

Microaerobic fermentation of algae biomass residuals for mixed alcohol production and nutrient recycling

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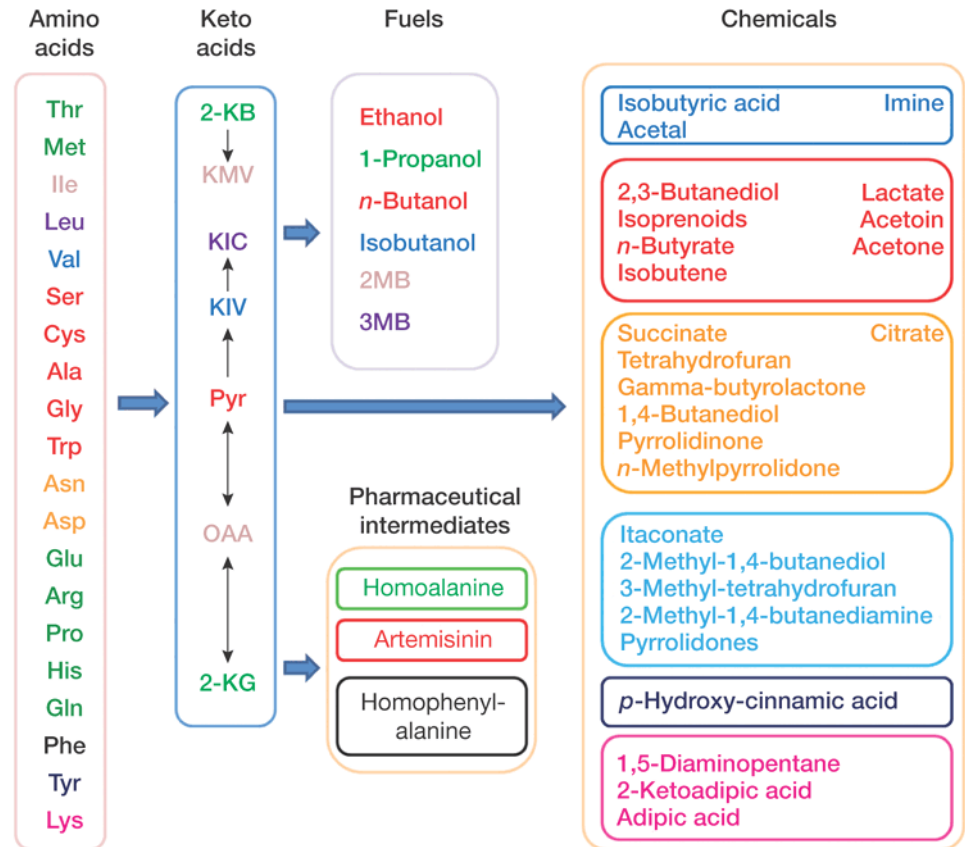
NREL, Golden CO

Conversion of amino acids to fuels, industrial chemicals, and pharmaceuticals

Chemical composition of algae

Strain	Protein	Carbohydrates	Lipids	Nucleic acid
<i>Scenedesmus obliquus</i>	50-56	10-17	12-14	3-6
<i>Scenedesmus quadricauda</i>	47	-	1.9	-
<i>Scenedesmus dimorphus</i>	8-18	21-52	16-40	-
<i>Chlamydomonas reinhardtii</i>	48	17	21	-
<i>Chlorella vulgaris</i>	51-58	12-17	14-22	4-5
<i>Chlorella pyrenoidosa</i>	57	26	2	-
<i>Spirogyra sp.</i>	6-20	33-64	11-21	-
<i>Dunaliella bioculata</i>	49	4	8	-
<i>Dunaliella salina</i>	57	32	6	-
<i>Euglena gracilis</i>	39-61	14-18	14-20	-
<i>Prymnesium parvum</i>	28-45	25-33	22-38	1-2
<i>Tetraselmis maculata</i>	52	15	3	-
<i>Porphyridium cruentum</i>	28-39	40-57	9-14	-
<i>Spirulina platensis</i>	46-63	8-14	4-9	2-5
<i>Spirulina maxima</i>	60-71	13-16	6-7	3-4.5
<i>Synechococcus sp.</i>	63	15	11	5
<i>Anabaena cylindrica</i>	43-56	25-30	4-7	-

