SD, Zhang C, Peck ML, Smith RA, Padmakshan D, Helmich KE, Free HCA, Lee S, Smith BG, Lu F, Sedbrook JC, Sibout R, Grabber JH, Runge TM, Mysore KS, Harris PJ, Bartley LE, Ralph J** (2016) Monolignol-ferulate conjugates are naturally incorporated into plant lignins. Science Advances **2:** e1600393
47. **Khadempour L, Burnum-Johnson KE, Baker ES, Nicora CD, Webb-Robertson B-JM, White RA, Monroe ME, Huang EL, Smith RD, Currie CR** (2016) The fungal cultivar of leaf-cutter ants produces specific enzymes in response to different plant substrates. Molecular Ecology **25:** 5795-5805
48. **Kim S, Dale BE** (2016) A distributed cellulosic biorefinery system in the US Midwest based on corn stover. Biofuels, Bioproducts and Biorefining **10:** 819-832
49. **Kim S-J, Brandizzi F** (2016) The plant secretory pathway for the trafficking of cell wall polysaccharides and glycoproteins. Glycobiology **26:** 940-949
50. **Kong L, Sen SM, Henao CA, Dumesic JA, Maravelias CT** (2016) A superstructure-based framework for simultaneous process synthesis, heat integration, and utility plant design. Computers & Chemical Engineering **91:** 68-84
51. **Kuang MC, Hutchins PD, Russell JD, Coon JJ, Hittinger CT** (2016) Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. eLife **5:** e19027
52. **Kumar R, Singh S, Balan V** (2016) Valorization of lignocellulosic biomass in a biorefinery: from logistics to environmental and performance impact. Nova Publishers
53. **Lacroix C, Renner K, Cole E, Seabloom EW, Borer ET, Malmstrom CM** (2016) Methodological guidelines for accurate detection of viruses in wild plant species. Applied and Environmental Microbiology **82:** 1966-1975
54. **Lan W, Morreel K, Lu F, Rencoret J, Carlos Del Rio J, Voorend W, Vermerris W, Boerjan W, Ralph J** (2016) Maize tricin-oligolignol metabolites and their implications for monocot lignification. Plant Physiology **171:** 810-820
55. **Lan W, Rencoret J, Lu F, Karlen SD, Smith BG, Harris PJ, del Rio JC, Ralph J** (2016) Tricin-lignins: occurrence and quantitation of tricin in relation to phylogeny. The Plant Journal **88:** 1046-1057
56. **Leducq J-B, Nielly-Thibault L, Charron G, Eberlein C, Verta J-P, Samani P, Sylvester K, Hittinger CT, Bell G, Landry CR** (2016) Speciation driven by hybridization and chromosomal plasticity in a wild yeast. Nature Microbiology **1:** 15003
57. **Lewin GR, Carlos C, Chevrette MG, Horn HA, McDonald BR, Stankey RJ, Fox BG, Currie CR** (2016) Evolution and ecology of *Actinobacteria* and their bioenergy applications. Annual Review of Microbiology **70:** 235-254
58. **Lewin GR, Johnson AL, Soto RD, Perry K, Book AJ, Horn HA, Pinto-Tomas AA, Currie CR** (2016) Cellulose-enriched microbial communities from leaf-cutter ant (*Atta colombica*) refuse dumps vary in taxonomic composition and degradation ability. PLOS ONE **11:** e0151840
59. **Liang C, da C. Jesus E, Duncan DS, Quensen JF, Jackson RD, Balser TC, Tiedje JM** (2016) Switchgrass rhizospheres stimulate microbial biomass but deplete microbial necromass in agricultural soils of the upper Midwest, USA. Soil Biology and Biochemistry **94:** 173-180
60. **Liang C, Kao-Kniffin J, Sanford GR, Wickings K, Balser TC, Jackson RD** (2016) Microorganisms and their residues under restored perennial grassland communities of varying diversity. Soil Biology and Biochemistry **103:** 192-200

61. **Lopes MR, Morais CG, Kominek J, Cadete RM, Soares MA, Uetanabaro APT, Fonseca C, Lachance M-A, Hittinger CT, Rosa CA** (2016) Genomic analysis and D-xylose fermentation of three novel *Spathaspora* species: *Spathaspora girioi* sp. nov., *Spathaspora Hagerdaliae f*. a., sp. nov. and *Spathaspora gorwiae* f. a., sp. nov. FEMS Yeast Research **16:** fw044

62. **Luo D, Callari R, Hamberger B, Wubshet SG, Nielsen MT, Andersen-Ranberg J, Hallstrom BM, Cozzi F, Heider H, Møller BL, Staerk D, Hamberger B** (2016) Oxidation and cyclization of casbene in the biosynthesis of *Euphorbia* factors from mature seeds of *Euphorbia lathyris* L. Proceedings of the National Academy of Sciences of the United States of America **113:** E5082-E5089

63. **Ma W, Kong Q, Mantyla JJ, Yang Y, Ohlrogge JB, Benning C** (2016) 14-3-3 protein mediates plant seed oil biosynthesis through interaction with AtWRI1. The Plant Journal **88:** 228-235

64. **McAndrew RP, Sathitsuksanoh N, Mbughuni MM, Heins RA, Pereira JH, George A, Sale KL, Fox BG, Simmons BA, Adams PD** (2016) Structure and mechanism of NOV1, a resveratrol-cleaving dioxygenase. Proceedings of the National Academy of Sciences **113:** 14324-14329

65. **McCormick RF, Truong SK, Mullet JE** (2016) 3D sorghum reconstructions from depth images identify QTL regulating shoot architecture. Plant Physiology **172:** 823-834

66. **McDaniel MD, Grandy AS, Tiemann LK, Weintraub MN** (2016) Eleven years of crop diversification alters decomposition dynamics of litter mixtures incubated with soil. Ecosphere **7:** e01426

67. **McIlwain SJ, Peris D, Sardi M, Moskvin OV, Zhan F, Myers KS, Riley NM, Buzzell A, Parreiras LS, Ong IM, Landick R, Coon JJ, Gasch AP, Sato TK, Hittinger CT** (2016) Genome sequence and analysis of a stress-tolerant, wild-derived strain of *Saccharomyces cerevisiae* used in biofuels research. G3: Genes | Genomes | Genetics **6:** 1757-1766

68. **McKinley B, Rooney W, Wilkerson C, Mullet J** (2016) Dynamics of biomass partitioning, stem gene expression, cell wall biosynthesis, and sucrose accumulation during development of *Sorghum bicolor*. The Plant Journal **88:** 662-680

69. **Montella S, Balan V, da Costa Sousa L, Gunawan C, Giacobbe S, Pepe O, Faraco V** (2016) Saccharification of newspaper waste after ammonia fiber expansion or extractive ammonia. AMB Express **6:** 18

70. **Motagamwala AH, Won W, Maravelias CT, Dumesic JA** (2016) An engineered solvent system for sugar production from lignocellulosic biomass using biomass derived γ-valerolactone. Green Chemistry **18:** 5756-5763

71. **Mottiar Y, Vanholme R, Boerjan W, Ralph J, Mansfield SD** (2016) Designer lignins: harnessing the plasticity of lignification. Current Opinion in Biotechnology **37:** 190-200

72. **Ng RTL, Maravelias CT** (2016) Design of cellulosic ethanol supply chains with regional depots. Industrial and Engineering Chemistry Research **55:** 3420-3432

73. **Oates LG, Duncan DS, Gelfand I, Millar N, Robertson GP, Jackson RD** (2016) Nitrous oxide emissions during establishment of eight alternative cellulosic bioenergy cropping systems in the North Central United States. Global Change Biology – Bioenergy **8:** 539-549

74. **Oates LG, Duncan DS, Sanford GR, Liang C, Jackson RD** (2016) Bioenergy cropping systems that incorporate native grasses stimulate growth of plant-associated soil microbes in the absence of nitrogen fertilization. Agriculture, Ecosystems & Environment **233:** 396-403

75. **Ong RG, Higbee A, Bottoms S, Dickinson Q, Xie D, Smith SA, Serate J, Pohlmann E, Jones AD, Coon JJ, Sato TK, Sanford GR, Eilert D, Oates LG, Piotrowski JS, Bates DM, Cavalier D, Zhang Y** (2016) Inhibition of microbial biofuel production in drought-stressed switchgrass hydrolysate. Biotechnology for Biofuels **9:** 237

76. **Pauly M, Keegstra K** (2016) Biosynthesis of the plant cell wall matrix polysaccharide xyloglucan. Annual Review of Plant Biology **67:** 235-259

77. **Paustian K, Lehmann J, Ogle S, Reay D, Robertson GP, Smith P** (2016) Climate-smart soils. Nature **532:** 49-57

78. **Pereira JH, Heins RA, Gall DL, McAndrew RP, Deng K, Holland KC, Donohue TJ, Noguera DR, Simmons BA, Sale KL, Ralph J, Adams PD** (2016) Structural and biochemical characterization of the early and late enzymes in the lignin β-aryl ether cleavage pathway from *Sphingobium* sp SYK-6. The Journal of Biological Chemistry **291:** 10228-10238
79. **Perez-Pimienta JA, Flores-Gomez CA, Ruiz HcA, Sathitsuksanoh N, Balan V, da Costa Sousa L, Dale BE, Singh S, Simmons BA** (2016) Evaluation of agave bagasse recalcitrance using AFEX™, autohydrolysis, and ionic liquid pretreatments. Bioresource Technology **211:** 216-223
80. **Peris D, Langdon Q, Moriarty RV, Sylvester K, Bontrager M, Charron G, LeDuc J-B, Landry CR, Libkind D, Hittinger CT** (2016) Complex ancestries of lager-brewing hybrids were shaped by standing variation in the wild yeast *Saccharomyces eubayanus*. PLOS Genetics **12:** e1006155
81. **Petrik DL, Cass CL, Padmakshan D, Foster CE, Vogel JP, Karlen SD, Ralph J, Sedbrook JC** (2016) *BdCESA7*, *BdCESA8*, and *BdPMT* utility promoter constructs for targeted expression to secondary cell-wall-forming cells of grasses. Frontiers in Plant Science **7:** 55
82. **Poovaiah CR, Bewg WP, Lan W, Ralph J, Coleman HD** (2016) Sugarcane transgenics expressing MYB transcription factors show improved glucose release. Biotechnology for Biofuels **9:** 143
83. **Ramstein GP, Evans J, Kaeppler SM, Mitchell RB, Vogel KP, Buell CR, Casler MD** (2016) Accuracy of genomic prediction in switchgrass (*Panicum virgatum* L.) improved by accounting for linkage disequilibrium. G3: Genes | Genomes | Genetics **6:** 1049-1062
84. **Rencoret J, del Río JC, Nierop KGJ, Gutiérrez A, Ralph J** (2016) Rapid Py-GC/MS assessment of the structural alterations of lignins in genetically modified plants. Journal of Analytical and Applied Pyrolysis **121:** 155-165
85. **Riley R, Haridas S, Wolfe KH, Lopes MR, Hittinger CT, Goker M, Salamov AA, Wisecaver JH, Long TM, Calvey CH, Aerts AL, Barry KW, Choi C, Clum A, Coughlan AY, Deshpande S, Douglass AP, Hanson SJ, Klenk H-P, LaButti KM, Lapidus A, Lindquist EA, Lipzen AM, Meier-Kolthoff JP, Ohm RA, Otillar RP, Pangilinan JL, Peng Y, Rokas A, Rosa CA, Scheuner C, Sibirny AA, Slot JC, Stielow JB, Sun H, Kurtzman CP, Blackwell M, Grigoriev IV, Jeffries TW** (2016) Comparative genomics of biotechnologically important yeasts. Proceedings of the National Academy of Sciences of the United States of America **113:** 9882-9887
86. **Rinaldi R, Jastrzebski R, Clough MT, Ralph J, Kennema M, Bruijnincx PCA, Weckhuysen BM** (2016) Paving the way for lignin valorisation: Recent advances in bioengineering, biorefining and catalysis. Angewandte Chemie (International Edition) **55:** 8164-8125
87. **Rinaldi R, Jastrzebski R, Clough MT, Ralph J, Kennema M, Bruijnincx PCA, Weckhuysen BM** (2016) Wege zur verwertung von lignin: Fortschritte in der biotechnik, der bioraffination und der katalyse. Angewandte Chemie **128:** 8296-8354
88. **Ro I, Sener C, Stadelman TM, Ball MR, Venegas JM, Burt SP, Hermans I, Dumesic JA, Huber GW** (2016) Measurement of intrinsic catalytic activity of Pt monometallic and Pt-MoO_x interfacial sites over visible light enhanced $PtMoO_x/SiO_2$ catalyst in reverse water gas shift reaction. Journal of Catalysis **344:** 784-794
89. **Ruan L, Bhardwaj AK, Hamilton SK, Robertson GP** (2016) Nitrogen fertilization challenges the climate benefit of cellulosic biofuels. Environmental Research Letters **11:** 064007
90. **Sanford GR, Oates LG, Jasrotia P, Thelen KD, Robertson GP, Jackson RD** (2016) Comparative productivity of alternative cellulosic bioenergy cropping systems in the North Central USA. Agriculture, Ecosystems & Environment **216:** 344-355
91. **Sardi M, Rovinskiy N, Zhang Y, Gasch AP** (2016) Leveraging genetic background effects in *Saccharomyces cerevisiae* to improve lignocellulosic hydrolysate tolerance. Applied and Environmental Microbiology **82:** 5838-5849

