

Genomics of “Candidatus Synechococcus spongiarum”, a Cyanobacterial Sponge Symbiont

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March 21, 2014

ACKNOWLEDGMENTS:

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231. Additional support was provided to Beate Slaby by a grant of the German Excellence Initiative to the Graduate School of Life Sciences, University of Wuerzburg and to Ute Hentschel by a DOE Joint Genome Institute grant (CSP 1291) .

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Background

- Marine sponges (Porifera): ancient metazoans of ecological importance, that produce bioactive secondary metabolites and interact with various microorganisms including cyanobacteria¹
- Marine *Synechococcus* spp.: cyanobacteria, important contributors to the global carbon cycle and major primary producers in the oceans²
- "Ca. *S. spongiarum*": an ecotype of this genus, widespread and abundant symbiont of various marine sponges around the world³, e.g. *Aplysina aerophoba*

Research questions

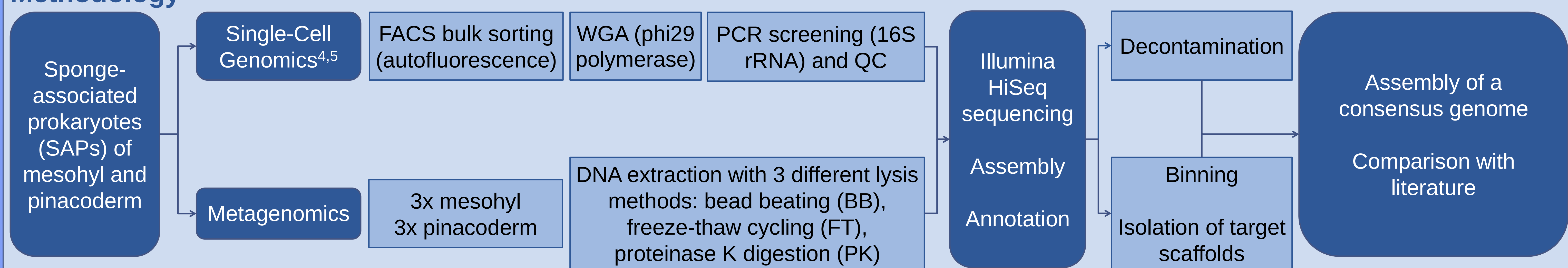
- What are the genomic differences between the cyanobacterial sponge symbiont and the free-living ecotypes?
- What are the adaptations of the symbiont's genome to an existence in sponges?
- What is the functional role of these symbionts within the context of the host sponge?



Aim

Create a consensus genome of "Ca. *S. spongiarum*" to investigate its adaptations to a symbiotic existence within marine sponges

Methodology



Sample name	Sample type	Derived from	Status	Total scaffold length (MB)	GC content (%)
Mesohyl BB	metagenome	<i>Aplysina aerophoba</i> SAPs	data ready	214.952	61.09
Mesohyl FT				217.671	61.09
Mesohyl PK				298.825	58.65
Pinacoderm BB				202.603	60.96
Pinacoderm FT				245.565	60.69
Pinacoderm PK				229.802	59.69
Marine sponge itags	iTags				
Bulk 10D	'single-cell' sample	FACS bulk sort 2013-05-10	in annotation		
Bulk 10E					
Bulk 15L					
Bulk 15M					
Bulk 15N					