Source: Becker (1994)



Consolidated Bioprocessing of Algae Biomass Residuals

Algae biomass is composed of roughly equal fractions of lipids, carbohydrates, and proteins

- Protein content is significantly higher than most terrestrial & multicellular organisms
- Protein compositional variation is low

Conversion of proteins to alcohols shows promise for **increasing fuel yields**, with significant potential for side benefits, including **boosting octane and reducing particulate emissions** via fuels blending

Ehrlich Mechanism

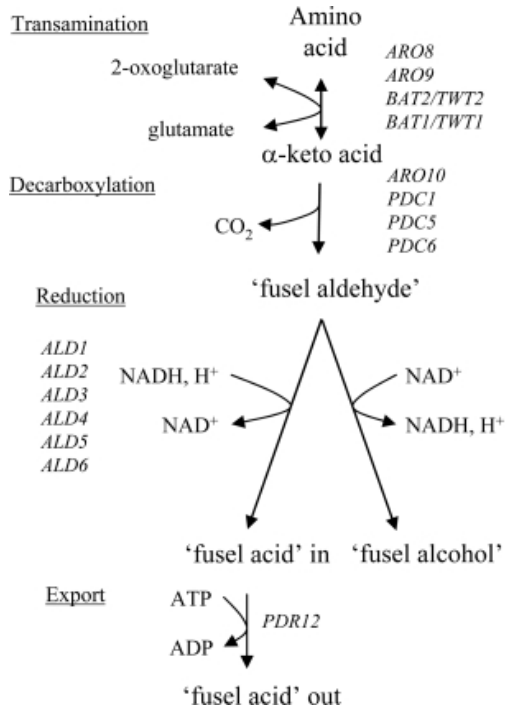
Pathway identified in *Saccharomyces* supporting amino acid metabolism

- Low yield, slow kinetics
- Inhibited by presence of fermentable sugars, etc.

Ehrlich pathway intermediates^a (from Hazelwood, et al. *Appl Environ Microbiol* 2008)