92. **Sarks C, Bals BD, Wynn J, Teymouri F, Schwegmann S, Sanders K, Jin M, Balan V, Dale BE** (2016) Scaling up and benchmarking of ethanol production from pelletized pilot scale AFEX treated corn stover using *Zymomonas mobilis* 8b. Biofuels **7:** 253-262
93. **Sarks C, Higbee A, Piotrowski J, Xue S, Coon JJ, Sato TK, Jin M, Balan V, Dale BE** (2016) Quantifying pretreatment degradation compounds in solution and accumulated by cells during solids and yeast recycling in the Rapid Bioconversion with Integrated recycling Technology process using AFEX™ corn stover. Bioresource Technology **205:** 24-33
94. **Sato TK, Tremaine M, Parreiras LS, Hebert AS, Myers KS, Higbee AJ, Sardi M, McIlwain SJ, Ong IM, Breuer RJ, Narasimhan RA, McGee MA, Dickinson Q, La Reau A, Xie D, Tian M, Piotrowski JS, Reed JL, Zhang Y, Coon JJ, Hittinger CT, Gasch AP, Landick R** (2016) Directed evolution reveals unexpected epistatic interactions that alter metabolic regulation and enable anaerobic xylose use by *Saccharomyces cerevisiae*. PLOS Genetics **12:** e1006372
95. **Schwartz TJ, Lyman SD, Motagamwala AH, Mellmer MA, Dumesic JA** (2016) Selective hydrogenation of unsaturated carbon-carbon bonds in aromatic-containing platform molecules. ACS Catalysis **6:** 2047-2054
96. **Sekhon RS, Breitzman MW, Silva RR, Santoro N, Rooney WL, De Leon N, Kaeppler SM** (2016) Stover composition in maize and sorghum reveals remarkable genetic variation and plasticity for carbohydrate accumulation. Frontiers in Plant Science **7:** 822
97. **Sener C, Wesley TS, Alba-Rubio AC, Kumbhalkar MD, Hakim SH, Riberio FH, Miller JT, Dumesic JA** (2016) PtMo bimetallic catalysts synthesized by controlled surface reactions for water gas shift. ACS Catalysis **6:** 1334-1344
98. **Shade A** (2016) Diversity is the question, not the answer. ISME Journal **11:** 1-6
99. **Shen X-X, Zhou X, Kominek J, Kurtzman CP, Hittinger CT, Rokas A** (2016) Reconstructing the backbone of the Saccharomycotina yeast phylogeny using genome-scale data. G3: Genes | Genomes | Genetics **6:** 3927-3939
100. **Shuai L, Amiri MT, Questell-Santiago YM, Héroguel F, Li Y, Kim H, Meilan R, Chapple C, Ralph J, Luterbacher JS** (2016) Formaldehyde stabilization facilitates lignin monomer production during biomass depolymerization. Science **354:** 329-333
101. **Simpson JP, Ohlrogge JB** (2016) A novel pathway for triacylglycerol biosynthesis is responsible for the accumulation of massive quantities of glycerolipids in the surface wax of Bayberry (*Myrica pensylvanica*) fruit. The Plant Cell **28:** 248-264
102. **Simpson JP, Thrower N, Ohlrogge JB** (2016) How did nature engineer the highest surface lipid accumulation among plants? Exceptional expression of acyl-lipid-associated genes for the assembly of extracellular triacylglycerol by Bayberry (*Myrica pensylvanica*) fruits. Biochimica et Biophysica Acta (BBA) - Molecular and Cell Biology of Lipids **1861:** 1243-1252
103. **Skevas T, Swinton SM, Tanner S, Sanford G, Thelen KD** (2016) Investment risks in bioenergy crops. Global Change Biology – Bioenergy **8:** 1162-1177
104. **Slininger PJ, Shea-Andersh MA, Thompson SR, Dien BS, Kurtzman CP, da Costa Sousa L, Balan V** (2016) Techniques for the evolution of robust pentose-fermenting yeast for bioconversion of lignocellulose to ethanol. Journal of Visualized Experiments **e54227:** 1-15
105. **Spero MA, Brickner JR, Mollet JT, Pisithkul T, Amador-Noguez D, Donohue TJ** (2016) Different functions of phylogenetically distinct bacterial complex I isozymes. Journal of Bacteriology **198:** 1268-1280
106. **Spero MA, Imam S, Noguera DR, Donohue TJ** (2016) Electron partitioning in anoxic phototrophic bacteria. *In* W. A. Cramer, T. Kallas, eds, Cytochrome Complexes: Evolution, Structures, Energy Transduction, and Signaling, Vol 41. Springer Verlag, pp 679-700
107. **Stahlheber KA, Watson B, Dickson TL, Disney R, Gross KL** (2016) Balancing biofuel production and biodiversity: Harvesting frequency effects on production and community composition in planted tallgrass prairie. Biomass and Bioenergy **92:** 98-105

108. **Stefely JA, Kwiecien NW, Freiberger EC, Richards AL, Jochem A, Rush MJP, Ulbrich A, Robinson KP, Hutchins PD, Veling MT, Guo X, Kemmerer ZA, Connors KJ, Trujillo EA, Sokol J, Marx H, Westphall MS, Hebert AS, Pagliarini DJ, Coon JJ** (2016) Mitochondrial protein functions elucidated by multi-omic mass spectrometry profiling. Nature Biotechnology **34:** 1191-1197

109. **Tumbalam P, Hard K, Thelen KD** (2016) Integrating winter annual cereal rye or triticale into a corn forage biofuel production system. Journal of Crop Improvement **30:** 526-540

110. **Tumbalam P, Thelen KD, Adkins A, Dale B, Balan V, Gunawan C, Gao J** (2016) Corn stover ethanol yield as affected by grain yield, Bt trait, and environment. Biomass and Bioenergy **85:** 119-125

111. **Vinay-Lara E, Wang S, Bai L, Phrommao E, Broadbent JR, Steele JL** (2016) *Lactobacillus casei* as a biocatalyst for biofuel production. Journal of Industrial Microbiology and Biotechnology **43:** 1205-1213

112. **Walker AM, Sattler SA, Regner M, Jones JP, Ralph J, Vermerris W, Sattler SE, Kang C** (2016) The structure and catalytic mechanism of *Sorghum bicolor* caffeoyl-CoA *O*-methyltransferase. Plant Physiology **172:** 78-92

113. **Wenninger A, Kim T, Spiesman B, Gratton C** (2016) Contrasting foraging patterns: testing resource-concentration and dilution effects with pollinators and seed predators. Insects **7:** 23

114. **Weraduwage SM, Kim S-J, Renna L, Anozie FC, Sharkey TD, Brandizzi F** (2016) Pectin methylesterification impacts the relationship between photosynthesis and plant growth. Plant Physiology **171:** 833-848

115. **Wisecaver JH, Alexander WG, King SB, Hittinger CT, Rokas A** (2016) Dynamic evolution of nitric oxide detoxifying flavohemoglobins, a family of single-protein metabolic modules in bacteria and eukaryotes. Molecular Biology and Evolution **33:** 1979-1987

116. **Woods DP, McKeown MA, Dong Y, Preston JC, Amasino RM** (2016) Evolution of *VRN2/Ghd7*-like genes in vernalization-mediated repression of grass flowering. Plant Physiology **170:** 2124-2135

117. **Wu W, Henao CA, Maravelias CT** (2016) A superstructure representation, generation, and modeling framework for chemical process synthesis. American Institute of Chemical Engineers Journal **62:** 3199-3214

118. **Xue C, Penton CR, Zhang B, Zhao M, Rothstein DE, Mladenoff DJ, Forrester JA, Shen Q, Tiedje JM** (2016) Soil fungal and bacterial responses to conversion of open land to short rotation woody biomass crops. Global Change Biology – Bioenergy **8:** 723-736

119. **Yang S, Fei Q, Zhang Y, Contreras LM, Utturkar SM, Brown SD, Himmel ME, Zhang M** (2016) *Zymomonas mobilis* as a model system for production of biofuels and biochemicals. Microbial Biotechnology **9:** 199-717

120. **Yelle DJ, Ralph J** (2016) Characterizing phenol–formaldehyde adhesive cure chemistry within the wood cell wall. International Journal of Adhesion & Adhesives **70:** 26-36

121. **Yoo CG, Kim H, Lu F, Azarpira A, Pan X, Oh KK, Kim JS, Ralph J, Kim TH** (2016) Understanding the physicochemical characteristics and the improved enzymatic saccharification of corn stover pretreated with aqueous and gaseous ammonia. BioEnergy Research **9:** 67-76

122. **Yue F, Lu F, Ralph S, Ralph J** (2016) Identification of 4-O-5-units in softwood lignins via definitive lignin models and NMR. Biomacromolecules **17:** 1909-1920

123. **Zenone T, Zona D, Gelfand I, Gielen B, Camino-Serrano M, Ceulemans R** (2016) CO_2 uptake is offset by CH_4 and N_2O emissions in a poplar short-rotation coppice. Global Change Biology – Bioenergy **8:** 524-538

124. **Zhang M, Cao X, Jia Q, Ohlrogge J** (2016) *FUSCA3* activates triacylglycerol accumulation in Arabidopsis seedlings and tobacco BY2 cells. The Plant Journal **88:** 95-107

125. **Zhou X, Peris D, Kominek J, Kurtzman CP, Hittinger CT, Rokas A** (2016) *In silico* whole genome sequencer and analyzer (iWGS): a computational pipeline to guide the design and analysis of *de novo* genome sequencing studies. G3: Genes | Genomes | Genetics **6:** 3655-3662

126. **Zienkiewicz K, Du Z-Y, Ma W, Vollheyde K, Benning C** (2016) Stress-induced neutral lipid biosynthesis in microalgae—Molecular, cellular and physiological insights. Biochimica et Biophysica Acta (BBA) - Molecular and Cell Biology of Lipids **1861:** 1269-1281

2017

1. **Adamczyk PA, Reed JL** (2017) *Escherichia coli* as a model organism for systems metabolic engineering. Current Opnion in Systems Biology **6:** 80-88
2. **Alameldin H, Izadi-Darbandi A, Smith SA, Balan V, Jones AD, Sticklen M** (2017) Production of seed-like storage lipids and increase in oil bodies in corn (Maize; *Zea mays* L.) vegetative biomass. Industrial Crops and Products **108:** 526-534
3. **Alonso DM, Hakim S, Zhou S, Won W, Hosseinaei O, Tao J, Garcia-Negron V, Motagamwala AH, Mellmer MA, Huang K, Houtman CJ, Labbe N, Harper DP, Maravelias C, Runge T, Dumesic JA** (2017) Increasing the revenue from lignocellulosic biomass: maximizing feedstock utilization. Science Advances **3:** e1603301
4. **Anderson W, Apweiler R, Bateman A, Bauer GA, Berman H, Blake JA, Blomberg N, Burley SK, Cochrane G, Di Francesco V, Donohue TJ, Durinx C, Game A, Green E, Gojobori T, Goodhand P, Hamosh A, Hermjakob H, Kanehisa M, Kiley R, McEntyre J, McKibbin R, Miyano S, Pauly B, Perrimon N, Ragan MA, Richards G, Teo Y-Y, Westerfield M, Westhof E, Lasko PF** (2017) Towards coordinated international support of core data resources for the life sciences. BioRxiv **10.1101/110825**
5. **Angelos E, Ruberti C, Kim S-J, Brandizzi F** (2017) Maintaining the factory: the roles of the unfolded protein response in cellular homeostasis in plants. The Plant Journal **90:** 671-682
6. **Austin EE, Wickings K, McDaniel MD, Robertson GP, Grandy AS** (2017) Cover crop root contributions to soil carbon in a no-till corn bioenergy cropping system. Global Change Biology – Bioenergy **9:** 1252-1263
7. **Bouché F, Woods DP, Amasino RM** (2017) Winter memory throughout the plant kingdom: different paths to flowering. Plant Physiology **173:** 27-35
8. **Burger BT, Imam S, Scarborough MJ, Noguera DR, Donohue TJ** (2017) Combining genome-scale experimental and computational methods to identify essential genes in *Rhodobacter sphaeroides*. mSystems **2:** e00015-00017
9. **Chundawat SPS, Uppugundla N, Gao D, Curran PG, Balan V, Dale BE** (2017) Shotgun approach to increasing enzymatic saccharification yields of ammonia fiber expansion pretreated cellulosic biomass. Frontiers in Energy Research **5:** 9
10. **Cronin KR, Runge TM, Zhang X, Izaurralde RC, Reinemann DJ, Sinistore JC** (2017) Spatially explicit life cycle analysis of cellulosic ethanol production scenarios in Southwestern Michigan. BioEnergy Research **10:** 13-25
11. **Cui L, Liang C, Duncan DS, Bao X, Xie H, He H, Wickings K, Zhang X, Chen F** (2017) Impacts of vegetation type and climatic zone on neutral sugar distribution in natural forest soils. Geoderma **282:** 139-146
12. **Dale B** (2017) A sober view of the difficulties in scaling cellulosic biofuels. Biofuels, Bioproducts and Biorefining **11:** 5-7
13. **del Río JC, Rencoret J, Gutiérrez A, Kim H, Ralph J** (2017) Hydroxystilbenes are monomers in palm fruit endocarp lignins. Plant Physiology **174:** 2072-2082
14. **Dulys-Nusbaum E** (2017) Timber residue supply for bioenergy in the northern tier of the Great Lakes: determinants and availability. Michigan State University, East Lansing, MI
15. **Eloy NB, Voorend W, Lan W, de Lyra Soriano Saleme M, Cesarino I, Vanholme R, Smith RA, Goeminne G, Pallidis A, Morreel K, Nicomedes Jr. J, Ralph J, Boerjan W** (2017) Silencing *CHALCONE SYNTHASE* in maize impedes the incorporation of tricin into lignin and increases lignin content. Plant Physiology **173:** 998-1016
16. **Emery SM, Reid ML, Bell-Dereske L, Gross KL** (2017) Soil mycorrhizal and nematode diversity vary in response to bioenergy crop identity and fertilization. Global Change Biology – Bioenergy **9:** 1644-1656