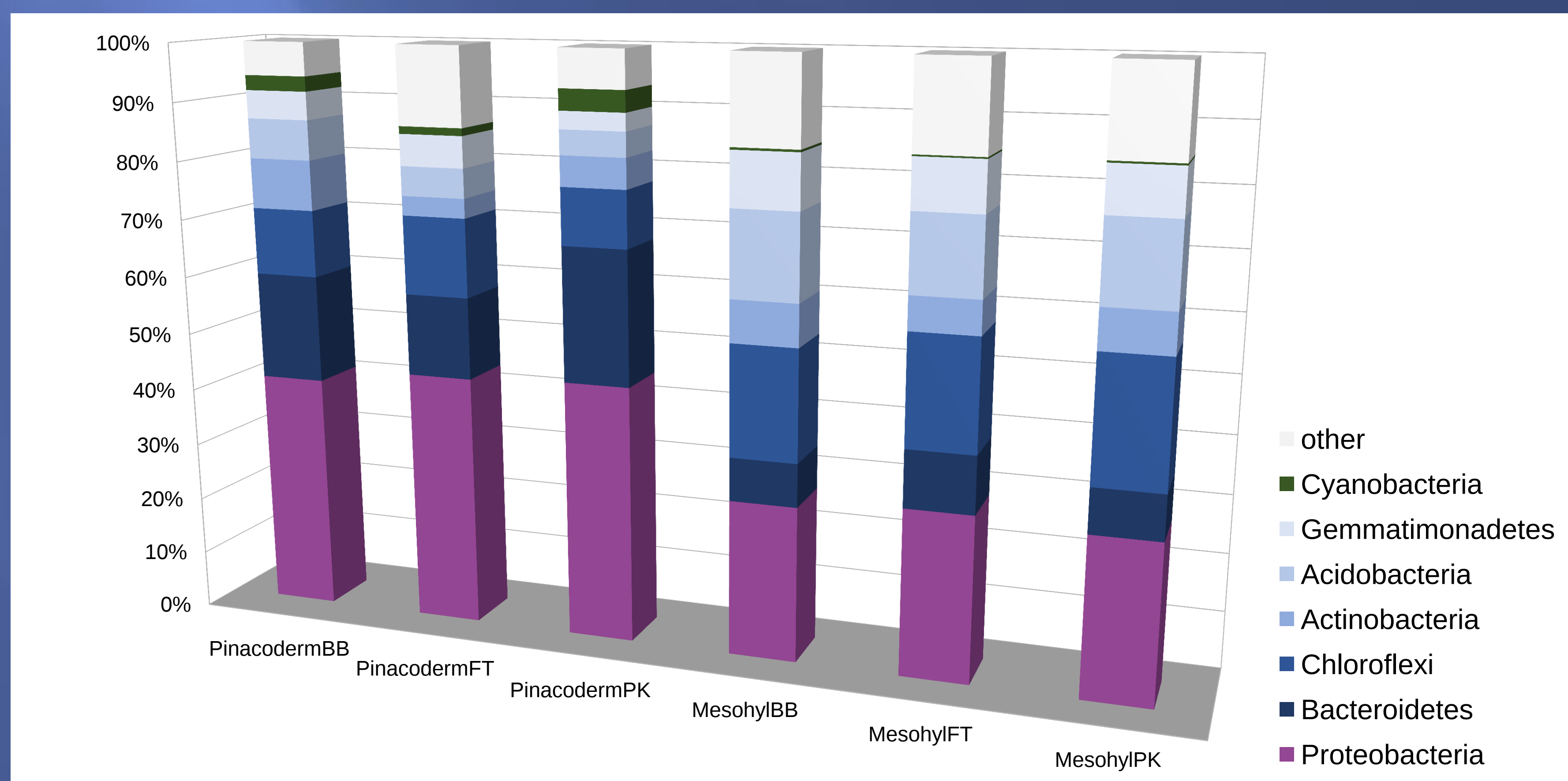


Fig. 1 Bacterial phylum composition per metagenome in the iTag dataset: pinacoderm (outer tissue) communities are more similar to each other than to mesohyl (inner tissue) communities. A trend towards differential coverage of bacterial phyla due to the different cell lysis methods is visible in comparison of the pinacoderm datasets to each other.