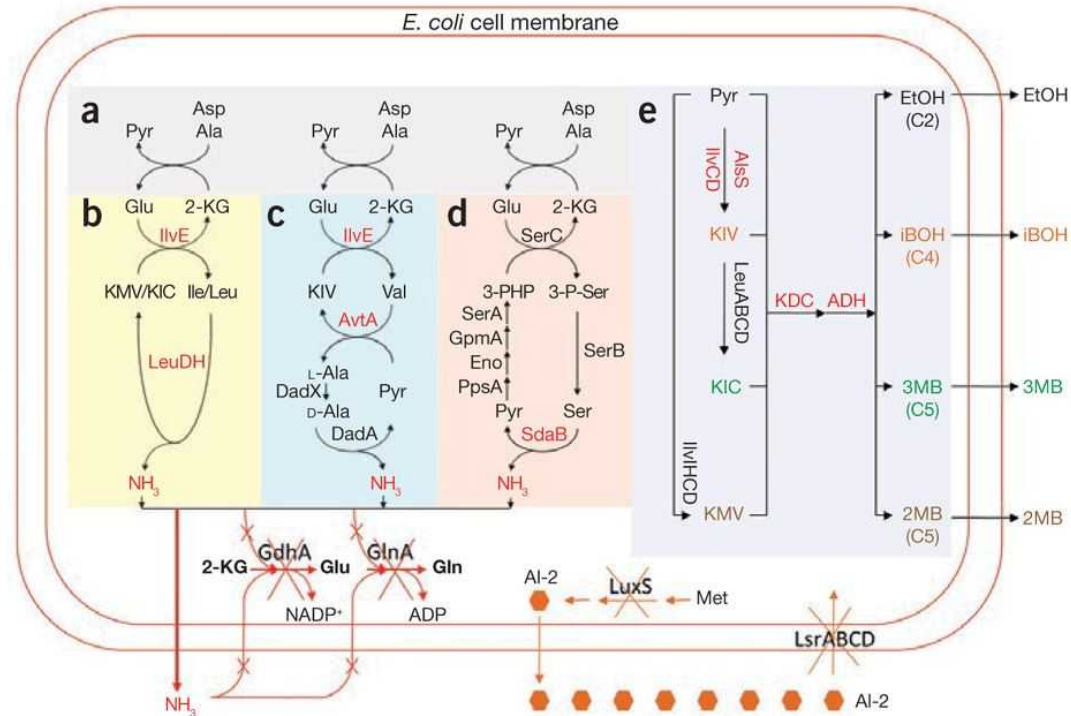
Amino acid	α-Keto acid		Fusel alcohol	
	Systematic	Traditional	Systematic	Traditional
Leu	4-Methyl-2-oxo-pentanoate	α-Ketoisocaproate	3-Methylbutanol	Isoamyl alcohol
Val	3-Methyl-2-oxo-butanoate	α-Ketoisovalerate	2-Methylpropanol	Isobutanol
Ile	3-Methyl-2-oxo-pentanoate	α-Ketomethylvalerate	2-Methylbutanol	Active amyl alcohol
Phe	3-Phenyl-2-oxo-propanoate	Phenylpyruvate	2-Phenylethanol	
Tyr	3-(4-Hydroxyphenyl)-2-oxopropanoate	p-Hydroxyphenylpyruvate	2-(4-Hydroxyphenyl)ethanol	p-Hydroxyphenylethanol or tyrosol
Trp	3-(Indol-3-yl)-2-oxopropanoate	3-Indole pyruvate	2-(Indol-3-yl)ethanol	Tryptophol
Met	4-Methylthio-2-oxobutanoate	α-Keto-γ-(methylthio)butyrate	3-(Methylthio)propanol	Methionol

Biochemical pathway & metabolic engineering



Oxidation

ADH1, *ADH2*, *ADH3*, *ADH4*, *ADH5*, *ADH6*, *SFA1*, *AAD3*, *AAD4*, *AAD6*, *AAD10*, *AAD14*, *AAD15*, *AAD16*, *YCR105W*, *YPL088W*



Pretreatment and fermentation conditions matrix

	Native SD 10% solids	Native SD 5% solids	DA SD liquor	DA SD solids	DA CZ solids	DA CZ liquor	SA SD liquor	DA, distilled light ferm bottoms	DA, distilled heavy ferm bottoms	IL prot-carb CZ
+ pronase	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗
- pronase	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗
+ IPTG	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗
- IPTG					✗	✗				
pH 7	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗
pH 5.2									✗	
+ vitamins					✗	✗				