17. **Forman V, Callari R, Folly C, Heider H, Hamberger B** (2017) Production of putative diterpene carboxylic acid intermediates of triptolide in yeast. Molecules **22:** 981
18. **Gage JL, Miller ND, Spalding EP, Kaeppler SM, de Leon N** (2017) TIPS: a system for automated image-based phenotyping of maize tassels. Plant Methods **13:** 21
19. **Gall DL, Ralph J, Donohue TJ, Noguera DR** (2017) Biochemical transformation of lignin for deriving valued commodities from lignocellulose. Current Opinion in Biotechnology **45:** 120-126
20. **Gasch AP, Yu FB, Hose J, Escalante LE, Place M, Bacher R, Kanbar J, Ciobanu D, Sandor L, Grigoriev IV, Kendziorski C, Quake SR, McClean MN** (2017) Single-cell RNA sequencing reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. PLOS Biology **15:** e2004050
21. **Gibson B, Geertman J-MA, Hittinger CT, Krogerus K, Libkind D, Louis EJ, Magalhães F, Sampaio JP** (2017) New yeasts - new brews: modern approaches to brewing yeast design and development. FEMS Yeast Research **17:** fox038
22. **Gontang EA, Aylward FO, Carlos C, Glavina del Rio T, Chovatia M, Fern A, Lo C-C, Malfatti SA, Tringe SG, Currie CR, Kolter R** (2017) Major changes in microbial diversity and community composition across gut sections of a juvenile *Panchlora* cockroach. PLOS ONE **12:** e0177189
23. **Gonzales-Vigil E, Hefer CA, von Loessl ME, La Mantia J, Mansfield SD** (2017) Exploiting natural variation to uncover an alkene biosynthetic enzyme in poplar. The Plant Cell **29:** 2000-2015
24. **Grabowski PP, Evans J, Daum C, Deshpande S, Barry KW, Kennedy M, Ramstein G, Kaeppler SM, Buell CR, Jiang Y, Casler MD** (2017) Genome-wide associations with flowering time in switchgrass using exome-capture sequencing data. New Phytologist **213:** 154-169
25. **Groendyk MA, Rothamer DA** (2017) Effect of increased fuel volatility on CDC operation in a light-duty CIDI engine. Fuel **194:** 195-210
26. **Gunawan C, Xue S, Pattathil S, da Costa Sousa L, Dale BE, Balan V** (2017) Comprehensive characterization of non-cellulosic recalcitrant cell wall carbohydrates in unhydrolyzed solids from AFEX-pretreated corn stover. Biotechnology for Biofuels **10:** 82
27. **Gurr GM, Wratten SD, Landis DA, You M** (2017) Habitat management to suppress pest populations: progress and prospects. Annual Review of Entomology **62:** 91-109
28. **Haase MAB, Kominek J, Langdon QK, Kurtzman CP, Hittinger CT** (2017) Genome sequence and physiological analysis of *Yamadazyma laniorum* f.a. sp. nov. and a reevaluation of the apocryphal xylose fermentation of its sister species *Candida tenuis*. FEMS Yeast Research **17:** fox019
29. **Hansen NL, Heskes AM, Hamberger B, Olsen CE, Hallström BM, Andersen-Ranberg J, Hamberger B** (2017) The terpene synthase gene family in *Tripterygium wilfordii* harbors a labdane-type diterpene synthase among the monoterpene synthase TPS-b subfamily. The Plant Journal **89:** 429-441
30. **Hansen NL, Nissen JN, Hamberger B** (2017) Two residues determine the product profile of the class II diterpene synthases TPS14 and TPS21 of *Tripterygium wilfordii*. Phytochemistry **138:** 52-56
31. **Hilley JL, Weers BD, Truong SK, McCormick RF, Mattison AJ, McKinley BA, Morishige DT, Mullet JE** (2017) Sorghum *Dw2* encodes a protein kinase regulator of stem internode length. Scientific Reports **7:** 4616
32. **Hittinger CT, Steele JL, Ryder DS** (2017) Diverse yeasts for diverse fermented beverages and foods. Current Opinion in Biotechnology **49:** 199-206
33. **Izaurralde RC, McGill WB, Williams JR, Jones CD, Link RP, Manowitz DH, Schwab DE, Zhang X, Robertson GP, Millar N** (2017) Simulating microbial denitrification with EPIC: model description and evaluation. Ecological Modeling **359:** 349-362
34. **Jakubowski AR, Casler MD, Jackson RD** (2017) Legume addition to perennial warm-season grass swards increases harvested biomass. Crop Science **57:** 3343-3351
35. **Jakubowski AR, Jackson RD, Casler MD** (2017) Can biomass yield of switchgrass be increased without increasing nitrogen requirements? Crop Science **57:** 2024-2031

36. **Jean M, Pennington D, Quigley M, Thelen K** (2017) Improving biomass and ethanol yield by intercropping a winter cereal with corn. Agronomy Journal **109:** 2530-2536

37. **Jensen A, Cabrera Y, Hsieh C-W, Nielsen J, Ralph J, Felby C** (2017) 2D NMR characterization of wheat straw residual lignin after dilute acid pretreatment with different severities. Holzforschung **71:** 461-469

38. **Jensen JK, Wilkerson CG** (2017) Brachypodium as an experimental system for the study of stem parenchyma biology in grasses. PLOS ONE **12:** e0173095

39. **Jin M, Liu Y, da Costa Sousa L, Dale BE, Balan V** (2017) Development of rapid bioconversion with integrated recycle technology for ethanol production from extractive ammonia pretreated corn stover. Biotechnology and Bioengineering **114:** 1713-1720

40. **Jin M, Sarks C, Bals BD, Posawatz N, Gunawan C, Dale BE, Balan V** (2017) Toward high solids loading process for lignocellulosic biofuel production at low cost. Biotechnology and Bioengineering **114:** 980-989

41. **Johnson AM, Kim H, Ralph J, Mansfield SD** (2017) Natural acetylation impacts carbohydrate recovery during deconstruction of *Populus trichocarpa* wood. Biotechnology for Biofuels **10:** 48

42. **Johnson RL, Hanrahan MP, Mellmer M, Dumesic JA, Rossini AJ, Shanks BH** (2017) Solvent-solid interface of acid catalysts studied by high resolution MAS NMR. The Journal of Physical Chemistry C **121:** 17226-17234

43. **Jones CD, Zhang X, Reddy AD, Robertson GP, Izaurralde RC** (2017) The greenhouse gas intensity and potential biofuel production capacity of maize stover harvest in the US Midwest. Global Change Biology – Bioenergy **9:** 1543-1554

44. **Jun S-Y, Walker AM, Kim H, Ralph J, Vermerris W, Sattler SE, Kang C** (2017) The enzyme activity and substrate specificity of two major cinnamyl alcohol dehydrogenases in sorghum (*Sorghum bicolor*), SbCAD2 and SbCAD4. Plant Physiology **174:** 2128-2145

45. **Karlen SD, Smith RA, Kim H, Padmakshan D, Bartuce A, Mobley JK, Free HCA, Smith BG, Harris PJ, Ralph J** (2017) Highly decorated lignins in leaf tissues of the Canary Island date palm *Phoenix canariensis*. Plant Physiology **175:** 1058-1067

46. **Kebrom TH, McKinley B, Mullet JE** (2017) Dynamics of gene expression during development and expansion of vegetative stem internodes of bioenergy sorghum. Biotechnology for Biofuels **10:** 159

47. **Kim H, Padmakshan D, Li Y, Rencoret J, Hatfield RD, Ralph J** (2017) Characterization and elimination of undesirable protein residues in plant cell wall materials for enhancing lignin analysis by solution-state nuclear magnetic resonance spectroscopy. Biomacromolecules **18:** 4184-4195

48. **Kim KH, Dutta T, Ralph J, Mansfield SD, Simmons BA, Singh S** (2017) Impact of lignin polymer backbone esters on ionic liquid pretreatment of poplar. Biotechnology for Biofuels **10:** 101

49. **Kim S-J, Zemelis-Durfee S, Wilkerson C, Brandizzi F** (2017) In *Brachypodium* a complex signaling is actuated to protect cells from proteotoxic stress and facilitate seed filling. Planta **246:** 75-89

50. **Kim TN, Fox AF, Wills BD, Meehan TD, Landis DA, Gratton C** (2017) Harvesting biofuel grasslands has mixed effects on natural enemy communities and no effects on biocontrol services. Journal of Applied Ecology **54:** 2011-2021

51. **Klammer SSH** (2017) To chip or not to chip: timber residue supply in Michigan's Upper Peninsula. Michigan State University, East Lansing, MI

52. **Kong L, Avadiappan V, Huang K, Maravelias CT** (2017) Simultaneous chemical process synthesis and heat integration with unclassified hot/cold process streams. Computers & Chemical Engineering **101:** 210-225

53. **Kong L, Wu Y, Maravelias CT** (2017) Simultaneous utility and heat exchanger area targeting for integrated process synthesis and heat integration. Industrial & Engineering Chemistry Research **56:** 11847-11859

54. **Kong Q, Ma W, Yang H, Ma G, Mantyla JJ, Benning C** (2017) The Arabidopsis WRINKLED1 transcription factor affects auxin homeostasis in roots. Journal of Experimental Botany **68:** 4627-4634

55. **Kravchenko AN, Toosi ER, Guber AK, Ostrom NE, Yu J, Azeem K, Rivers ML, Robertson GP** (2017) Hotspots of soil N_2O emission enhanced through water absorption by plant residue. Nature Geoscience **10:** 496-500

56. **Lam CH, Das S, Erickson NC, Hyzer CD, Garedew M, Anderson JE, Wallington TJ, Tamor MA, Jackson JE, Saffron CM** (2017) Towards sustainable hydrocarbon fuels with biomass fast pyrolysis oil and electrocatalytic upgrading. Sustainable Energy & Fuels **1:** 258-266

57. **Landis DA** (2017) Designing agricultural landscapes for biodiversity-based ecosystem services. Basic and Applied Ecology **18:** 1-12

58. **LeDuc SD, Zhang X, Clark CM, Izaurralde RC** (2017) Cellulosic feedstock production on Conservation Reserve Program land: potential yields and environmental effects. Global Change Biology – Bioenergy **9:** 460-468

59. **Lemmer KC, Zhang W, Langer SJ, Dohnalkova AC, Hu D, Lemke RA, Piotrowski JS, Orr G, Noguera DR, Donohue TJ** (2017) Mutations that alter the bacterial cell envelope increase lipid production. mBio **8:** e00513-00517

60. **Li B, Walton JD** (2017) Functional diversity for biomass deconstruction in family 5 subfamily 5 (GH5_5) of fungal endo-β1,4-glucanases. Applied Microbiology and Biotechnology **101:** 4093-4101

61. **Li H, Yelle DJ, Li C, Yang M, Ke J, Zhang R, Liu Y, Zhu N, Liang S, Mo X, Ralph J, Currie CR, Mo J** (2017) Lignocellulosic pretreatment in a fungus-cultivating termite. Proceedings of the National Academy of Sciences of the United States of America **114:** 4709-4714

62. **Li M, Williams DL, Heckwolf M, de Leon N, Kaeppler S, Sykes RW, Hodge D** (2017) Prediction of cell wall properties and response to deconstruction using alkaline pretreatment in diverse maize genotypes using Py-MBMS and NIR. BioEnergy Research **10:** 329-343

63. **MacMillan CP, Birke H, Chuah A, Brill E, Tsuji Y, Ralph J, Dennis ES, Llewellyn D, Pettolino FA** (2017) Tissue and cell-specific transcriptomes in cotton reveal the subtleties of gene regulation underlying the diversity of plant secondary cell walls. BMC Genomics **18:** 539

64. **Martien JI, Amador-Noguez D** (2017) Recent applications of metabolomics to advance microbial biofuel production. Current Opinion in Biotechnology **43:** 118-126

65. **McClelland DJ, Motagamwala AH, Li Y, Rover MR, Wittrig AM, Wu C, Buchanan JS, Brown RC, Ralph J, Dumesic JA, Huber GW** (2017) Functionality and molecular weight distribution of red oak lignin before and after pyrolysis and hydrogenation. Green Chemistry **19:** 1378-1389

66. **McDonald BR, Currie CR** (2017) Lateral gene transfer dynamics in the ancient bacterial genus *Streptomyces*. mBio **8:** e00644-00617

67. **Miesel JR, Jach-Smith LC, Renz MJ, Jackson RD** (2017) Distribution of switchgrass (*Panicum virgatum* L.) aboveground biomass in response to nitrogen addition and across harvest dates. Biomass and Bioenergy **100:** 74-83

68. **Mnich E, Vanholme R, Oyarce P, Liu S, Lu F, Goeminne G, Jørgensen B, Motawie MS, Boerjan W, Ralph J, Ulvskov P, Møller BL, Bjarnholt N, Harholt J** (2017) Degradation of lignin β-aryl ether units in *Arabidopsis thaliana* expressing *LigD*, *LigF* and *LigG* from *Sphingomonas paucimobilis* SYK-6. Plant Biotechnology Journal **15:** 581-593

69. **Morais CG, Batista TM, Kominek J, Borelli BM, Furtado C, Moreira RG, Franco GR, Rosa LH, Fonseca C, Hittinger CT, Lachance M-A, Rosa CA** (2017) *Spathaspora boniae* sp. nov., a D-xylose-fermenting species in the *Candida albicans*/*Lodderomyces* clade. International Journal of Systematic and Evolutionary Microbiology **67:** 3798-3805

70. **Ng RTL, Maravelias CT** (2017) Design of biofuel supply chains with variable regional depot and biorefinery locations. Renewable Energy **100:** 90-102

71. **Ng RTL, Maravelias CT** (2017) Economic and energetic analysis of biofuel supply chains. Applied Energy **205:** 1571-1582

