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The supragenome and the world of non-coding RNAs in cyanobacteria

Analyses of 22 total genome sequences of closely related marine picocyanobacteria showed an unprecedented number of differences in their genome size, the number of annotated protein-coding genes and GC content. These cyanobacteria belong to only two genera, the chlorophyll *b*-possessing *Prochlorococcus* and *Synechococcus*. The population size of marine unicellular cyanobacteria in the ocean has been estimated at $>10^{27}$ and their genes amount to a significant share in marine metagenome projects. We have determined the core genome at 1201 – 1206 genes, which is consequently the minimum number of genes for a free-living photosynthetic organism. In contrast, the total number of protein-coding genes available to *Prochlorococcus/Synechococcus* according to the distributed genome model amounts to about 35,000. However, these numbers do not include yet the genes for regulatory and non-coding RNA (ncRNA). Regulatory RNA has been discovered in all three domains of life. Thus far, in cyanobacteria only a small number of ncRNAs has been described. We have used 5 different methods for the identification of novel non-coding and antisense RNAs in various cyanobacteria, yielding about 150 ncRNAs within the more compact genomes of marine cyanobacteria, several hundred putative transcripts within intergenic spacers or in antisense orientation in the model cyanobacterium *Synechocystis* PCC6803, and possibly up to 1.000 in the most complex genomes of nitrogen-fixing cyanobacteria. Among these, IsrR, an antisense RNA to the *Synechocystis isiA* gene regulates the expression of *isiA* under iron and redox stress. Although functions are still unknown for the vast majority of cyanobacterial ncRNAs, and for *cis*-encoded antisense RNAs even their systems principles of action still need to be elucidated, it is apparent that it is not possible to understand the intracellular regulatory network in all its complexity without detailed information about the numbers and functions of these regulators.

CV

Jan 2008 – present	Full Professor for Genetics (W3), University Freiburg, Germany
Sep 2006 – present	Speaker of the Freiburg Initiative in Systems Biology (“FRISYS”)
Apr 2004 – Dec 2007	Professor for Experimental Bioinformatics (C3), Univ. Freiburg, Germany
Jan 2003 – Aug 2004	Funding Director of Ocean Genome Legacy Foundation in Beverly, U.S.
1999 – Dec 2002	Associate Professor Genetics (C2), Humboldt-University Berlin
Sep – Dec 2000	MIT, Cambridge, U.S. (Fellow Human Frontier Science Program)
1999	Habilitation (Genetics) Humboldt-University Berlin, Germany
1994 – 1999	Assistant Professor Genetics (C1), Humboldt-University Berlin
1993 – 1994	Postdoctoral Research Fellow, Observatoire Océanologique de Roscoff, CNRS, France
1990 - 1993	Research Assistant, Humboldt-University Berlin
Sep – Dec 1990	Friedrich-Miescher-Institut Basel, Switzerland, EMBO Fellow
1987 - 1990	Reading for a PhD in Plant Molecular Genetics. *Thesis* 1990.
1983 - 1987	Student, Humboldt-University Berlin (Biology)
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