SD = *Scenedesmus sp.*

CZ = *Chlorella sp.*

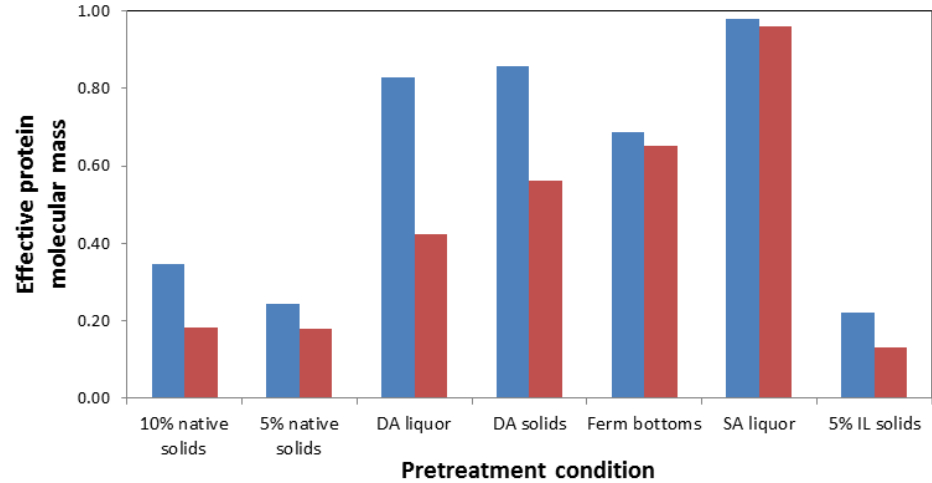
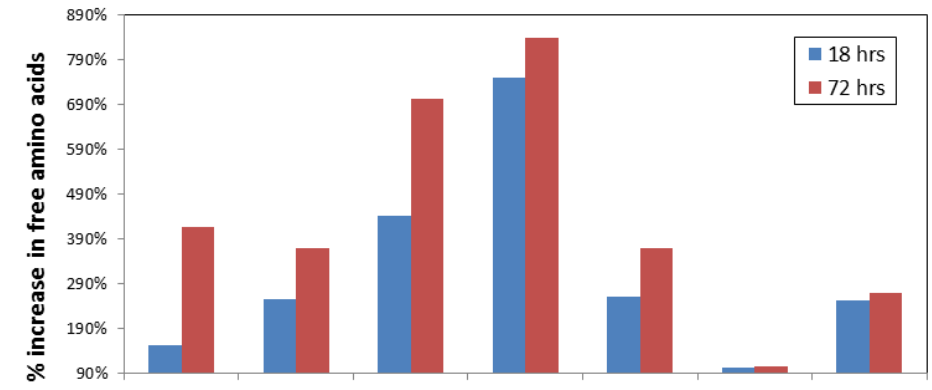
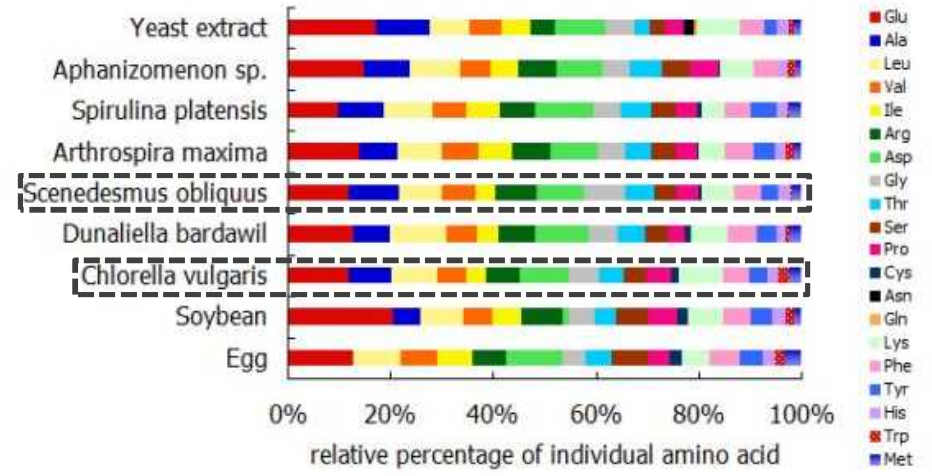
DA = dilute acid hydrolysis