72. **Ng RTL, Patchin S, Wu W, Sheth N, Maravelias CT** (2017) An optimization-based web application for synthesis and analysis of biomass-to-fuel strategies. Biofuels, Bioproducts and Biorefining **DOI: 10.1002/bbb.1821**
73. **Novo M, Silvar C, Merino F, Martínez-Cortés T, Lu F, Ralph J, Pomar F** (2017) Deciphering the role of the phenylpropanoid metabolism in the tolerance of *Capsicum annuum* L. to *Verticillium dahliae* Kleb. Plant Science **258:** 12-20
74. **Oates LG, Read HW, Gutknecht JLM, Duncan DS, Balser TC, Jackson RD** (2017) A lipid extraction and analysis method for characterizing soil microbes in experiments with many samples. Journal of Visualized Experiments **125:** e55310
75. **Ostrom NE, Ostrom PH** (2017) Mining the isotopic complexity of nitrous oxide: a review of challenges and opportunities. Biogeochemistry **132:** 359-372
76. **Pateraki I, Andersen-Ranberg J, Jensen NB, Wubshet SG, Heskes AM, Forman V, Hallström B, Hamberger B, Motawia MS, Olsen CE, Staerk D, Hansen J, Møller BL, Hamberger B** (2017) Total biosynthesis of the cyclic AMP booster forskolin from *Coleus forskohlii*. eLife **6:** e23001
77. **Peris D, Moriarty RV, Alexander WG, Baker E, Sylvester K, Sardi M, Langdon QK, Libkind D, Wang Q-M, Bai F-Y, Leducq J-B, Charron G, Landry CR, Sampaio JP, Goncalves P, Hyma KE, Fay JC, Sato TK, Hittinger CT** (2017) Hybridization and adaptive evolution of diverse *Saccharomyces* species for cellulosic biofuel production. Biotechnology for Biofuels **10:** 78
78. **Proemse BC, Murray AE, Schallenberg C, McKiernan B, Glazer BT, Young SA, Ostrom NE, Bowie AR, Wieser ME, Kenig F, Doran PT, Edwards R** (2017) Iron cycling in the anoxic cryo-ecosystem of Antarctic Lake Vida. Biogeochemistry **134:** 17-27
79. **Qureshi AS, Zhang J, da Costa Sousa L, Bao J** (2017) Antibacterial peptide secreted by *Pediococcus acidilactici* enables efficient cellulosic open L-lactic acid fermentation. ACS Sustainable Chemistry & Engineering **5:** 9254-9262
80. **Robertson GP, Hamilton SK, Barham BL, Dale BE, Izaurralde RC, Jackson RD, Landis DA, Swinton SM, Thelen KD, Tiedje JM** (2017) Cellulosic biofuel contributions to a sustainable energy future: choices and outcomes. Science **356:** pii: eaal2324
81. **Rosenheim JA, Gratton C** (2017) Ecoinformatics (big data) for agricultural entomology: pitfalls, progress, and promise. Annual Review of Entomology **62:** 399-417
82. **Sakai S, Rothamer DA** (2017) Effect of ethanol blending on particulate formation from premixed combustion in spark-ignition engines. Fuel **196:** 154-168
83. **Saleme MLS, Cesarino I, Vargas L, Kim H, Vanholme R, Goeminne G, Van Acker R, Fonseca FCA, Pallidis A, Voorend W, Nicomedes Jr. J, Padmakshan D, Van Doorsselaere J, Ralph J, Boerjan W** (2017) Silencing *CAFFEOYL SHIKIMATE ESTERASE* affects lignification and improves saccharification in poplar. Plant Physiology **175:** 1040-1057
84. **Sanford GR, Oates LG, Roley SS, Duncan DS, Jackson RD, Robertson GP, Thelen KD** (2017) Biomass production a stronger driver of cellulosic ethanol yield than biomass quality. Agronomy Journal **109:** 1-12
85. **Sardi M, Gasch AP** (2017) Incorporating comparative genomics into the design-test-learn cycle of microbial strain engineering. FEMS Yeast Research **17:** fox042
86. **Sarks C, Jin M, Balan V, Dale BE** (2017) Fed-batch hydrolysate addition and cell separation by settling in high cell density lignocellulosic ethanol fermentations on AFEX™ corn stover in the Rapid Bioconversion with Integrated recycling Technology process. Journal of Industrial Microbiology & Biotechnology **144:** 1261-1272
87. **Shade A, Jacques M-A, Barret M** (2017) Ecological patterns of seed microbiome diversity, transmission, and assembly. Current Opinion in Microbiology **37:** 15-22
88. **Shen X-X, Hittinger CT, Rokas A** (2017) Contentious relationships in phylogenomic studies can be driven by a handful of genes. Nature Ecology and Evolution **1:** 0126

89. **Singh R, Hu J, Regner MR, Round JW, Ralph J, Saddler JN, Eltis LD** (2017) Enhanced delignification of steam-pretreated poplar by a bacterial laccase. Scientific Reports **7:** 42121

90. **Skevas T, Skevas I, Swinton SM** (2017) Does spatial dependence affect the intention to make land available for bioenergy crops? Journal of Agricultural Economics **69:** 393-412

91. **Smith RA, Cass CL, Mazaheri M, Sekhon RS, Heckwolf M, Kaeppler H, de Leon N, Mansfield SD, Kaeppler SM, Sedbrook JC, Karlen SD, Ralph J** (2017) Suppression of *CINNAMOYL-CoA REDUCTASE* increases the level of monolignol ferulates incorporated into maize lignins. Biotechnology for Biofuels **10:** 109

92. **Smith RA, Schuetz M, Karlen SD, Bird D, Tokunaga N, Sato Y, Mansfield SD, Ralph J, Samuels AL** (2017) Defining the diverse cell populations contributing to lignification in Arabidopsis stems. Plant Physiology **174:** 1028-1036

93. **Spiesman BJ, Bennett A, Isaacs R, Gratton C** (2017) Bumble bee colony growth and reproduction depend on local flower dominance and natural habitat area in the surrounding landscape. Biological Conservation **206:** 217-223

94. **Sprunger CD, G. OL, Jackson RD, Robertson GP** (2017) Plant community composition influences fine root production and biomass allocation in perennial bioenergy cropping systems of the upper Midwest, USA. Biomass and Bioenergy **105:** 248-258

95. **Stappler E, Walton JD, Beier S, Schmoll M** (2017) Abundance of secreted proteins of *Trichoderma reesei* Is regulated by light of different intensities. Frontiers in Microbiology **8:** 2586

96. **Steffan SA, Dharampal PS, Diaz-Garcia L, Currie CR, Zalapa J, Hittinger CT** (2017) Empirical, metagenomic, and computational techniques illuminate the mechanisms by which fungicides compromise bee health. Journal of Visualized Experiments **(128):** e54631

97. **Stoklosa RJ, del Pilar Orjuela A, da Costa Sousa L, Uppugundla N, Williams DL, Dale BE, Hodge DB, Balan V** (2017) Techno-economic comparison of centralized versus decentralized biorefineries for two alkaline pretreatment processes. Bioresource Technology **226:** 9-17

98. **Swinton SM, Tanner S, Barham BL, Mooney DF, Skevas T** (2017) How willing are landowners to supply land for bioenergy crops in the Northern Great Lakes region? Global Change Biology – Bioenergy **9:** 414-428

99. **Tian M, Kumar P, Gupta STP, Reed JL** (2017) Metabolic modeling for design of cell factories. *In* Jens Nielsen, Stefan Hohmann, eds, Systems Biolgoy, Ed First Edition. Wiley-VCH Verlag GmbH & Co. KGaA, pp 71-107

100. **Tornqvist C-E, Vaillancourt B, Kim J, Buell CR, Kaeppler SM, Casler MD** (2017) Transcriptional analysis of flowering time in switchgrass. BioEnergy Research **10:** 700-713

101. **Tran TNT, Breuer RJ, Narasimhan RA, Parreiras LS, Zhang Y, Sato TK, Durrett TP** (2017) Metabolic engineering of *Saccharomyces cerevisiae* to produce a reduced viscosity oil from lignocellulose. Biotechnology for Biofuels **10:** 69

102. **Truong SK, McCormick RF, Mullet JE** (2017) Bioenergy sorghum crop model predicts VPD-limited transpiration traits enhance biomass yield in water-limited environments. Frontiers in Plant Science **8:** 335

103. **Unda F, Kim H, Hefer C, Ralph J, Mansfield SD** (2017) Altering carbon allocation in hybrid poplar (*Populus alba × grandidentata*) impacts cell wall growth and development. Plant Biotechnology Journal **15:** 865-878

104. **Vakirlis N, Hebert AS, Opulente DA, Achaz G, Hittinger CT, Fischer G, Coon JJ, Lafontaine I** (2017) A molecular portrait of de novo genes in yeasts. Molecular Biology and Evolution **35:** 631-645

105. **Valdez ZP, Hockaday WC, Masiello CA, Gallagher ME, Philip Robertson G** (2017) Soil carbon and nitrogen responses to nitrogen fertilizer and harvesting rates in switchgrass cropping systems. BioEnergy Research **10:** 456-464

106. **Van Acker R, Dejardin A, Desmet S, Hoengenaert L, Vanholme R, Morreel K, Laurans F, Kim H, Santoro N, Foster C, Goeminne G, Legee F, Lapierre C, Pilate G, Ralph J, Boerjan W** (2017) Different routes for conifer- and sinapaldehyde and higher saccharification upon deficiency in the dehydrogenase CAD1. Plant Physiology **175:** 1018-1039
107. **Walker JA, Pattathil S, Bergeman LF, Beebe ET, Deng K, Mirzai M, Northen TR, Hahn MG, Fox BG** (2017) Determination of glycoside hydrolase specificities during hydrolysis of plant cell walls using glycome profiling. Biotechnology for Biofuels **10:** 31
108. **Wang K, Froehlich JE, Zienkiewicz A, Hersh HL, Benning C** (2017) A plastid phosphatidylglycerol lipase contributes to the export of acyl groups from plastids for seed oil biosynthesis. The Plant Cell **29:** 1678-1696
109. **Won W, Motagamwala AH, Dumesic JA, Maravelias CT** (2017) A co-solvent hydrolysis strategy for the production of biofuels: process synthesis and technoeconomic analysis. Reaction Chemistry and Engineering **2:** 397-405
110. **Woods DP, Bednarek R, Bouché F, Gordon SP, Vogel JP, Garvin DF, Amasino RM** (2017) Genetic architecture of flowering-time variation in *Brachypodium distachyon*. Plant Physiology **173:** 269-279
111. **Woods DP, Ream TS, Bouché F, Lee J, Thrower N, Wilkerson C, Amasino RM** (2017) Establishment of a vernalization requirement in *Brachypodium distachyon* requires *REPRESSOR OF VERNALIZATION1*. Proceedings of the National Academy of Sciences of the United States of America **114:** 6623-6628
112. **Wu W, Yenkie K, Maravelias CT** (2017) A superstructure-based framework for bio-separation network synthesis. Computers & Chemical Engineering **96:** 1-17
113. **Wyche TP, Alvarenga RFR, Piotrowski JS, Duster MN, Warrack SR, Cornilescu G, De Wolfe TJ, Hou Y, Braun DR, Ellis GA, Simpkins SW, Nelson J, Myers CL, Steele J, Mori H, Safdar N, Markley JL, Rajski SR, Bugni TS** (2017) Chemical genomics, structure elucidation, and *in vivo* studies of the marine-derived anticlostridial ecteinamycin. ACS Chemical Biology **12:** 2287-2295
114. **Yang Q, Zhang X, Abraha M, Del Grosso S, Robertson GP, Chen J** (2017) Enhancing the soil and water assessment tool model for simulating N_2O emissions of three agricultural systems. Ecosystem Health and Sustainability **3:** e01259
115. **Yang Y, Zienkiewicz A, Lavell A, Benning C** (2017) Coevolution of domain interactions in the chloroplast TGD1, 2, 3 lipid transfer complex specific to Brassicaceae and Poaceae plants. The Plant Cell **29:** 1500-1515
116. **Yenkie KM, Wu W, Maravelias CT** (2017) Synthesis and analysis of separation networks for the recovery of intracellular chemicals generated from microbial-based conversions. Biotechnology for Biofuels **10:** 119
117. **Yeung LY, Li S, Kohl IE, Haslun JA, Ostrom NE, Hu H, Fischer TP, Schauble EA, Young ED** (2017) Extreme enrichment in atmospheric $^{15}N^{15}N$. Science Advances **3:** eaao6741
118. **Yue F, Gao R, Piotrowski JS, Kabbage M, Lu F, Ralph J** (2017) Scaled-up production of poacic acid, a plant-derived antifungal agent. Industrial Crops and Products **130:** 240-243
119. **Yue F, Lu F, Regner M, Sun R, Ralph J** (2017) Lignin-derived thioacidolysis dimers: reevaluation, new products, authentication, and quantification. ChemSusChem **10:** 830-835
120. **Zeng Y, Himmel ME, Ding S-y** (2017) Visualizing chemical functionality in plant cell walls. Biotechnology for Biofuels **10:** 263
121. **Zhang B, Penton CR, Xue C, Quensen JF, Roley SS, Guo J, Garoutte A, Zheng T, Tiedje JM** (2017) Soil depth and crop determinants of bacterial communities under ten biofuel cropping systems. Soil Biology and Biochemistry **112:** 140-152
122. **Zhang J, Lei C, Liu G, Bao Y, Balan V, Bao J** (2017) In-situ vacuum distillation of ethanol helps to recycle cellulase and yeast during SSF of delignified corncob residues. ACS Sustainable Chemistry & Engineering **5:** 11676–11685

123. **Zhou S, Runge T, Karlen SD, Ralph J, Gonzales-Vigil E, Mansfield SD** (2017) Chemical pulping advantages of Zip-lignin hybrid poplar. ChemSusChem **10:** 3565-3573
124. **Zienkiewicz K, Zienkiewicz A, Poliner E, Du Z-Y, Vollheyde K, Herrfurth C, Marmon S, Farre EM, Feussner I, Benning C** (2017) Nannochloropsis, a rich source of diacylglycerol acyltransferases for engineering of triacylglycerol content in different hosts. Biotechnology for Biofuels **10:** 8

