

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

Beate M. Slaby^{1*}, Alex Copeland², Tanja Woyke², Ute Hentschel¹

¹ Department of Botany II, Julius-von Sachs Institute of Biological Sciences, University of Wuerzburg - Germany

² LBNL Department of Energy Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, USA

**To whom correspondence should be addressed:* Email: beate.slaby@uni-wuerzburg.de

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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Beate M. Slaby*,¹ Alex Copeland,² Tanja Woyke,² and Ute Hentschel¹

¹Department of Botany II, Julius-von-Sachs Institute of Biological Sciences, University of Wuerzburg

²DOE Joint Genome Institute, Walnut Creek, California, USA

contact: beate.slaby@uni-wuerzburg.de



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

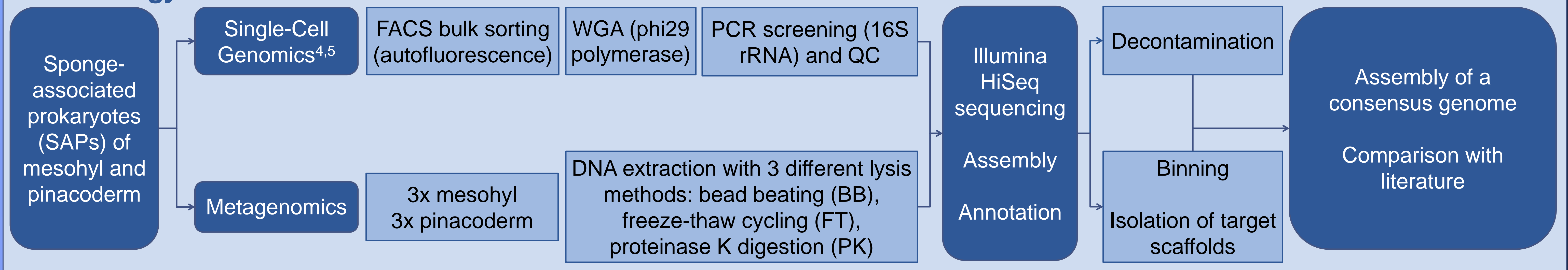
- What are the genomic differences between the cyanobacterial sponge symbiont and the free-living ecotypes?
- What are the adaptations of the symbiont's genome to an existence in sponges?
- What is the functional role of these symbionts within the context of the host sponge?



