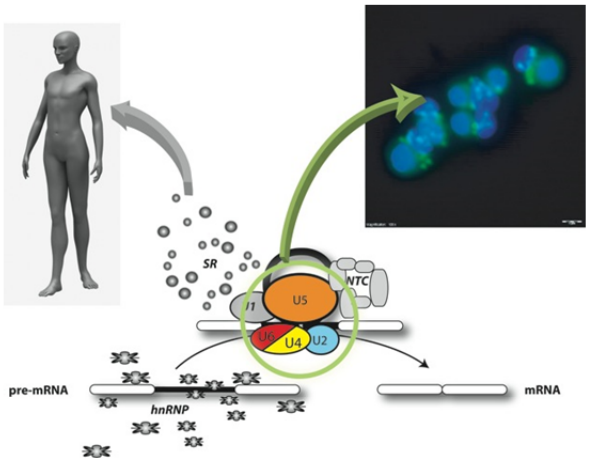
SFB 960-/BZR – Kolloquium

21. September 2017, 14.00 Uhr
H53



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The Highly Reduced Spliceosome of *Cyanidioschyzon merolae*

Genomic intron densities are highly variable across species, ranging from many introns per transcript in humans to fewer than one per transcript in some microbes. The extremophilic red alga, *C. merolae*, has taken intron reduction to an extreme, harboring only ~40 introns in its 5000-gene genome. This raises the question of whether this alga contains the canonical set of splicing machinery, which in humans comprises 5 small, nuclear RNAs and over 200 proteins.

To study the biological role of this tiny intron complement, Stephen and his group have characterized the splicing machinery in *C. merolae*. Surprisingly, it is completely lacking the U1 snRNP, comprises only~40 core proteins, has but a single LSm complex, and appears to have an RNA degradation complex associated with it.

The unexpected observation of apparent splicing regulatory proteins raised the possibility that the splicing events in *C. merolae*, few though they are, are regulated in response to environmental conditions or other cues. Stephen will discuss current efforts to investigate this possibility. The small size of the *C. merolae* spliceosome make this a promising system in which to study core features of the splicing pathway, as well as the evolutionary pressures that result in reduced splicing systems.