2018

1. **Abraha M, Gelfand I, Hamilton SK, Chen J, Robertson GP** (2018) Legacy effects of land use on soil nitrous oxide emissions in annual crop and perennial grassland ecosystems. Ecological Applications **28:** 1362-1369
2. **Abraha M, Hamilton SK, Chen J, Robertson GP** (2018) Ecosystem carbon exchange on conversion of Conservation Reserve Program grasslands to annual and perennial cropping systems. Agricultural and Forest Meteorology **253-254:** 151-160
3. **Banerjee A, Hamberger B** (2018) P450s controlling metabolic bifurcations in plant terpene specialized metabolism. Phytochemistry Reviews **17:** 81-111
4. **Bhalla A, Bansal N, Pattathil S, Li M, Shen W, Particka CA, Karlen SD, Phongpreecha T, Semaan RR, Gonzales-Vigil E, Ralph J, Mansfield SD, Ding S-Y, Hodge DB, Hegg EL** (2018) Engineered lignin in poplar biomass facilitates Cu-catalyzed alkaline-oxidative pretreatment. ACS Sustainable Chemistry & Engineering **6:** 2932-2941
5. **Bhalla A, Fasahati P, Particka CA, Assad AE, Stoklosa RJ, Bansal N, Semaan R, Saffron CM, Hodge DB, Hegg EL** (2018) Integrated experimental and technoeconomic evaluation of two-stage Cu-catalyzed alkaline–oxidative pretreatment of hybrid poplar. Biotechnology for Biofuels **11:** 143
6. **Bottoms S, Dickinson Q, McGee M, Hinchman L, Higbee A, Hebert A, Serate J, Xie D, Zhang Y, Coon JJ, Myers CL, Landick R, Piotrowski JS** (2018) Chemical genomic guided engineering of gamma-valerolactone tolerant yeast. Microbial Cell Factories **17:** 5
7. **Carlos C, Fan H, Currie CR** (2018) Substrate shift reveals roles for members of bacterial consortia in degradation of plant cell wall polymers. Frontiers in Microbiology **9:** 364
8. **Casto AL, McKinley BA, Yu KMJ, Rooney WL, Mullet JE** (2018) Sorghum stem aerenchyma formation is regulated by *SbNAC_D* during internode development. Plant Direct **2:** e00085
9. **Cates AC, Jackson RD** (2018) Cover crop effects on net ecosystem carbon balance in grain and silage maize. Agronomy Journal **110:** 30-38
10. **Cates AM, Sanford GR, Ward Good L, Jackson RD** (2018) What do we know about cover crop efficacy in the North Central United States? Journal of Soil and Water Conservation **73:** 153A-157A
11. **Cheng H-Y, Masiello CA, Del Valle I, Gao X, Bennett GN, Silberg JJ** (2018) Ratiometric gas reporting: a nondisruptive approach to monitor gene expression in soils. ACS Synthetic Biology **7:** 903-911
12. **Das A, Rahimi A, Ulbrich A, Alherech M, Motagamwala AH, Bhalla A, da Costa Sousa L, Balan V, Dumesic JA, Hegg EL, Dale BE, Ralph J, Coon J, J., Stahl SS** (2018) Lignin conversion to low-molecular-weight aromatics via an aerobic oxidation-hydrolysis sequence: comparison of different lignin sources. ACS Sustainable Chemistry & Engineering **6:** 3367-3374
13. **de los Santos-Villalobos S, Kremer JM, Parra-Cota FI, Hayano-Kanashiro AC, García-Ortega LF, Gunturu SK, Tiedje JM, He SY, Peña-Cabriales JJ** (2018) Draft genome of the fungicidal biological control agent *Burkholderia anthina* strain XXVI. Archives of Microbiology **200:** 803-810
14. **de Souza WR, Martins PK, Freeman J, Pellny TK, Michaelson LV, Sampaio BL, Vinecky F, Ribeiro AP, da Cunha BADB, Kobayashi AK, de Oliveira PA, Campanha RB, Pacheco TaF, Martarello DCI, Marchiosi Re, Ferrarese-Filho O, dos Santos WD, Tramontina R, Squina FM, Centeno DC, Gaspar M, Braga MR, Tine MAS, Ralph J, Mitchell RAC, Molinari HBC** (2018) Suppression of a single BAHD gene in *Setaria viridis* causes large, stable decreases in cell wall feruloylation and increases biomass digestibility. New Phytologist **218:** 81-93

15. **del Rio JC, Rencoret J, Gutierrez A, Kim H, Ralph J** (2018) Structural characterization of lignin from maize (*Zea mays* L.) fibers: evidence for diferuloylputrescine incorporated into the lignin polymer in maize kernels. Journal of Agricultural and Food Chemistry **66:** 4402-4413
16. **Dou J, Kim H, Li Y, Padmakshan D, Yue F, Ralph J, Vuorinen T** (2018) Structural characterization of lignins from willow bark and wood. Journal of Agricultural and Food Chemistry **66:** 7294-7300
17. **Dou J, Xu W, Koivisto JJ, Mobley JK, Padmakshan D, Kögler M, Xu C, Willför S, Ralph J, Vuorinen T** (2018) Characteristics of hot water extracts from the bark of cultivated willow (*Salix* sp.). ACS Sustainable Chemistry & Engineering **6:** 5566–5573
18. **Du Z-Y, Alvaro J, Hyden B, Zienkiewicz K, Benning N, Zienkiewicz A, Bonito G, Benning C** (2018) Enhancing oil production and harvest by combining the marine alga *Nannochloropsis oceanica* and the oleaginous fungus *Mortierella elongata*. Biotechnology for Biofuels **11:** 174
19. **Eizaguirre JI, Peris D, Rodriguez ME, Lopes CA, De Los Rios P, Hittinger CT, Libkind D** (2018) Phylogeography of the wild Lager-brewing ancestor (*Saccharomyces eubayanus*) in Patagonia. Environmental Microbiology **20:** 3732-3743
20. **Emery SM, Kinnetz ER, Bell-Dereske L, Stahlheber KA, Gross KL, Pennington D** (2018) Low variation in arbuscular mycorrhizal fungal associations and effects on biomass among switchgrass cultivars. Biomass and Bioenergy **119:** 503-508
21. **Evans J, Sanciangco MD, Lau KH, Crisovan E, Barry K, Daum C, Hundley H, Jenkins J, Kennedy M, Kunde-Ramamoorthy G, Vaillancourt B, Acharya A, Schmutz J, Saha M, Kaeppler SM, Brummer EC, Casler MD, Buell CR** (2018) Extensive genetic diversity is present within North American switchgrass germplasm. The Plant Genome **11:** 170055
22. **Fan M, Herburger K, Jensen JK, Zemelis-Durfee S, Brandizzi F, Fry SC, Wilkerson CG** (2018) A trihelix family transcription factor is associated with key genes in mixed-linkage glucan accumulation. Plant Physiology **178:** 1207-1221
23. **Flores-Gómez CA, Escamilla Silva EM, Zhong C, Dale BE, da Costa Sousa L, Balan V** (2018) Conversion of lignocellulosic agave residues into liquid biofuels using an AFEX™-based biorefinery. Biotechnology for Biofuels **11:** 7
24. **Gall DL, Kontur WS, Lan W, Kim H, Li Y, Ralph J, Donohue TJ, Noguera DR** (2018) *In vitro* enzymatic depolymerization of lignin with release of syringyl, guaiacyl, and tricin units. Applied and Environmental Microbiology **84:** e02076-02017
25. **Gomes EA, Lana UGP, Quensen JF, de Sousa SM, Oliveira CA, Guo J, Guimarães LJM, Tiedje JM** (2018) Root-associated microbiome of maize genotypes with contrasting phosphorus use efficiency. Phytobiomes **2:** 129-137
26. **Goncalves C, Wisecaver JH, Kominek J, Oom MS, Leandro MJ, Shen X-X, Opulente DA, Zhou X, Peris D, Kurtzman CP, Hittinger CT, Rokas A, Goncalves P** (2018) Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. eLife **7:** e33034
27. **Gould BA, Palacio-Mejia JD, Jenkins J, Mamidi S, Barry K, Schmutz J, Juenger TE, Lowry DB** (2018) Population genomics and climate adaptation of a C4 perennial grass, *Panicum hallii* (Poaceae). BMC Genomics **19:** 792
28. **Guber A, Kravchenko A, Razavi BS, Uteau D, Peth S, Blagodatskaya E, Kuzyakov Y** (2018) Quantitative soil zymography: mechanisms, processes of substrate and enzyme diffusion in porous media. Soil Biology and Biochemistry **127:** 156-167
29. **Hamilton SK, Hussain MZ, Lowrie C, Basso B, Robertson GP** (2018) Evapotranspiration is resilient in the face of land cover and climate change in a humid temperate catchment. Hydrological Processes **32:** 655-663
30. **Haslun JA, Ostrom NE, Hegg EL, Ostrom PH** (2018) Estimation of isotope variation of N2O during denitrification by *Pseudomonas aureofaciens* and *Pseudomonas chlororaphis:* implications for N_2O source apportionment. Biogeosciences **15:** 3873–3882

31. **Higgins DA, Young MK, Tremaine M, Sardi M, Fletcher JM, Agnew M, Liu L, Dickinson Q, Peris D, Wrobel RL, Hittinger CT, Gasch AP, Singer SW, Simmons BA, Landick R, Thelen MP, Sato TK** (2018) Natural variation in the multidrug efflux pump SGE1 underlies ionic liquid tolerance in yeast. Genetics **210:** 219-234
32. **Hutchins PD, Russell JD, Coon JJ** (2018) LipiDex: an integrated software package for high-confidence lipid identification. Cell Systems **6:** 621-625.e625
33. **Jach-Smith LC, Jackson RD** (2018) N addition undermines N supplied by arbuscular mycorrhizal fungi to native perennial grasses. Soil Biology and Biochemistry **116:** 148-157
34. **Jones CD, Oates LG, Robertson GP, Izaurralde RC** (2018) Perennialization and cover cropping mitigate soil carbon loss from residue harvesting. Journal of Environmental Quality **47:** 710-717
35. **Karlen SD, Free HCA, Padmakshan D, Smith BG, Ralph J, Harris PJ** (2018) Commelinid monocotyledon lignins are acylated by *p*-coumarate. Plant Physiology **177:** 513-521
36. **Kim S, Zhang X, Dale B, Reddy AD, Jones CD, Cronin K, Izaurralde RC, Runge T, Sharara M** (2018) Corn stover cannot simultaneously meet both the volume and GHG reduction requirements of the renewable fuel standard. Biofuels, Bioproducts and Biorefining **12:** 203-212
37. **Kim S, Zhang X, Dale BE, Reddy AD, Jones CD, Izaurralde RC** (2018) EISA (Energy Independence and Security Act) compliant ethanol fuel from corn stover in a depot-based decentralized system. Biofuels, Bioproducts and Biorefining **12:** 873-881
38. **Kim S-J, Zemelis-Durfee S, Jensen JK, Wilkerson CG, Keegstra K, Brandizzi F** (2018) In the grass species *Brachypodium distachyon*, the production of mixed-linkage (1,3;1,4)-β-glucan (MLG) occurs in the Golgi apparatus. The Plant Journal **93:** 1062-1075
39. **Kim TN, Bartel S, Wills BD, Landis DA, Gratton C** (2018) Disturbance differentially affects alpha and beta diversity of ants in tallgrass prairies. Ecosphere **9:** e02399
40. **Kong L, Maravelias CT** (2018) An optimization-based approach for simultaneous chemical process and heat exchanger network synthesis. Industrial & Engineering Chemistry Research **57:** 6330-6343
41. **Kontur WS, Bingman CA, Olmsted CN, Wassarman DR, Ulbrich A, Gall DL, Smith RW, Yusko LM, Fox BG, Noguera DR, Coon JJ, Donohue TJ** (2018) *Novosphingobium aromaticivorans* uses a Nu-class glutathione *S*-transferase as a glutathione lyase in breaking the β-aryl ether bond of lignin. Journal of Biological Chemistry **293:** 4955-4968
42. **Krassowski T, Coughlan AY, Shen X-X, Zhou X, Kominek J, Opulente DA, Riley R, Grigoriev IV, Maheshwari N, Shields DC, Kurtzman CP, Hittinger CT, Rokas A, Wolfe KH** (2018) Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. Nature Communications **9:** 1887
43. **Krause DJ, Kominek J, Opulente DA, Shen X-X, Zhou X, Langdon QK, DeVirgilio J, Hulfachor AB, Kurtzman CP, Rokas A, Hittinger CT** (2018) Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. Proceedings of the National Academy of Sciences of the United States of America **115:** 11030-11035
44. **Kravchenko AN, Guber AK, Quigley MY, Koestel J, Gandhi H, Ostrom NE** (2018) X-ray computed tomography to predict soil N_2O production via bacterial denitrification and N_2O emission in contrasting bioenergy cropping systems. Global Change Biology – Bioenergy **10:** 894-909
45. **Kuang MC, Kominek J, Alexander WG, Cheng J-F, Wrobel RL, Hittinger CT** (2018) Repeated cis-regulatory tuning of a metabolic bottleneck gene during evolution. Molecular Biology and Evolution **35:** 1968-1981
46. **Kumar R, Bhagia S, Smith MD, Petridis L, Ong RG, Cai CM, Mittal A, Himmel MH, Balan V, Dale BE, Ragauskas AJ, Smith JC, Wyman CE** (2018) Cellulose-hemicellulose interactions at elevated temperatures increase cellulose recalcitrance to biological conversion. Green Chemistry **20:** 921-934
47. **Kutlu T, Guber AK, Rivers ML, Kravchenko AN** (2018) Moisture absorption by plant residue in soil. Geoderma **316:** 47-55

48. **Lai Y-S, Stefano G, Zemelis-Durfee S, Ruberti C, Gibbons L, Brandizzi F** (2018) Systemic signaling contributes to the unfolded protein response of the plant endoplasmic reticulum. Nature Communications **9:** 3918
49. **Lan W, Yue F, Rencoret J, del Rio JC, Boerjan W, Lu F, Ralph J** (2018) Elucidating tricin-lignin structures: assigning correlations in HSQC spectra of monocot lignins. Polymers **10:** 916
50. **Landis DA, Gratton C, Jackson RD, Gross KL, Duncan DS, Liang C, Meehan TD, Robertson BA, Schmidt TM, Stahlheber KA, Tiedje JM, Werling BP** (2018) Biomass and biofuel crop effects on biodiversity and ecosystem services in the North Central US. Biomass and Bioenergy **114:** 18-29
51. **Langdon QK, Peris D, Kyle B, Hittinger CT** (2018) sppIDer: a species identification tool to investigate hybrid genomes with high-throughput sequencing. Molecular Biology and Evolution **35:** 2835-2849
52. **Lapierre C, Voxeur A, Karlen SD, Helm RF, Ralph J** (2018) Evaluation of feruloylated and *p*-coumaroylated arabinosyl units in grass arabinoxylans by acidolysis in dioxane/methanol. Journal of Agricultural and Food Chemistry **66:** 5418-5424
53. **Lettow MC, Brudvig LA, Bahlai CA, Gibbs J, Jean RP, Landis DA** (2018) Bee community responses to a gradient of oak savanna restoration practices. Restoration Ecology **26:** 882-890
54. **Li M, Yan G, Bhalla A, Maldonado-Pereira L, RUssell PR, Ding S-Y, Mullet JE, Hodge DB** (2018) Physical fractionation of sweet sorghum and forage/energy sorghum for optimal processing in a biorefinery. Industrial Crops and Products **124:** 607-616
55. **Li Y, Shuai L, Kim H, Motagamwala AH, Mobley JK, Yue F, Tobimatsu Y, Havkin-Frenkel D, Chen F, Dixon RA, Luterbacher JS, Dumesic JA, Ralph J** (2018) An “ideal lignin” facilitates full biomass utilization. Science Advances **4:** eaau2968
56. **Lin Y, Karlen SD, Ralph J, King JY** (2018) Short-term facilitation of microbial litter decomposition by ultraviolet radiation. Science of the Total Environment **615:** 838-848
57. **Lomax A, Woods DP, Dong Y, Bouch e Fee, Rong Y, Mayer KS, Zhong X, Amasino RM** (2018) An ortholog of *CURLY LEAF/ENHANCER OF ZESTE like-1* is required for proper flowering in *Brachypodium distachyon*. The Plant Journal **93:** 871-882
58. **Lovell JT, Jenkins J, Lowry DB, Mamidi S, Sreedasyam A, Weng X, Barry K, Bonnette J, Campitelli B, Daum C, Gordon SP, Gould BA, Khasanova A, Lipzen A, MacQueen A, Palacio-Mejía JD, Plott C, Shakirov EV, Shu S, Yoshinaga Y, Zane M, Kudrna D, Talag JD, Rokhsar D, Grimwood J, Schmutz J, Juenger TE** (2018) The genomic landscape of molecular responses to natural drought stress in *Panicum hallii*. Nature Communications **9:** 5213
59. **MacGilvray ME, Shishkova E, Chasman D, Place M, Gitter A, Coon JJ, Gasch AP** (2018) Network inference reveals novel connections in pathways regulating growth and defense in the yeast salt response. PLOS Computational Biololgy **13:** e1006088
60. **Mackelprang R, Grube AM, Lamendella R, Jesus EdC, Copeland A, Liang C, Jackson RD, Rice CW, Kapucija S, Parsa B, Tringe SG, Tiedje JM, Jansson JK** (2018) Microbial community structure and functional potential in cultivated and native tallgrass prairie soils of the midwestern United States. Frontiers in Microbiology **9:** 1775
61. **McCormick RF, Truong SK, Sreedasyam A, Jenkins J, Shu S, Sims D, Kennedy M, Amirebrahimi M, Weers BD, McKinley B, Mattison A, Morishige DT, Grimwood J, Schmutz J, Mullet JE** (2018) The *Sorghum bicolor* reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. The Plant Journal **93:** 338-354
62. **McDaniel EA, Stuecker TN, Veluvolu M, Gasch AP, Lewis JA** (2018) Independent mechanisms for acquired salt tolerance versus growth resumption induced by mild ethanol pretreatment in *Saccharomyces cerevisiae*. mSphere **3:** e00574-00518
63. **McKinley BA, Casto AL, Rooney WL, Mullet JE** (2018) Developmental dynamics of stem starch accumulation in *Sorghum bicolor*. Plant Direct **2:** e00074

