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Mating-system evolution in *Euplotes*, from the Mendelian to a molecular approach
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Euplotes evolved multiple mating systems which have for long been assumed to be determined by "open" series of alleles at a single *mat* locus. Families of mating type-specific pheromones and of their *mat* coding genes have been extensively characterized from *Euplotes* species lying in different positions of *Euplotes* phylogenetic tree, and this characterization permitted the study of *Euplotes* mating systems to evolve from a Mendelian to a molecular approach. While early branching species (e.g. *E. raikovi*) show a mating-type determination at a single *mat* locus in accord with Mendelian genetics, late branching species (e.g. *E. crassus*) revealed, in disagreement with Mendelian genetics, a mating-type determination at two distinct *mat* loci implying an event of *mat*-gene locus duplication. One locus (orthologous) appears to be multi-allelic and deputed to synthesize pheromones distinctive of different mating types, and the second one (paralogous) deputed to synthesize pheromones that are structurally identical among different mating types.

12B-5

Evolution and distribution of MAT and MATX genes in euglenids
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Methionine adenosyltransferase (MAT) is an ubiquitous, essential enzyme that occurs in eukaryotes in two paralogs, MAT and MATX. MATX was found in a variety of unrelated organisms. Its distribution in the tree is punctuated, which could have arisen by differential losses of old paralogs or by horizontal gene transfers of one of them between eukaryotes. Our aim was to map the distribution of MAT/MATX genes in euglenids. We gained data from 23 various euglenids and one prasinophyte alga *Pyramimonas parkae*, the closest known relative of euglenid secondary plastid. In two euglenid species we found both types MAT and MATX. MATX was present only in the photoautotrophic euglenids, while heterotrophs, mixotroph *Rapaza viridis* and *Pyramimonas* possess MAT form. Our results suggest that the MATX distribution is restricted to photoautotrophs. If it was introduced into this clade by HGT, the transfer was not connected to the origin of secondary plastid.

12B-6

Comparison of pre-mRNA splicing in two unicellular eukaryotes
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The process of spliceosomal intron removal from pre-mRNA is conserved across eukaryotes, and is catalyzed by one of the largest molecular machines in the cell. The spliceosome is made up of five small nuclear RNAs (snRNAs) and many associated proteins, ranging from 100 in yeast to more than 200 in humans. In the unicellular eukaryotes *Encephalitozoon cuniculi* and *Cyanidioschyzon merolae*, genomic reduction has resulted in the loss of many genes, including those that encode spliceosomal components. *E. cuniculi* has just 30 spliceosomal proteins, while fewer than 10 are predicted in *C. merolae*. Surprisingly, we cannot identify the U1