

Protists as a goldmine of non-standard variants of the genetic code.

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Most translation systems employ the same genetic code to interpret the nucleotide sequence in mRNA, but exceptions described from various organisms revealed an unexpected evolutionary flexibility of this fundamental molecular mechanism. A series of groundbreaking discoveries in past two years have fundamentally expanded the known diversity of genetic codes in eukaryotic nuclear genomes and unveiled new aspects of the evolutionary processes behind the origin of non-standard code. My lab substantially contributed to this progress by discovering three novel genetic code variants. One, reported from a clade of trypanosomatid, is striking in that the codons UAG and UAA have a context-dependent meaning as sense or stop codons, depending on their position in mRNA. Two other codes, found in the fornicate *Iotanema spirale* and in a novel elusive rhizarian from the Sainouroidea group, share the unique property of having reassigned the UAG codon as a sense one while keeping UAA as the termination codon. This finding for the first time shows that the eukaryotic translation apparatus can evolve to discriminate between the UAG and UAA codons. In the first part of the presentation I will provide a review of these and other already published exciting discoveries. In its second part I will present new findings concerning alternative genetic codes achieved in a broader collaborative project led by my lab. Firstly, I will report on our discovery of three additional organisms from three different taxonomic groups (Ciliophora, Stramenopiles, Heterolobosea) that have the same genetic code as we previously described in *Iotanema spirale*, i.e. that have reassigned the UAG (but not UAA) codon to encode glutamine. Secondly, I will summarize our new findings about the distribution and evolution of genetic code variants in ciliates. Our results further support the view that protists are a fascinating resource of non-standard biology at the molecular level.