64. **Mellmer MA, Sanpitakseree C, Demir B, Bai P, Ma K, Neurock M, Dumesic JA** (2018) Solvent-enabled control of reactivity for liquid-phase reactions of biomass-derived compounds. Nature Catalysis **1:** 199-207

65. **Meyer JR, Waghmode SB, He J, Gao Y, Hoole D, da Costa Sousa L, Balan V, Foston MB** (2018) Isolation of lignin from Ammonia Fiber Expansion (AFEX) pretreated biorefinery waste. Biomass and Bioenergy **119:** 446-455

66. **Mokomele T, da Costa Sousa L, Balan V, van Rensburg E, Dale BE, Görgens JF** (2018) Ethanol production potential from AFEX™ and steam-exploded sugarcane residues for sugarcane biorefineries. Biotechnology for Biofuels **11:** 127

67. **Mokomele T, da Costa Sousa L, Bals B, Balan V, Goosen N, Dale BE, Görgens JF** (2018) Using steam explosion or AFEX™ to produce animal feeds and biofuel feedstocks in a biorefinery based on sugarcane residues. Biofuels, Bioproducts and Biorefining **12:** 978-996

68. **Motagamwala AH, Won W, Sener C, Alonso DM, Maravelias CT, Dumesic JA** (2018) Toward biomass-derived renewable plastics: production of 2,5-furandicarboxylic acid from fructose. Science Advances **4:** eaap9722

69. **Ng RTL, Kurniawan D, Wang H, Mariska B, Wu W, Maravelias CT** (2018) Integrated framework for designing spatially explicit biofuel supply chains. Applied Energy **216:** 116-131

70. **Nuoendagula, Tsuji Y, Takata N, Sakamoto S, Nakagawa-Izumi A, Taniguchi T, Ralph J, Mitsuda N, Kajita S** (2018) Change in lignin structure, but not in lignin content, in transgenic poplar overexpressing the rice master regulator of secondary cell wall biosynthesis. Physiologia Plantarum **163:** 170-182

71. **Nutting JE, Rafiee M, Stahl SS** (2018) Tetramethylpiperidine *N*-Oxyl (TEMPO), phthalimide *N*-Oxyl (PINO), and related *N*-Oxyl species: electrochemical properties and their use in electrocatalytic reactions. Chemical Reviews **118:** 4834-4885

72. **Ong RG, Shinde S, da Costa Sousa L, Sanford GR** (2018) Pre-senescence harvest of switchgrass inhibits xylose utilization by engineered yeast. Frontiers in Energy Research **6:** 52

73. **Opulente DA, Rollinson EJ, Bernick-Roehr C, Hulfachor AB, Rokas A, Kurtzman CP, Hittinger CT** (2018) Factors driving metabolic diversity in the budding yeast subphylum. BMC Biology **16:** 26

74. **Ostrom NE, Gandhi H, Coplen TB, Toyoda S, Böhlke JK, Brand WA, Casciotti KL, Dyckmans J, Giesemann A, Mohn J, Well R, Yu L, Yoshida N** (2018) Preliminary assessment of stable nitrogen and oxygen isotopic composition of USGS51 and USGS52 nitrous oxide reference gases and perspectives on calibration needs. Rapid Communications in Mass Spectrometry **32:** 1207-1214

75. **Pan S, Reed JL** (2018) Advances in gap-filling genome-scale metabolic models and model-driven experiments lead to novel metabolic discoveries. Current Opinion in Biotechnology **51:** 103-108

76. **Peris D, Pérez-Torrado R, Hittinger CT, Barrio E, Querol A** (2018) On the origins and industrial applications of *Saccharomyces cerevisiae* x *Saccharomyces kudriavzevii* hybrids. Yeast **35:** 51-69

77. **Poliner E, Pulman JA, Zienkiewicz K, Childs K, Benning C, Farre EM** (2018) A toolkit for *Nannochloropsis oceanica* CCMP1779 enables gene stacking and genetic engineering of the eicosapentaenoic acid pathway for enhanced long-chain polyunsaturated fatty acid production. Plant Biotechnology Journal **16:** 298-309

78. **Ramstein GP, Evans J, Nandety A, Saha MC, Brummer EC, Kaeppler SM, Buell CR, Casler MD** (2018) Candidate variants for additive and interactive effects on bioenergy traits in switchgrass (*Panicum virgatum* L.) identified by genome-wide association analyses. The Plant Genome **11:** 180002

79. **Regner M, Bartuce A, Padmakshan D, Ralph J, Karlen SD** (2018) Reductive cleavage method for quantitation of monolignols and low-abundance monolignol conjugates. ChemSusChem **11:** 1600-1605

80. **Regner M, Bartuce A, Padmakshan D, Ralph J, Karlen SD** (2018) Cover Profile: Reductive cleavage method for quantitation of monolignols and low-abundance monolignol conjugates. ChemSusChem **11:** 1580

81. **Rencoret J, Kim H, Evaristo AB, Gutiérrez A, Ralph J, del Rio JC** (2018) Variability in lignin composition and structure in cell walls of different parts of macaúba (*Acrocomia aculeata*) palm fruit. Journal of Agricultural and Food Chemistry **66:** 138-153
82. **Rodriguez-R LM, Gunturu S, Tiedje JM, Cole JR, Konstantinidis KT** (2018) Nonpareil 3: fast estimation of metagenomic coverage and sequence diversity. mSystems **3:** e00039-00018
83. **Roley SS, Duncan DS, Liang D, Garoutte A, Jackson RD, Tiedje JM, Robertson GP** (2018) Associative nitrogen fixation (ANF) in switchgrass (*Panicum virgatum*) across a nitrogen input gradient. PLOS ONE **13:** e0197320
84. **Sardi M, Krause M, Heilberger J, Gasch AP** (2018) Genotype-by-environment-by-environment interactions in the *Saccharomyces cerevisiae* transcriptomic response to alcohols and anaerobiosis. G3: Genes | Genomes | Genetics **8:** 3881-3890
85. **Sardi M, Paithane V, Place M, Robinson DE, Hose J, Wohlbach DJ, Gasch AP** (2018) Genome-wide association across *Saccharomyces cerevisiae* strains reveals substantial variation in underlying gene requirements for toxin tolerance. PLOS Genetics **14:** e1007217
86. **Scarborough MJ, Lawson CE, Hamilton JJ, Donohue TJ, Noguera DR** (2018) Metatranscriptomic and thermodynamic insights into medium-chain fatt acid production using an anaerobic microbiome. mSystems **3:** e00221-00218
87. **Scarborough MJ, Lynch G, Dickson M, McGee M, Donohue TJ, Noguera DR** (2018) Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. Biotechnology for Biofuels **11:** 200
88. **Sener C, Motagamwala AH, Alonso DM, Dumesic JA** (2018) Enhanced furfural yields from xylose dehydration in the γ-valerolactone/water solvent system at elevated temperatures. ChemSusChem **11:** 2321-2331
89. **Shade A** (2018) Understanding microbiome stability in a changing world. mSystems **3:** 00157-00117
90. **Shen X-X, Opulente DA, Kominek J, Zhou X, Steenwyk JL, Buh KV, Haase MAB, Wisecaver JH, Wang M, Doering DT, Boudouris JT, Schneider RM, Langdon QK, Ohkuma M, Endoh R, Takashima M, Manabe R-i, Cadez N, Libkind D, Rosa CA, DeVirgilio J, Hulfachor AB, Groenewald M, Kurtzman CP, Hittinger CT, Rokas A** (2018) Tempo and mode of genome evolution in the budding yeast subphylum. Cell **175:** 1533-1545
91. **Song B, Li B, Wang X, Shen W, Park S, Collings C, Feng A, Smith SJ, Walton JD, Ding S-Y** (2018) Real-time imaging reveals that lytic polysaccharide monooxygenase promotes cellulase activity by increasing cellulose accessibility. Biotechnology for Biofuels **11:** 11
92. **Song Y, Mobley JK, Motagamwala AH, Isaacs M, Dumesic JA, Ralph J, Lee AF, Wilson K, Crocker M** (2018) Gold-catalyzed conversion of lignin to low molecular weight aromatics. Chemical Science **9:** 8127-8133
93. **Spiesman BJ, Kummel H, Jackson RD** (2018) Carbon storage potential increases with increasing ratio of C4 to C3 grass cover and soil productivity in restored tallgrass prairies. Oecologia **186:** 565-576
94. **Sprunger CD, Robertson GP** (2018) Early accumulation of active fraction soil carbon in newly established cellulosic biofuel systems. Geoderma **318:** 42-51
95. **Stanton CL, Reinhard CT, Kasting JF, Ostrom NE, Haslun JA, Lyons TW, Glass JB** (2018) Nitrous oxide from chemodenitrification: a possible missing link in the Proterozoic greenhouse and the evolution of aerobic respiration. Geobiology **16:** 597-609
96. **Takeda Y, Tobimatsu Y, Karlen SD, Koshiba T, Suzuki S, Yamamura M, Murakami S, Mukai M, Hattori T, Osakabe K, Ralph J, Sakamoto M, Umezawa T** (2018) Downregulation of *p-COUMAROYL ESTER 3-HYDROXYLASE* in rice leads to altered cell wall structures and improves biomass saccharification. The Plant Journal **96:** 796-811
97. **Taylor M, Tornqvist C-E, Zhao X, Grabowski P, Doerge R, Ma J, Volenec J, Evans J, Ramstein GP, Sanciangco MD, Buell CR, Casler MD, Jiang Y** (2018) Genome-wide association study in pseudo-F2

populations of switchgrass identifies genetic loci affecting heading and anthesis dates. Frontiers in Plant Science **9:** 1250

98. **Tian L, Chen J, Shao C** (2018) Interdependent dynamics of LAI-albedo across the roofing landscapes: Mongolian and Tibetan plateaus. Remote Sensing **10:** 1159
99. **Tian M, Reed JL** (2018) Integrating proteomic or transcriptomic data into metabolic models using linear bound flux balance analysis. Bioinformatics **34:** 3882-3888
100. **Timokhin V, Regner M, Tsuji Y, Grabber J, Ralph J** (2018) Synthesis of nepetoidin B. Synlett **29:** 1229-1231
101. **Tornqvist C-E, Taylor M, Jiang Y, Evans J, Buell CR, Kaeppler SM, Casler MD** (2018) Quantitative Trait Locus mapping for flowering time in a lowland x upland switchgrass pseudo-F2 population. The Plant Genome **11:** 170093
102. **Walker TW, Chew AK, Li H, Demir B, Zhang ZC, Huber GW, Van Lehn RC, Dumesic JA** (2018) Universal kinetic solvent effects in acid-catalyzed reactions of biomass-derived oxygenates. Energy and Environmental Science **11:** 617-628
103. **Wang JP, Matthews ML, Williams CM, Shi R, Yang C, Tunlaya-Anukit S, Chen H-C, Li Q, Liu J, Lin C-Y, Naik P, Sun Y-H, Loziuk PL, Yeh T-F, Kim H, Gjersing E, Shollenberger T, Shuford CM, Song J, Miller Z, Huang Y-Y, Edmunds CW, Liu B, Sun Y, Lin Y-CJ, Li W, Chen H, Peszlen I, Ducoste JJ, Ralph J, Chang H-M, Muddiman DC, Davis MF, Smith C, Isik F, Sederoff R, Chiang VL** (2018) Improving wood properties for wood utilization through multi-omics integration in lignin biosynthesis. Nature Communications **9:** 1579
104. **Wang K, Guo Q, Froehlich JE, Hersh HL, Zienkiewicz A, Howe GA, Benning C** (2018) Two abscisic acid-responsive plastid lipase genes involved in jasmonic acid biosynthesis in *Arabidopsis thaliana*. The Plant Cell **30:** 1006-1022
105. **Wang X, He Q, Yang Y, Wang J, Haning K, Hu Y, Wu B, He M, Zhang Y, Bao J, Contreras LM, Yang S** (2018) Advances and prospects in metabolic engineering of *Zymomonas mobilis*. Metabolic Engineering **50:** 57-73
106. **Wills BD, Landis DA** (2018) The role of ants in north temperate grasslands: a review. Oecologia **186:** 323-338
107. **Wu W, Long MR, Zhang X, Reed JL, Maravelias CT** (2018) A framework for the identification of promising bio-based chemicals. Biotechnology and Bioengineering **115:** 2328-2340
108. **Xue S, Jones AD, Sousa L, Piotrowski J, Jin M, Sarks C, Dale BE, Balan V** (2018) Water-soluble phenolic compounds produced from extractive ammonia pretreatment exerted binary inhibitory effects on yeast fermentation using synthetic hydrolysate. PLOS ONE **13:** e0194012
109. **Yang S, Vera JM, Grass J, Savvakis G, Moskvin OV, Yang Y, McIlwain SJ, Lyu Y, Zinonos I, Hebert AS, Coon JJ, Bates DM, Sato TK, Brown SD, Himmel ME, Zhang M, Landick R, Pappas KM, Zhang Y** (2018) Complete genome sequence and the expression pattern of plasmids of the model ethanologen *Zymomonas mobilis* ZM4 and its xylose-utilizing derivatives 8b and 2032. Biotechnology for Biofuels **11:** 125
110. **Yang Y, Benning C** (2018) Functions of triacylglycerols during plant development and stress. Current Opinion in Biotechnology **49:** 191-198
111. **Yao S, Mobley JK, Ralph J, Crocker M, Parkin S, Selegue JP, Meier MS** (2018) Mechanochemical treatment facilitates two-step oxidative depolymerization of kraft lignin. ACS Sustainable Chemistry & Engineering **6:** 5990–5998
112. **Zhang Y, Oates LG, Serate J, Xie D, Pohlmann E, Bukhman YV, Karlen SD, Young MK, Higbee A, Eilert D, Sanford GR, Piotrowski JS, Cavalier D, Ralph J, Coon JJ, Sato TK, Ong RG** (2018) Diverse lignocellulosic feedstocks can achieve high field-scale ethanol yields while providing flexibility for the biorefinery and landscape-level environmental benefits. Global Change Biology – Bioenergy **10:** 825-840