SA = strong acid hydrolysis

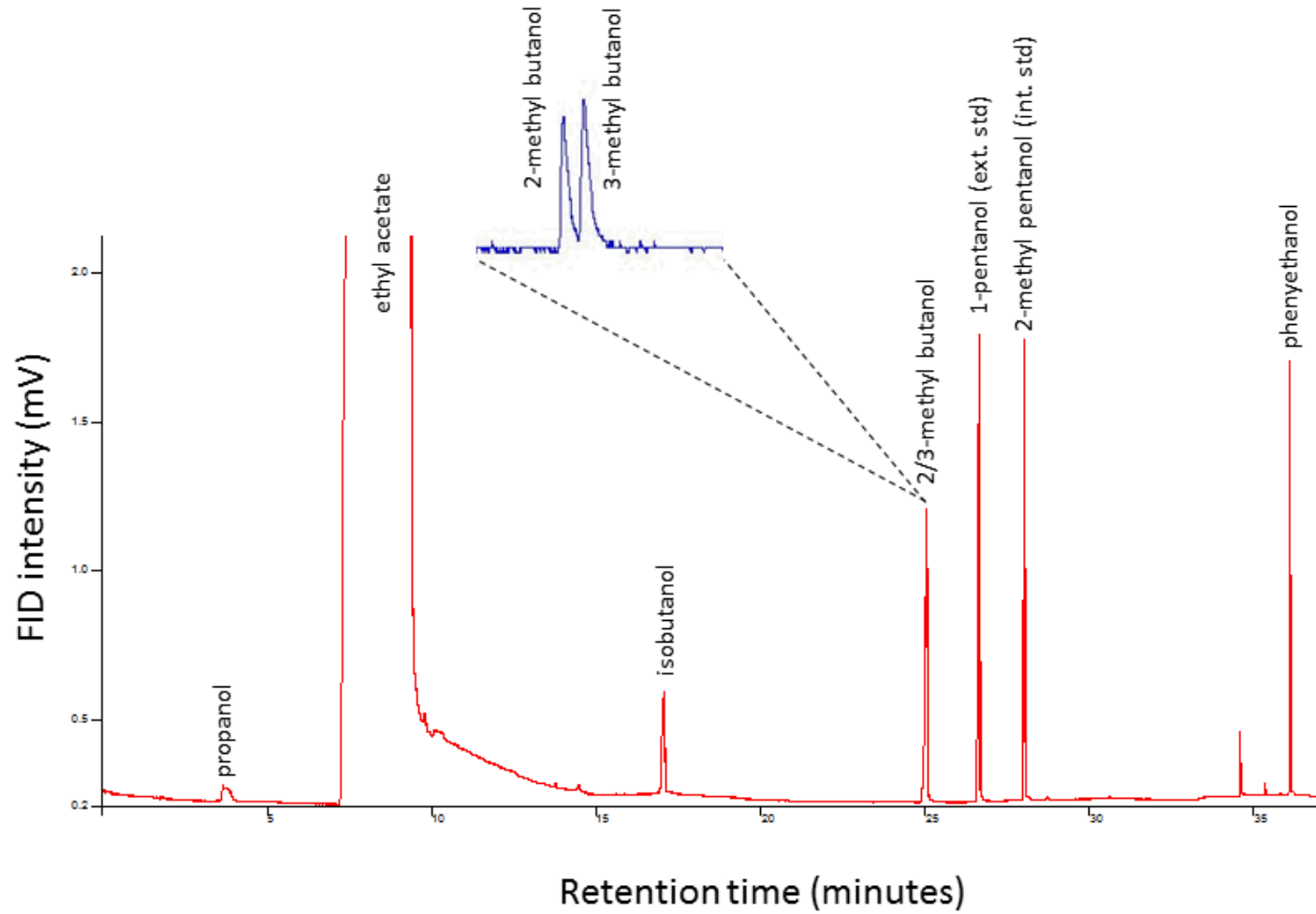
IL prot-carb = ionic liquid extracted protein/carbohydrate fraction

Hydrolysis of *Scenedesmus* and *Chlorella* biomass

- Dilute acid hydrolysis converts majority of carbohydrates to glucose (~90%)
- Proteins are only ~40% hydrolyzed to amino acids
- Strong preference for amino acids for conversion to mixed alcohols
- Enzymatic (pronase) digestion yields ~80% protein hydrolysis



Chromatographic analysis of alcohol production



Microaerobic fermentation of algae biomass residuals for fuel production and nutrient recycling

Goal: Develop process to maximize conversion of microalgal residuals to fuels and liberate N/P

Strategy: Subject pretreated microalgae biomass to microaerobic fermentation using a metabolically engineered *E. coli* strain, developed by J. Liao and co-workers (Xin Huo, et al *Nature Biotech*, 2011)

- Alcohol tolerance
- Assimilation of nitrogenous carbon sources
- Knock-down of quorum sensing

