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Chromosomes of Protists: the crucible of evolution

Marie-Odile Gobillard
Observatoire Oceanologique (CNRS-Université Paris 6), Banyuls-sur-Mer, France

As early as 1925, the great protozoologist Edouard Chatton classified microorganisms into two categories, the prokayotic and the eukaryotic microbes, according to the only observation of their nuclear organization by means of light microscopy. Now, by means of TEM, we know that prokaryotic microbes are characterized by the absence of nuclear envelope surrounding the bacterial chromosome, which is more or less condensed and whose chromatin is deprived of histone proteins but presents specific basic proteins. Eukayotic microbes, the Protists, have nucleus surrounded by nuclear envelope and chromosomes more or less condensed whose chromatin are provided with classical histone proteins organized into nucleosomes. The extraordinary diversity of the mitotic systems presented by the 36 phyla of Protists (according to Margulis et al, 1990, Handbook of Protoctista) is in opposition with the relative homogeneity of their chromosome structure and chromatin components, except for the Mesokaryotes Mesokaryotes comprise essentially the 4,000 species of Dinoflagellates, in which the original features presented by their nucleus (dinokaryon), their dinomitosis and chromosome organization as well as their chromatin composition, question us. Although their DNA synthesis is typically eukaryotic, Dinoflagellates are the only eukaryotes in which the chromatin, organized into quasi permanently condensed chromosomes, is totally devoid of histones and nucleosomes. It contains specific DNA-binding basic proteins and the permanent compaction of their chromosomes during the whole cell cycle puts the question of modalities of their division and transcription. Since the genesis of the Last Eukaryotic Common Ancestor (LECA), Protists have ceaselessly colonized every biotope on our planet. They have left fossil traces (i.e. dinosteranes in the early Cambrian stratus, and petroleum layers) as well as current (planktonic food chains, Ciliates in the ruminant paunch, HyperMastigines in the Termite digestive gut, parasite protists in human, etc.). All these microorganisms form a “gigantic Protist planet” whose phylogenetic tree, via genome and chromosome studies, is far from being achieved.