113. **Zhou L, da Costa Sousa L, Dale BE, Feng J-X, Balan V** (2018) The effect of alkali-soluble lignin on purified core cellulase and hemicellulase activities during hydrolysis of extractive ammonia-pretreated lignocellulosic biomass. Royal Society Open Science **5:** 171529
114. **Zhou X, Shen X-X, Hittinger CT, Rokas A** (2018) Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets. Molecular Biology and Evolution **35:** 486-503

2019

1. **Abraha M, Gelfand I, Hamilton SK, Chen J, Robertson GP** (2019) Carbon debt of field-scale conservation reserve program grasslands converted to annual and perennial bioenergy crops. Environmental Research Letters **14:** 024019
2. **Agarwal UP, Ralph SA, Padmakshan D, Liu S, Foster CE** (2019) Estimation of syringyl units in wood lignins by FT-Raman spectroscopy. Journal of Agricultural and Food Chemistry **67:** 4367-4374
3. **Avci U, Zhou X, Pattathil S, da Costa Sousa L, Hahn MG, Dale B, Xu Y, Balan V** (2019) Effects of extractive ammonia pretreatment on the ultrastructure and gllycan composition of corn stover. Frontiers in Energy Research **7:** 85
4. **Baker EP, Hittinger CT** (2019) Evolution of a novel chimeric maltotriose transporter in *Saccharomyces eubayanus* from parent proteins unable to perform this function. PLOS Genetics **15:** e1007786
5. **Baker EP, Peris D, Moriarty RV, Li XC, Fay JC, Hittinger CT** (2019) Mitochondrial DNA and temperature tolerance in lager yeasts. Science Advances **5:** eaav1869
6. **Banerjee A, Arnesen JA, Moser D, Motsa BB, Johnson SR, Hamberger B** (2019) Engineering modular diterpene biosynthetic pathways in *Physcomitrella patens*. Planta **249:** 221-233
7. **Basso B, Shuai G, Zhang J, Robertson GP** (2019) Yield stability analysis reveals sources of large-scale nitrogen loss from the US Midwest. Scientific Reports **9:** 5774
8. **Bhalla A, Cai CM, Xu F, Singh SK, Bansal N, Phongpreecha T, Dutta T, Foster CE, Kumar R, Simmons BA, Singh S, Wyman CE, Hegg EL, Hodge DB** (2019) Performance of three delignifying pretreatments on hardwoods: hydrolysis yields, comprehensive mass balances, and lignin properties. Biotechnology for Biofuels **12:** 213
9. **Bowsher AW, Kearns PJ, Shade A** (2019) 16S rRNA/rRNA gene ratios and cell activity staining reveal consistent patterns of microbial activity in plant-associated soil. mSystems **4:** e00003-00019
10. **Cadez N, Bellora N, Ulloa R, Hittinger CT, Libkind D** (2019) Genomic content of a novel yeast species *Hanseniaspora gamundiae* sp. nov. from fungal stromata (*Cyttaria*) associated with a unique fermented beverage in Andean Patagonia, Argentina. PLOS ONE **14:** e0210792
11. **Chen J, Sciusco P, Ouyang Z, Zhang R, Henebry GM, John R, Roy DP** (2019) Linear downscaling from MODIS to landsat: connecting landscape composition with ecosystem functions. Landscape Ecology **34:** 2917–2934
12. **da Costa Sousa L, Humpula J, Balan V, Dale BE, Chundawat SPS** (2019) Impact of ammonia pretreatment conditions on the cellulose III allomorph ultrastructure and its enzymatic digestibility. ACS Sustainable Chemistry & Engineering **7:** 14411-14424
13. **Daly P, McClellan C, Maluk M, Oakey H, Lapierre C, Waugh R, Stephens J, Marshall D, Barakate A, Tsuji Y, Goeminne G, Vanholme R, Boerjan W, Ralph J, Halpin C** (2019) RNAi-suppression of barley caffeic acid *O*-methyltransferase modifies lignin despite redundancy in the gene family. Plant Biotechnology Journal **17:** 594-607
14. **Donohue TJ** (2019) Shedding light on a Group IV (ECF11) alternative sigma factor. Molecular Microbiology **112:** 374-384
15. **Doud DFR, Bowers RM, Schulz F, De Raad M, Deng K, Tarver A, Glasgow E, Vander Meulen K, Fox B, Deutsch S, Yoshikuni Y, Trent N, Hedlund BP, Singer SW, Ivanova N, Woyke T** (2019) Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. The ISME Journal **DOI: 10.1038/s41396-019-0557-y**

16. **Du Z-Y, Zienkiewicz K, Vande Pol N, Ostrom NE, Benning C, Bonito GM** (2019) Algal-fungal symbiosis leads to photosynthetic mycelium. eLife **8:** e47815
17. **Dulys-Nusbaum E, Klammer SSH, Swinton SM** (2019) How willing are different types of landowner to supply hardwood timber residues for bioenergy? Biomass and Bioenergy **122:** 45-52
18. **Duncan DS, Oates LG, Gelfand I, Millar N, Robertson GP, Jackson RD** (2019) Environmental factors function as constraints on soil nitrous oxide fluxes in bioenergy feedstock cropping systems. Global Change Biology – Bioenergy **11:** 416-426
19. **Elder T, del Río JC, Ralph J, Rencoret J, Kim H, Beckham GT** (2019) Radical coupling reactions of piceatannol and monolignols: A density functional theory study. Phytochemistry **164:** 12-23
20. **Fasahati P, Liu JJ, Ohlrogge JB, Saffron CM** (2019) Process design and economics for production of advanced biofuels from genetically modified lipid-producing sorghum. Applied Energy **239:** 1459-1470
21. **Felczak MM, Jacobson TB, Ong WK, Amador-Noguez D, TerAvest MA** (2019) Expression of phosphofructokinase is not sufficient to enable Embden-Meyerhof-Parnas glycolysis in *Zymomonas mobilis* ZM4. Frontiers in Microbiology **10:** 2270
22. **Gage JL, Vaillancourt B, Hamilton JP, Manrique-Carpintero NC, Gustafson TJ, Barry K, Lipzen A, Tracy WF, Mikel MA, Kaeppler SM, Buell CR, de Leon N** (2019) Multiple maize reference genomes impact the identification of variants by genome-wide association study in a diverse inbred panel. The Plant Genome **12:** 1-12
23. **Garedew M, Young-Farhat D, Jackson JE, Saffron CM** (2019) Electrocatalytic upgrading of phenolic compounds observed after lignin pyrolysis. ACS Sustainable Chemistry & Engineering **7:** 8375-8386
24. **Ghosh IN, Martien J, Hebert AS, Zhang Y, Coon JJ, Amador-Noguez D, Landick R** (2019) OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. Metabolic Engineering **52:** 324-340
25. **Glasgow EM, Vander Meulen KA, Takasuka TE, Bianchetti CM, Bergeman LF, Deutsch S, Fox BG** (2019) Extent and origins of functional diversity in a subfamily of glycoside hydrolases. Journal of Molecular Biology **431:** 1217-1233
26. **Grabber JH, Davidson C, Tobimatsu Y, Kim H, Lu F, Zhu Y, Opietnik M, Santoro N, Foster CE, Yue F, Ress D, Pan X, Ralph J** (2019) Structural features of alternative lignin monomers associated with improved digestibility of artificially lignified maize cell walls. Plant Science **287:** 110070
27. **Grady KL, Sorensen JW, Stopnisek N, Guittar J, Shade A** (2019) Assembly and seasonality of core phyllosphere microbiota on perennial biofuel crops. Nature Communications **10:** 4135
28. **Graham BJ, Raines RT** (2019) Efficient metal-free conversion of glucose to 5-hydroxymethylfurfural using a boronic acid. Biomass Conversion and Biorefinery **9:** 471-477
29. **Groendyk M, Rothamer DA** (2019) Optical investigation of mixing controlled combustion using a novel transgenic plant oil. Fuel **252:** 675-698
30. **Guber AK, Kravchenko AN, Razavi BS, Blagodatskaya E, Kuzyakov Y** (2019) Calibration of 2-D soil zymography for correct analysis of enzyme distribution. European Journal of Soil Science **70:** 715-726
31. **Haan NL, Landis DA** (2019) Grassland disturbance increases monarch butterfly oviposition and decreases arthropod predator abundance. Biological Conservation **233:** 185-192
32. **Haan NL, Landis DA** (2019) The importance of shifting disturbance regimes in monarch butterfly decline and recovery. Frontiers in Ecology and Evolution **7:** 191
33. **Hussain MZ, Bhardwaj AK, Basso B, Robertson GP, Hamilton SK** (2019) Nitrate leaching from continuous corn, perennial grasses, and poplar in the US Midwest. Journal of Environmental Quality **48:** 1849-1855
34. **Hussain MZ, Hamilton SK, Bhardwaj AK, Basso B, Thelen KD, Robertson GP** (2019) Evapotranspiration and water use efficiency of continuous maize and maize and soybean in rotation in the upper Midwest U.S. Agricultural Water Management **221:** 92-98

35. **Hutchins PD, Russell JD, Coon JJ** (2019) Mapping lipid fragmentation for tailored mass spectral libraries. Journal of the American Society for Mass Spectrometry **30:** 659-668
36. **Jacobson TB, Adamczyk PA, Stevenson DM, Regner M, Ralph J, Reed JL, Amador-Noguez D** (2019) ^{2}H and ^{13}C metabolic flux analysis elucidates *in vivo* thermodynamics of the ED pathway in *Zymomonas mobilis*. Metabolic Engineering **54:** 301-316
37. **Johnson SR, Bhat WW, Bibik J, Turmo A, Hamberger B, Evolutionary Mint Genomics Consortium, Hamberger B** (2019) A database-driven approach identifies additional diterpene synthase activities in the mint family (Lamiaceae). Journal of Biological Chemistry **294:** 1349-1362
38. **Johnson SR, Bhat WW, Sadre R, Miller GP, Garcia AS, Hamberger B** (2019) Promiscuous terpene synthases from *Prunella vulgaris* highlight the importance of substrate and compartment switching in terpene synthase evolution. New Phytologist **223:** 323-335
39. **Kim J, Tremaine M, Grass JA, Purdy HM, Landick R, Kiley PJ, Reed JL** (2019) Systems metabolic engineering of *Escherichia coli* improves co-conversion of lignocellulose-derived sugars. Biotechnology Journal **14:** 1800441
40. **Kim S, Dale BE, Jin M, Thelen KD, Zhang X, Meier P, Reddy AD, Jones CD, Izaurralde RC, Balan V, Runge T, Sharara M** (2019) Integration in a depot-based decentralized biorefinery system: corn stover-based cellulosic biofuel. Global Change Biology – Bioenergy **11:** 871-882
41. **Kim S, Dale BE, Zhang X, Jones CD, Reddy AD, Izaurralde RC** (2019) The Renewable Fuel Standard may limit overall greenhouse gas savings by corn stover-based cellulosic biofuels in the U.S. Midwest: effects of the regulatory approach on projected emissions. Environmental Science & Technology **53:** 2288-2294
42. **Klinger GE, Zhou Y, Hao P, Robbins J, Aquilina JM, Jackson JE, Hegg EL** (2019) Biomimetic reductive cleavage of keto aryl ether bonds by small-molecule thiols. ChemSusChem **12:** 4775-4779
43. **Kominek J, Doering DT, Opulente DA, Shen X-X, Zhou X, DeVirgilio J, Hulfachor AB, Groenewald M, Mcgee MA, Karlen SD, Kurtzman CP, Rokas A, Hittinger CT** (2019) Eukaryotic acquisition of a bacterial operon. Cell **176:** 1356-1366
44. **Kontur WS, Olmsted CN, Yusko LM, Niles AV, Walters KA, Beebe ET, Vander Meulen KA, Karlen SD, Gall DL, Noguera DR, Donohue TJ** (2019) A heterodimeric glutathione *S*-transferase that stereospecifically breaks lignin's β(R)-aryl ether bond reveals the diversity of bacterial β-etherases. Journal of Biological Chemistry **294:** 1877-1890
45. **Kravchenko AN, Guber AK, Razavi BS, Koestel J, Quigley MY, Robertson GP, Kuzyakov Y** (2019) Microbial spatial footprint as a driver of soil carbon stabilization. Nature Communications **10:** 3121
46. **Lal PB, Wells F, Lyu Y, Ghosh I, Landick R, Kiley PJ** (2019) A markerless method for genome engineering in *Zymomonas mobilis* ZM4. Frontiers in Microbiology **10:** 2216
47. **Lam PY, Tobimatsu Y, Matsumoto N, Suzuki S, Lan W, Takeda Y, Yamamura M, Sakamoto M, Ralph J, Lo C, Umezawa T** (2019) OsCAldOMT1 is a bifunctional *O*-methyltransferase involved in the biosynthesis of tricin lignins in rice cell walls. Scientific Reports **9:** 11597
48. **Lan W, Rencoret J, del Rio JC, Ralph J** (2019) Tricin in grass lignin: biosynthesis, characterization, and quantitation. *In* Fachuang Lu and Fengxia Yue, ed, Lignin: Biosynthesis, Functions and Economic Significance. Nova Science Publishers, Inc., Hauppauge, New York, USA, pp 51-78
49. **Langdon QK, Peris D, Baker EP, Opulente DA, Nguyen H-V, Bond U, Goncalves P, Sampaio JP, Libkind D, Hittinger CT** (2019) Fermentation innovation through complex hybridization of wild and domesticated yeasts. Nature Ecology & Evolution **3:** 1576-1586
50. **Lee M-H, Jeon HS, Kim SH, Chung JH, Roppolo D, Lee H-J, Cho HJ, Tobimatsu Y, Ralph J, Park OK** (2019) Lignin-based barrier restricts pathogens to the infection site and confers resistance in plants. The EMBO Journal **38:** e101948
51. **Li XC, Peris D, Hittinger CT, Sia EA, Fay JC** (2019) Mitochondria-encoded genes contribute to evolution of heat and cold tolerance in yeast. Science Advances **5:** eaav1848

