



Bacterial Genes in a Eukaryote

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Importance of Malaria

- 270-515 million clinical cases each year
- 1-2.7 million deaths, mainly attributable to *Plasmodium falciparum*
- An estimated 2.2 billion at risk of contracting the disease

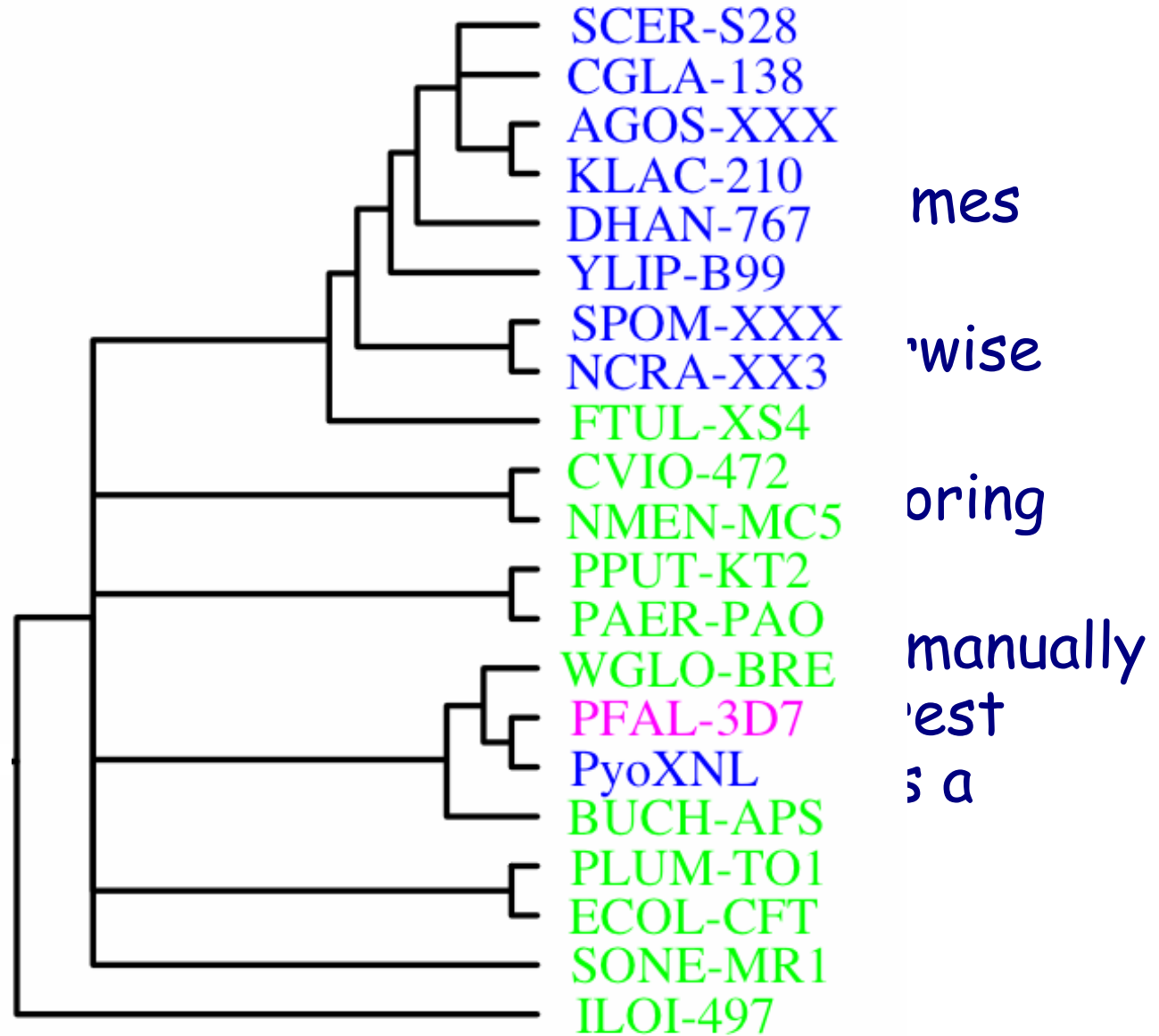


The *P. falciparum* genome

- 23Mb nuclear genome
- ~5300 genes
- Most (A+T)-rich genome sequenced to date (~81%)
- 60% genes unique
- 5% hypothetical functions (counterparts with unknown function)

Method

- Create c
- Compare sequence comparison
- Align the protein
- Maximum likelihood analysis of prokaryotic





Results

- Identified 155 genes where the nearest neighbour was a prokaryotic sequence
- 54 of these are Apicoplast targeted
- In particular, 35 genes were identified where a query *P. falciparum* gene was found to have homologues from bacterial genomes, but not from any archaeal or other eukaryotic genomes.