"Eukaryote Genome Evolution: A View from Plasmodium falciparum, the Causative Agent of Malaria"

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Whole-genome sequencing strategies have revolutionized biology. Genomes contain evidence for the history of life and furthermore, they contain evidence for Lateral Gene Transfer (LGT), which plays an indisputable role in overall genome plasticity and therefore an important part in the history of life. Using these vast amounts of molecular data, together with novel methodologies, long-standing and contentious questions in evolutionary biology can be addressed.

In particular, there are conflicting theories for the evolution of the three eukaryotic kingdoms Plantae, Animalia and Fungi. The bulk of previously published work has suggested an Animalia-Fungi clade named the Opisthokonta, however support has been shown for the alternative hypotheses. Similarly, within the Metazoa, researchers have often been divided on the relationship of nematodes to arthropods and vertebrates. Traditionally, vertebrates and arthropods have been grouped together with nematodes occupying a basal position. This classic hypothesis, named "Coelomata" argues that vertebrates and arthropods are more closely related as they have a true body cavity (coelom), which nematodes lack. However, a recent hypothesis now joins the nematodes with the arthropods in a molting clade, the Ecdysozoa. Since the publication of the Ecdysozoa hypothesis, evidence has appeared both for and against it. These hypotheses were tested through the construction of a "supertree" using all the single gene families identified from available completed eukaryotic genomes. The results found a supertree supporting the traditional Coelomata hypothesis, with the vertebrates more closely related to the arthropods. Moreover, support was unexpectedly found for an animal-plant grouping rather than the Opisthokonta. Additionally,completed genomes were used to trace the ancestry of all the Plasmodium falciparum genes in order to investigate both the overall and specific contribution of the prokaryotic Domains in the evolution of the eukaryotes. The results reveal the uniqueness of the Plasmodium gene repertoire and also conflict slightly with previous work on the importance of the bacterial contribution to the eukaryote. Furthermore, 155 putative LGT genes were identified, many of which may be potential drug targets.