Results Overview

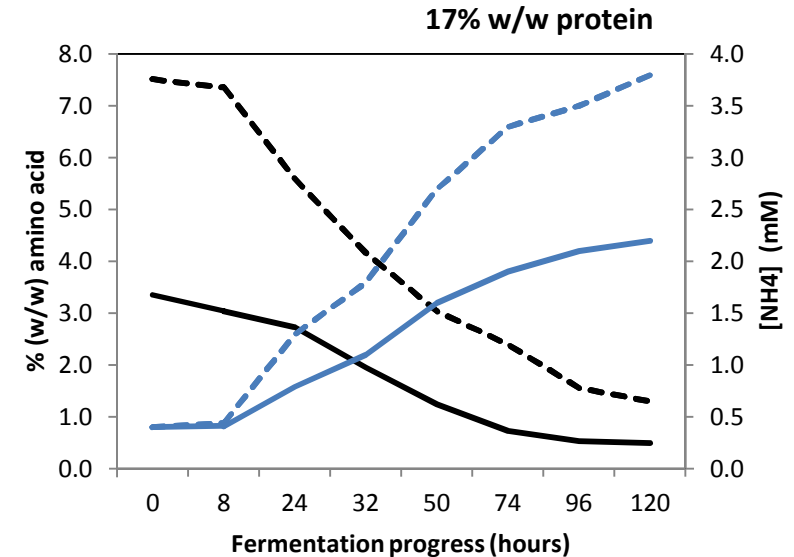
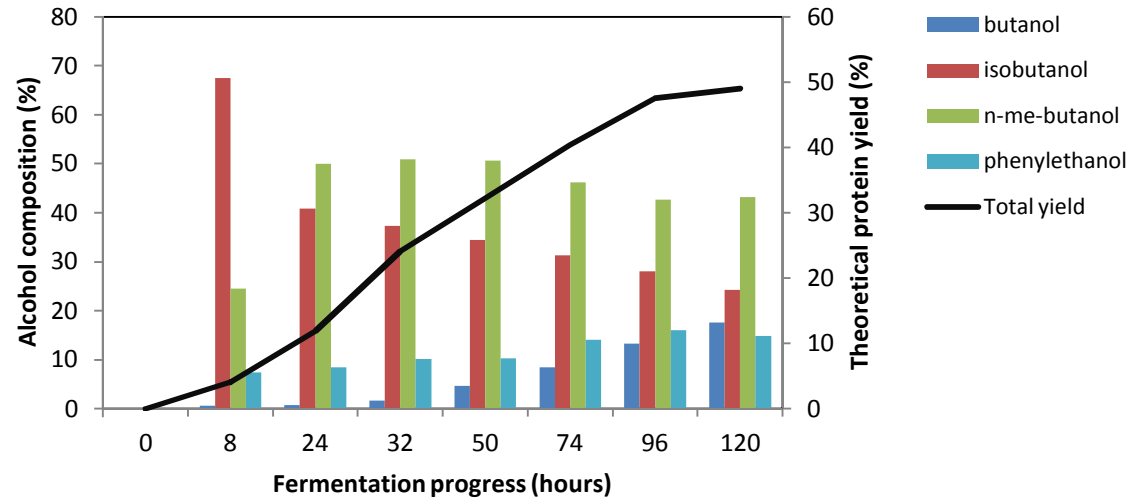
1) Mixed alcohols = 50% protein yield using 5-step process:

dilute acid pretreatment -> ethanolic fermentation -> distillation -> enzymatic digestion (proteins) -> microaerobic fermentation (37°C, 96-120 hrs)

2) Alcohol components do not significantly vary with biomass type
3) Accumulation of alcohols proceeds in distinct temporal phases:

isobutanol -> n-methyl-butanol -> phenylethanol and n-butanol

4) Ammonium is accumulated in fermentation liquor as amino acid breakdown product (stoichiometric with alcohol production)



- [amino acid]+enzyme
- [amino acid]-enzyme
- [NH4]+enzyme
- [NH4]-enzyme

Nuances, Challenges, & Opportunities

1.) Evidence for metabolic inhibition by some chemical components of algae biomass slurry: more aggressively lipid extracted biomass provides increased higher alcohol yields; ionic liquid pretreatment outperforms dilute acid for alcohol production: ammonium + alcohol products, TAG/phospholipids, sugars/sugar degradation products are likely to be inhibitory

2.) Different catalysis rates for different amino acids -or- are products re-entering metabolic pathways?