52. **Liu N, Li H, Chevrette MG, Zhang L, Cao L, Zhou H, Zhou X, Zhou Z, Pope PB, Currie CR, Huang Y, Wang Q** (2019) Functional metagenomics reveals abundant polysaccharide-degrading gene clusters and cellobiose utilization pathways within gut microbiota of a wood-feeding higher termite. The ISME Journal **13:** 104-117
53. **Liu X, Gupta STP, Bhimsaria D, Reed JL, Rodriguez-Martinez JA, Ansari AZ, Raman S** (2019) *De novo* design of programmable inducible promoters. Nucleic Acids Research **47:** 10452-10463
54. **Liu Y, Landick B, Raman S** (2019) A regulatory NADH/NAD+ redox biosensor for bacteria. ACS Synthetic Biology **8:** 264-273.
55. **Manning P, Loos J, Barnes AD, Batáry P, Bianchi FJJA, Buchmann N, De Deyn GB, Ebeling A, Eisenhauer N, Fischer M, Fründ J, Grass I, Isselstein J, Jochum M, Klein AM, Klingenberg EOF, Landis DA, Lepš J, Lindborg R, Meyer ST, Temperton VM, Westphal C, Tscharntke T** (2019) Transferring biodiversity-ecosystem function research to the management of ‘real-world’ ecosystems. Advances in Ecological Research **61:** 323-356
56. **Martien JI, Hebert AS, Stevenson DM, Regner MR, Khana DB, Coon JJ, Amador-Noguez D** (2019) Systems-level analysis of oxygen exposure in *Zymomonas mobilis*: implications for isoprenoid production. mSystems **4:** e00284-00218
57. **Mehrer CR, Rand JM, Incha MR, Cook TB, Demir B, Motagamwala AH, Kim D, Dumesic JA, Pfleger BF** (2019) Growth-coupled bioconversion of levulinic acid to butanone. Metabolic Engineering **55:** 92-101
58. **Mellmer MA, Sanpitakseree C, Demir B, Ma K, Elliott WA, Bai P, Johnson RL, Walker TW, Shanks BH, Rioux RM, Neurock M, Dumesic JA** (2019) Effects of chloride ions in acid-catalyzed biomass dehydration reactions in polar aprotic solvents. Nature Communications **10:** 1132
59. **Mokomele T, da Costa Sousa L, Balan V, van Rensburg E, Dale BE, Görgens JF** (2019) Incorporating anaerobic co-digestion of steam exploded or ammonia fiber expansion pretreated sugarcane residues with manure into a sugarcane-based bioenergy-livestock nexus. Bioresource Technology **272:** 326-336
60. **Myers KS, Riley NM, MacGilvray ME, Sato TK, McGee M, Heilberger J, Coon JJ, Gasch AP** (2019) Rewired cellular signaling coordinates sugar and hypoxic responses for anaerobic xylose fermentation in yeast. PLOS Genetics **15:** e1008037
61. **Oyarce P, De Meester B, Fonseca F, de Vries L, Goeminne G, Pallidis A, De Rycke R, Tsuji Y, Li Y, Van den Bosch S, Sels B, Ralph J, Vanholme R, Boerjan W** (2019) Introducing curcumin biosynthesis in *Arabidopsis* enhances lignocellulosic biomass processing. Nature Plants **5:** 225-237
62. **Perez JM, Kontur WS, Alherech M, Coplien J, Karlen SD, Stahl SS, Donohue TJ, Noguera DR** (2019) Funneling aromatic products of chemically depolymerized lignin into 2-pyrone-4-6- dicarboxylic acid with *Novosphingobium aromaticivorans*. Green Chemistry **21:** 1340-1350
63. **Rafiee M, Alherech M, Karlen SD, Stahl SS** (2019) Electrochemical aminoxyl-mediated oxidation of primary alcohols in lignin to carboxylic acids: polymer modification and depolymerization. Journal of the American Chemical Society **141:** 15266-15276
64. **Ralph J, Lapierre C, Boerjan W** (2019) Lignin structure and its engineering. Current Opinion in Biotechnology **56:** 240-249
65. **Ramstein GP, Casler MD** (2019) Extensions of BLUP models for genomic prediction in heterogeneous populations: application in a diverse switchgrass sample. G3: Genes | Genomes | Genetics **9:** 789-805
66. **Reed DE, Chen J, Abraha M, Robertson GP, Dahlin KM** (2019) The shifting role of mRUE for regulating ecosystem production. Ecosystems **DOI: 10.1007/s10021-019-00407-4**
67. **Roley SS, Xue C, Hamilton SK, Tiedje JM, Robertson GP** (2019) Isotopic evidence for episodic nitrogen fixation in switchgrass (*Panicum virgatum* L.). Soil Biololgy and Biochemistry **129:** 90-98
68. **Sadre R, Kuo P, Chen J, Yang Y, Banerjee A, Benning C, Hamberger B** (2019) Cytosolic lipid droplets as engineered organelles for production and accumulation of terpenoid biomaterials in leaves. Nature Communications **10:** 853

69. **Sakai S, Rothamer D** (2019) Impact of ethanol blending on particulate emissions from a spark-ignition direct-injection engine. Fuel **236:** 1548-1558
70. **Schuh MK, Bahlai CA, Malmstrom CM, Landis DA** (2019) Effect of switchgrass ecotype and cultivar on establishment, feeding, anddevelopment of fall armyworm (Lepidoptera: Noctuidae). Journal of Economic Entomology **112:** 440-449
71. **Shcherbak I, Robertson GP** (2019) Nitrous oxide (N_2O) emissions from subsurface soils of agricultural ecosystems. Ecosystems **22:** 1650–1663
72. **Shen W, Collings C, Li M, Markovicz J, Ralph J, Mansfield SD, Ding S-Y** (2019) Imaging changes in cell walls of engineered poplar by stimulated Raman scattering and atomic force microscopy. ACS Sustainable Chemistry & Engineering **7:** 10616-10622
73. **Shuai G, Martinez-Feria RA, Zhang J, Li S, Price R, Basso B** (2019) Capturing maize stand heterogeneity across yield-stability zones using unmanned aerial vehicles (UAV). Sensors **19:** 4446
74. **Smercina DN, Evans SE, Friesen ML, Tiemann LK** (2019) To fix or not to fix: controls on free-living nitrogen fixation in the rhizosphere. Applied and Environmental Microbiology **85:** e02546-02518
75. **Smercina DN, Evans SE, Friesen ML, Tiemann LK** (2019) Optimization of the $^{15}N_2$ incorporation and acetylene reduction methods for free-living nitrogen fixation. Plant and Soil **445:** 595-611
76. **Song Y, Motagamwala AH, Karlen SD, Dumesic JA, Ralph J, Mobley JK, Crocker M** (2019) A comparative study of secondary depolymerization methods on oxidized lignins. Green Chemistry **21:** 3940-3947
77. **Spiesman BJ, Bennett A, Isaacs R, Gratton C** (2019) Harvesting effects on wild bee communities in bioenergy grasslands depend on nesting guild. Ecological Applications **29:** e01828
78. **Steenwyk JL, Opulente DA, Kominek J, Shen X-X, Zhou X, Labella AL, Bradley NP, Eichman BF, Cadez N, Libkind D, DeVirgilio J, Hulfachor AB, Kurtzman CP, Hittinger CT, Rokas A** (2019) Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. PLOS Biology **17:** e3000255
79. **Szymanski LM, Sanford GR, Heckman KA, Jackson RD, Marín-Spiotta E** (2019) Conversion to bioenergy crops alters the amount and age of microbially-respired soil carbon. Soil Biology and Biochemistry **128:** 35-44
80. **Tobimatsu Y, Takano T, Umezawa T, Ralph J** (2019) Solution-state multidimensional NMR of lignins: approaches and applications. *In* Fachuang Lu and Fengxia Yue, ed, Lignin: Biosynthesis, Functions and Economic Significance. Nova Science Publishers, Inc., Hauppauge, New York, USA, pp 79-110
81. **von Haden AC, Kucharik CJ, Jackson RD, Marín-Spiotta E** (2019) Litter quantity, litter chemistry, and soil texture control changes in soil organic carbon fractions under bioenergy cropping systems of the North Central U.S. Biogeochemistry **143:** 313-326
82. **Walker TW, Motagamwala AH, Dumesic JA, Huber GW** (2019) Fundamental catalytic challenges to design improved biomass conversion technologies. Journal of Catalysis **369:** 518-525
83. **Williams DL, Ong RG, Mullet JE, Hodge DB** (2019) Integration of pretreatment with simultaneous counter-current extraction of energy sorghum for high-titer mixed sugar production. Frontiers in Energy Research **6:** 133
84. **Wills BD, Kim TN, Fox AF, Gratton C, Landis DA** (2019) Reducing native ant abundance decreases predation rates in Midwestern grasslands. Environmental Entomology **48:** 1360-1368
85. **Woods D, Dong Y, Bouche F, Bednarek R, Rowe M, Ream T, Amasino R** (2019) A florigen paralog is required for short-day vernalization in a pooid grass. eLife **8:** e42153
86. **Xue C, Hao Y, Pu X, Ryan Penton C, Wang Q, Zhao M, Zhang B, Ran W, Huang Q, Shen Q, Tiedje JM** (2019) Effect of LSU and ITS genetic markers and reference databases on analyses of fungal communities. Biology and Fertility of Soils **55:** 79-88
87. **Yan X, Liu J, Kim H, Liu B, Huang X, Yang Z, Lin Y-C, Chen H, Yang C, Wang JP, Muddiman DC, Ralph J, Sederoff RR, Li Q, Chiang VL** (2019) CAD1 and CCR2 protein complex formation in monolignol biosynthesis in *Populus trichocarpa*. New Phytologist **222:** 244-260

88. **Zhang Y, Vera JM, Xie D, Serate J, Pohlmann E, Russell JD, Hebert AS, Coon JJ, Sato TK, Landick R** (2019) Multiomic fermentation using chemically defined synthetic hydrolyzates revealed multiple effects of lignocellulose-derived inhibitors on cell physiology and xylose utilization in *Zymomonas mobilis*. Frontiers in Microbiology **10:** 2596

2020

1. **Abraha M, Chen J, Hamilton SK, Robertson GP** (2020) Long-term evapotranspiration rates for rainfed corn and perennial bioenergy crops in a mesic landscape. Hydrological Processes **34:** 810-822
2. **Chew AK, Walker TW, Shen Z, Demir B, Witteman L, Euclide J, Huber GW, Dumesic JA, Van Lehn RC** (2020) Effect of mixed-solvent environments on the selectivity of acid-catalyzed dehydration reactions. ACS Catalysis **10:** 1679-1691
3. **Haan NL, Zhang Y, Landis DA** (2020) Predicting landscape configuration effects on agricultural pest suppression. Trends in Ecology & Evolution **35:** 175-186
4. **Helms JA, Ijelu SE, Wills BD, Landis DA, Haddad NM** (2020) Ant biodiversity and ecosystem services in bioenergy landscapes. Agriculture, Ecosystems & Environment **290:** 106780
5. **Kabbage M, Piotrowski JS, Thill E, Westrck NM, Ralph J, Hockemeyer K, Koch PL** (2020) Poacic acid suppresses dollar spot and snow mould in amenity turfgrass. Plant Pathology **69:** 112-119
6. **Karlen SD, Fasahati P, Mazaheri M, Serate J, Smith RA, Sirobhushanam S, Chen M, Tymkhin VI, Cass CL, Liu S, Padmakshan D, Xie D, Zhang Y, McGee MA, Russell JD, Coon JJ, Kaeppler HF, de Leon N, Maravelias CT, Runge TM, Kaeppler SM, Sedbrook JC, Ralph J** (2020) Assessing the viability of recovering hydroxycinnamic acids from lignocellulosic biorefinery alkaline pretreatment waste streams. ChemSusChem **DOI: 10.1002/cssc.201903345**
7. **Oshlag JZ, Ma Y, Morse K, Burger BT, Lemke RA, Karlen SD, Myers KS, Donohue TJ, Noguera DR** (2020) Anaerobic degradation of syringic acid by an adapted strain of *Rhodopseudomonas palustris*. Applied and Environmental Microbiology **86:** e01888-01819
8. **Petipas RH, Bowsher AW, Bekkerring C, Jack CN, McLachlan EE, White RAI, Younginger BS, Tiemann LK, Evans SE, Friesen ML** (2020) Interactive effects of microbes and nitrogen on *Panicum virgatum* root functional traits and patterns of phenotypic selection. International Journal of Plant Sciences **181:** 20-32
9. **Srivastava PA, Hegg EL, Fox BG, Yennamalli RM** (2020) PreDSLpmo: a neural network-based prediction tool for functional annotation of lytic polysaccharide monooxygenases. Journal of Biotechnology **308:** 148-155