this phagomixotroph's genome was found to retain a unique combination of genes not present in obligate photoautotrophs or heterotrophs. Additional prasinophytes have been found to ingest fluorescently-tagged bacteria and synthetic particles. To investigate drivers of bacterivory in *Cymbomonas*, cultures of the alga were grown under limited N, P and light regimes and fed bacteria as a rescue source of nutrients. The *Cymbomonas* genome was also mined for metabolic genes related to nutrient uptake and assimilation. Surprisingly, bacteria only rescued *Cymbomonas* growth under phosphate-limited conditions, but not when nitrogen or light-limited. The genome contains genes related to phosphate metabolism that are not present in other Chloroplastida. A full GS-GOGAT pathway is present and no unique nitrogen-related genes were found. These results suggest that *Cymbomonas* retains the ability to extract phosphorous from prey, but relies on photoautotrophic pathways for nitrogen and carbon. This trait gives *Cymbomonas* a competitive advantage in P-limited cultures and may drive retention of bacterivory in this species.

SUPPLIMENTING SYMBIONTS: PATHWAY RESTORATION IN A LONG TIME PARASITE

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Apicomplexans are highly successful parasites, infecting every major metazoan lineage. The genus *Nephromyces* has recently been described as having a mutualistic relationship to its host *Molgula tunicates* (Saffo et al., 2010), making *Nephromyces* the only reported mutualistic apicomplexan genus. Apicomplexans have reduced genomes and have lost the ability to make many essential metabolites. These essential metabolites are instead scavenged from their host. Species of *Nephromyces* are known to have three different bacterial endosymbionts. Our data show that the bacterial endosymbionts encode a number of essential pathways lost in Apicomplexans. Here we describe insights from the transcriptome from *Nephromyces*, all three bacterial endosymbionts and the tunicate host. These data gives us a glimpse of the complex metabolic relationships and intertwined pathways of hosts and endosymbionts, with a particular focus on the biosynthesis of amino acids and vitamins.

TWO NEW NON-CANONICAL NUCLEAR GENETIC CODES FROM A RHIZARIAN AND A FORNICATE WITH UAG, BUT NOT UAA, AS A SENSE CODON

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The original presumption that all organisms use the same (standard) genetic code for translation of mRNA sequences into proteins has been challenged by discoveries of deviations of this universal language in both prokaryotes and eukaryotes. In eukaryotes the nuclear genetic code has proven to be much more conservative than that of mitochondria, and plastids; just a few its variants are known. Generally, we can sort them into 3 groups: (1) UGA serves as a sense codon; (2) UAA and UAG simultaneously serve as sense codons; (3) CUG encodes serine or alanine (rather than leucine). We analyzed transcriptomic data from two unrelated protists and found out that these organisms, as only eukaryotes known so far, use UAG as a sense codon in nuclear genetic code while retaining UAA as a termination codon. One of these organisms uses UAG as codon for leucine, similarly to a code variant described from certain mitochondria. The other one instead uses UAG to encode glutamine, resembling thus the non-canonical genetic code of several eukaryotic groups including many ciliates, hexamitin diplomonads, some oxymonads, and some ulvophytes; however, all these taxa have at the same time reassigned also the UAA codon. Phylogenetic analyses place the first organism into the rhizarian lineage Sainouroidea, whereas the second one represents an undescribed lineage of "*Carpediemonas*-like organisms" in Fornicata (Metamonada). Our findings thus once again show protists as an inexhaustible resource of peculiar departures from the "standard" biology.

AGAMOCOCCIDIANS: COCCIDIANS OR GREGARINES? NEW SPECIES AND NEW DATA ON THE PHYLOGENETIC POSITION OF THE GROUP

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Agamococcidians (Agamococcidiorida Levine, 1979) represent an enigmatic group of Apicomplexa. The life cycle of these parasites is characterised by presence of oocysts with sporocysts (similar to coccidian), sporozoites and trophozoites, and by absence of merogony and gamogony. This group combines two families Rhytidocystidae Levine, 1979, parasites of polychaetes, and Gemmocystidae Upton & Peters, 1986, parasites of stony corals. The phylogenetic position of these organisms is still unclear. Previous phylogenetic studies brought agamococcidians together with gregarines and cryptosporidians (Leander, Ramey, 2006; Rueckert, Leander, 2009; Kristmundsson et al., 2011; Cavalier-Smith, 2014). In contrast, morphological data (oocysts with sporocysts and nonmotile trophozoites located within host epithelial tissues) indicate a relationship of agamococcidians with coccidians. We isolated two putative new species of *Rhytidocystis* from polychaetes *Pectinaria hyperborea* and *Ophelia limacina* collected in the Keret Archipelago of the White Sea, Russia. The SSU rDNA sequences obtained from these new parasites clustered strongly with *Rhytidocystis cyamus* and *R. polygordiae* within the rhytidocystid clade. Phylogenies inferred from these sequences demonstrate a close relationship between rhytidocystids and marine coccidians. Interestingly, some coccidians closely related to rhytidocystids, such as *Margolisiella islandica* or *Aggregata* sp., have all three types of reproduction found among apicomplexans: sporogony, merogony and gamogony in their life cycles. Thus, our molecular data agree with known morphological data. We discuss the phylogenetic position and perspectives of further investigations of agamococcidians for more deep understanding of Apicomplexa evolution.

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CAPSASPORA OWCZARZAKI AS A UNICELLULAR MODEL TO STUDY CO-OPTION OF THE ANCESTRAL INTEGRIN ADHESOME

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Adhesion systems and signaling networks are both essential in multicellular organisms. Some elements of the adhesion and signaling pathways of metazoans, such as proteins from the integrin adhesome are conserved in their closest unicellular relatives. This means these proteins already existed in the unicellular ancestor of metazoans and that they were co-opted for a multicellular lifestyle. To understand how the integrin adhesome was co-opted at the onset of Metazoa, we aim to unravel its function in a close unicellular relative of animals, the filasterean *Capsaspora owczarzaki*. This protist is the closest unicellular relative to metazoans that contains in its genome the basic core of proteins that constitutes the integrin adhesome. The expression of these proteins is upregulated during the aggregative stage in culture conditions. In order to understand its role, we are developing some molecular and genetic tools, such as immunostaining, transfection, and CRISPR/cas9. We will discuss preliminary data on the localization of several cytoskeletal and adhesion proteins of the integrin adhesome in *C. owczarzaki*, obtained by overexpression and by immunostaining with antibodies raised against our proteins of interest. We will also discuss the development of CRISPR system in this organism with the aim to develop a complete model system to analyze the origin of animals.

ORAL PROTISTS: IMPORTANCE TO CANINE PERIODONTAL DISEASE

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