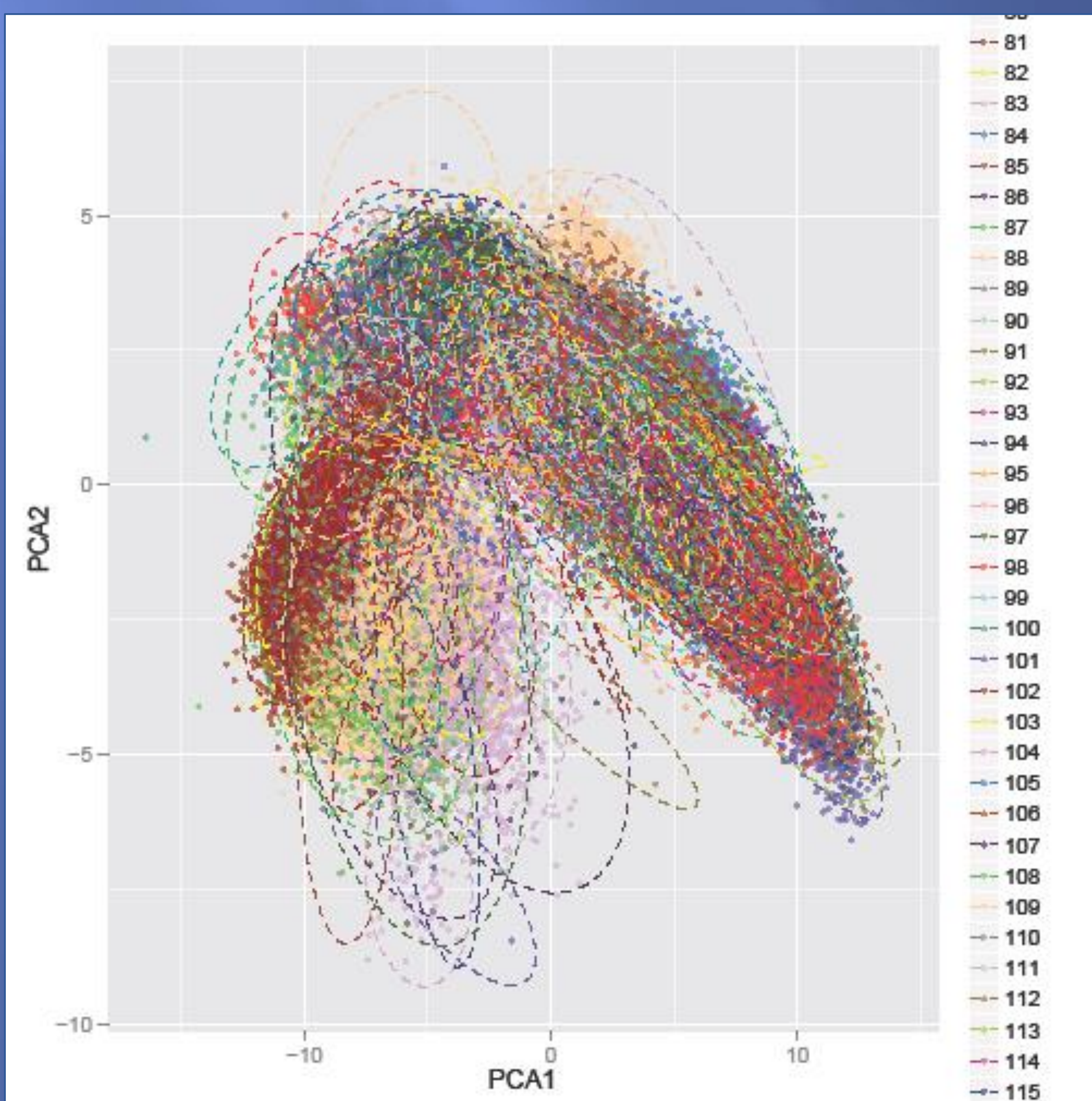
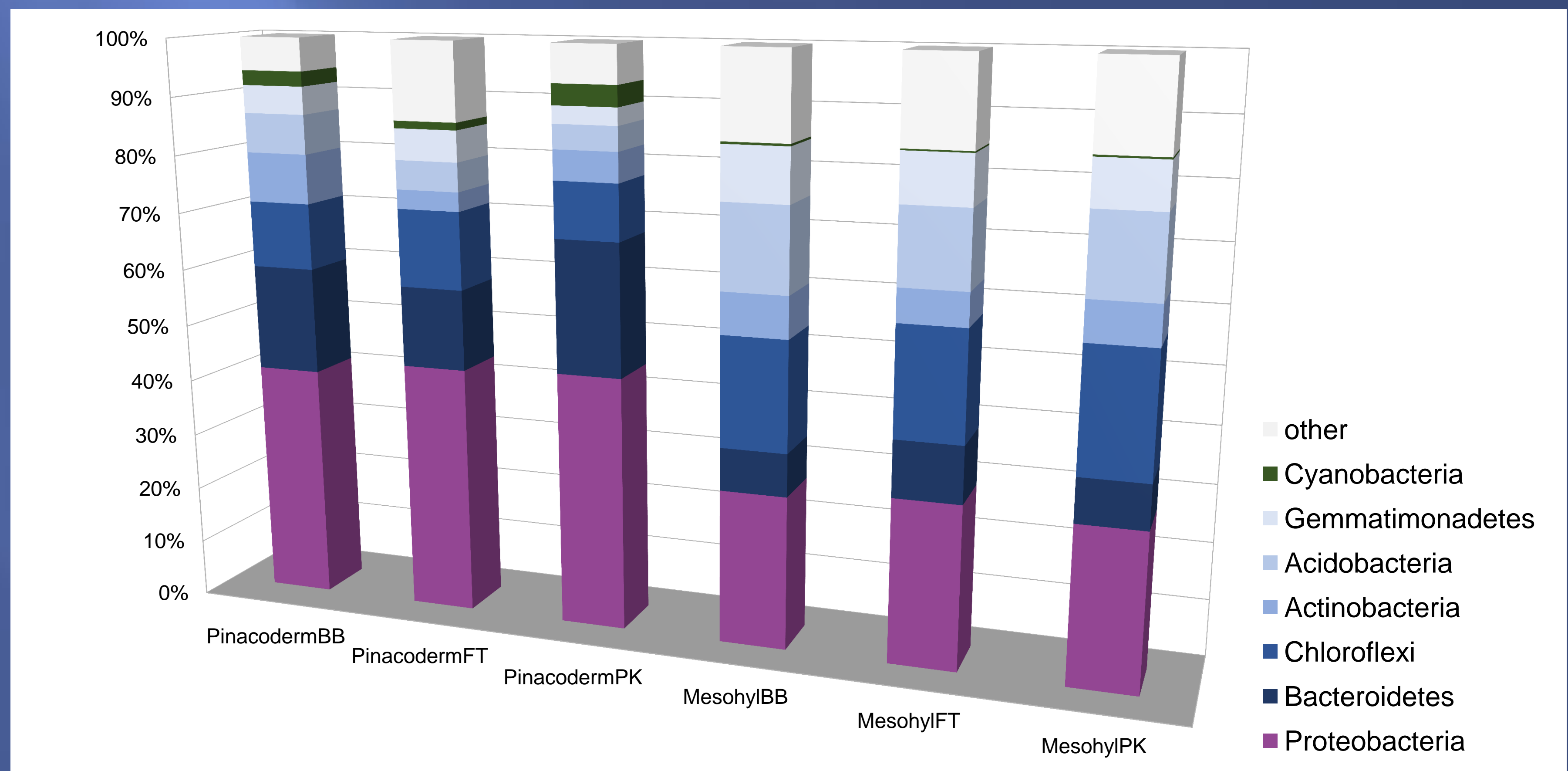
Aim

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				FACS bulk sort 2013-05-15	in sequencing		
Bulk 15M							
Bulk 15N							



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.

References

- ¹ Hentschel U, Piel J, Degnan SM, Taylor MW (2012) Nat Rev Microbiol 10:641-654
- ² Coelho SM, Simon N, Ahmed S, Cock JM, Partensky F (2013) Mol Ecol 22:867-907
- ³ Erwin PM, Legentil SL, Turon X (2012) Microb Ecol 64:771-783
- ⁴ Kamke J, Sczyrba A, Ivanova N, Schwientek P, Rinke C, Mavromatis K, Woyke T, Hentschel U (2013) ISME J 7:2287-2300
- ⁵ Kamke J, Bayer K, Woyke T, Hentschel U (2012) Biol Bull 223:30-43
- ⁶ Alneberg J, Bjarnason BS, de Bruijn I, Schirmer M, Quick J, Ijaz UZ, Loman NJ, Andersson AF, Quince C (2013) arXiv:1312.4038

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).