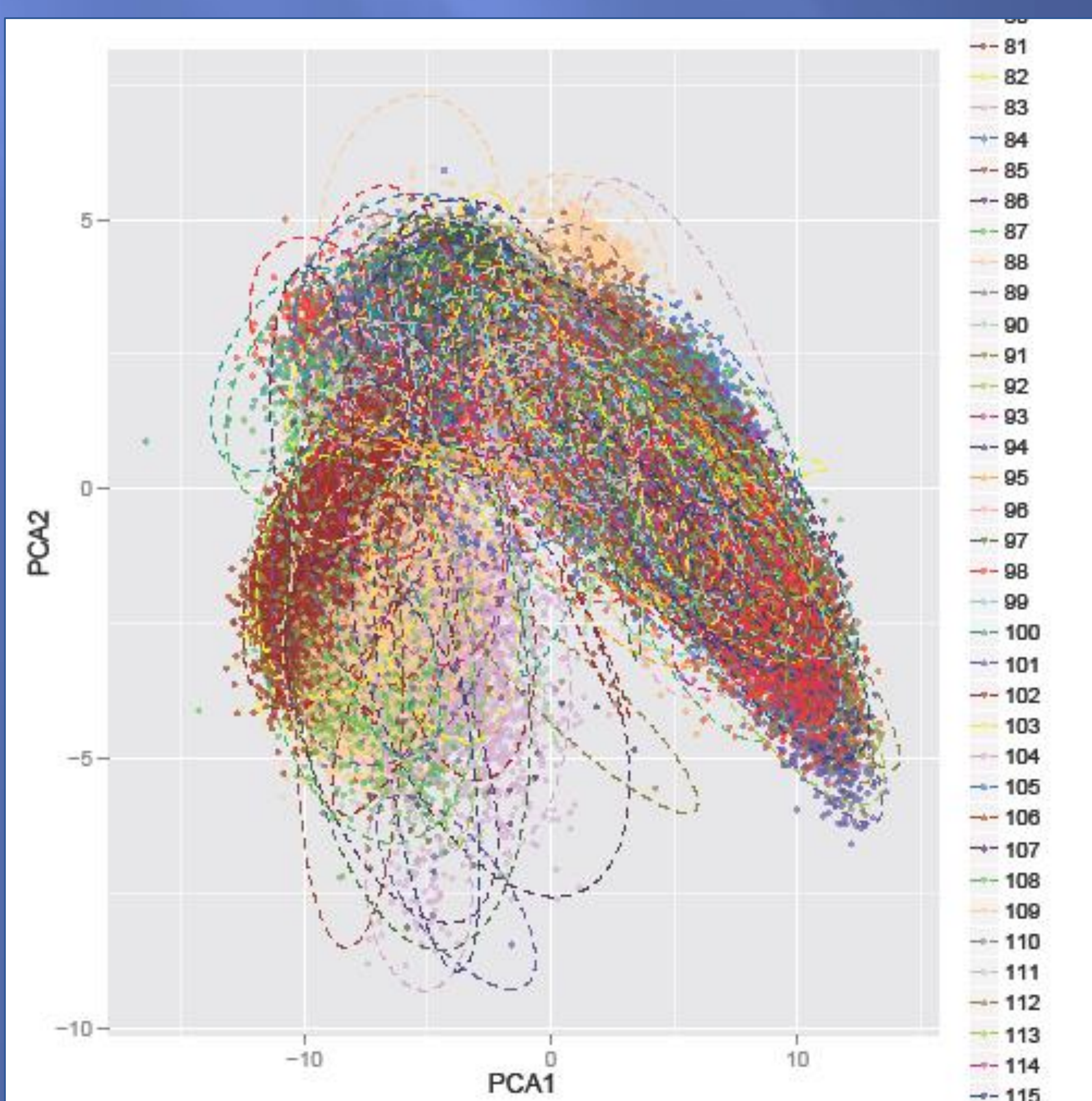


Fig. 2 PCA plot: binning with Concoct⁶ of a combined assembly (SOAPdenovo) of all six metagenomic datasets using differential coverage. Numbers/colors are bin numbers determined by Concoct. While a visual differentiation of bins is not possible in such a complex microbial community, the table of bins (not shown) can be used to find the target scaffolds.

Work in Progress

- Implementation of phylogenetic data
- Continued implementation of other binning methods
- Tracking of bins containing cyanobacterial scaffolds and assembly of a consensus genome of "Ca. *S. spongiarum*"
- Implementation of single-cell data to complete the consensus genome and get insight into differences between individual genomes, depending on quality of single-cell data
- Analysis of metabolic pathways
- Comparison with genomes of free-living *Synechococcus* spp.

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Acknowledgements

Support was provided to B.S. by a grant of the German Excellence Initiative to the Graduate School of Life Sciences, University of Wuerzburg, and to U.H. by a DOE Joint Genome Institute grant (CSP 1291).