→ Optimization necessary for removing both desired and undesired products:

- Thermal trapping of alcohols during fermentation
- Precipitation of accumulated ammonium as phosphate mineral salts

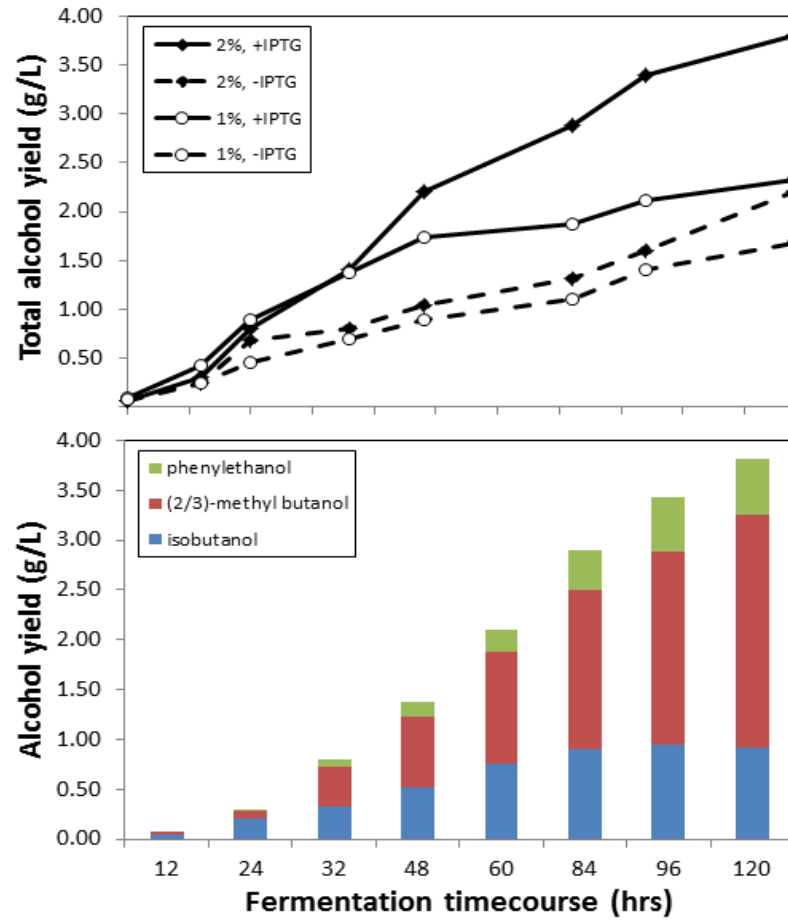
3.) How to eliminate dependence on enzymatic treatment?

Observation: NO alcohol production in dilute acid pretreated samples without enzymes; however we do observe alcohol production on native (untreated biomass), and biomass that has undergone preliminary ethanolic fermentation. In most cases, enzymes increase the total alcohol yield by **2x**. Furthermore, we observe release of distinct intermediates (dialcohols/ketones) with/without enzymatic treatment

→ Steps toward maximal consolidation of bioprocess:

- Co-fermentation of sugars & proteins (*Saccharomyces* + *E. coli* YH83, with thermal ramp)
- Heterologous expression of proteases in *Saccharomyces* and/or *E. coli* YH83
- Combine metabolic carbohydrate and protein -> mixed alcohol pathways in *E. coli* YH83
- Triggered protease expression based on carbon source, stabilization of expressed pathways
- Engineered intermediates via keto-isovalerate pathway up-regulation & thermophilicity (J. Takasumi)

Contribution of induced vs constitutively expressed genes to total mixed alcohol yield



Conclusions

- Conditions identified for optimal hydrolysis of algae biomass
- High yield of mixed alcohols from hydrolyzed algae biomass protein residuals
- Significant release of ammonium and phosphate for nutrient recycling
- Non-aerobic conditions offer significant cost reduction for biomass processing
- No need for co-factors (vitamins, trace elements)