

Evolutionary history of FtsZ/Tubulin GTPase superfamily protein

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Abstract One important step in the eukaryogenesis process was the development of the cytoskeleton. The evolutionary transition from FtsZ to tubulin could provide a window into the transition from prokaryotic to eukaryotic cells. The study of phylogenetic analysis together with the genomic context of prokaryotic FtsZ shows two evolutionary paths for bacteria and archaea, bacterial FtsZ associated with bacterial division and archaea FtsZ associated with information genes

Introduction One of the major cytoskeletal elements in eukaryotic cells is the microtubule forming tubulin, whose prokaryotic counterpart is the FtsZ protein^{2,3}.

We focused on the phylogenetic relationship between the members of the FtsZ/Tubulin superfamily of proteins.

Methods Protein searches in the NCBI database, following GTDB taxonomic nomenclature were realized through HMMSEARCH using the Pfam model of tubulin, with an E-value threshold of $1e^{-5}$, filtering out those sequences with an alignment coverage below 70%. We reduce the dataset at 70% redundancy. We aligned the resulting sequences using different mafft modes, removed gappy position (95%) and removed the disordered region in the C-terminal of these proteins. Phylogenetic reconstruction was carried out using IQTREE. For each protein, we took the genomic context of 10 Kb up and down stream of the respective coding gene. Then, we predicted the genes using Prodigal, and annotated the predicted proteins through HMMSCAN using Pfam database. Then, we looked at the most abundant Pfam domains in the genomic context of FtsZ homologues.

Results The Figure 1 show the phylogeny for all the members of the FtsZ/Tubulin superfamily and their representative domains protein: tubulin, artubulin, CetZ, artubulin-like and FtsZ.

Conclusions Through phylogenetic reconstruction and analyses of the genomic context, we infer the evolutionary history of the FtsZ/tubulin protein family. The broad distribution of FtsZ in bacteria suggest that FtsZ was present in the bacterial common ancestor. On the other hand the monophyletic behaviour of the archaeal FtsZ1 and FtsZ2, suggests that the archaeal common ancestor duplicated its FtsZ before the archaeal diversification. These two facts in combination with the different genomic organizations around the bacterial and archaeal FtsZs unveil the early evolutionary paths of FtsZ for the origin of the Bacterial and Archaeal domains respectively (Figure 3). These facts raise new questions in the field, such as what was the trigger for such genomic contexts to originate? Was there a LUCA or was there an evolutionary transition between bacteria and archaea? Addressing these questions will improve our understanding of the evolution of the three domains of life.

References

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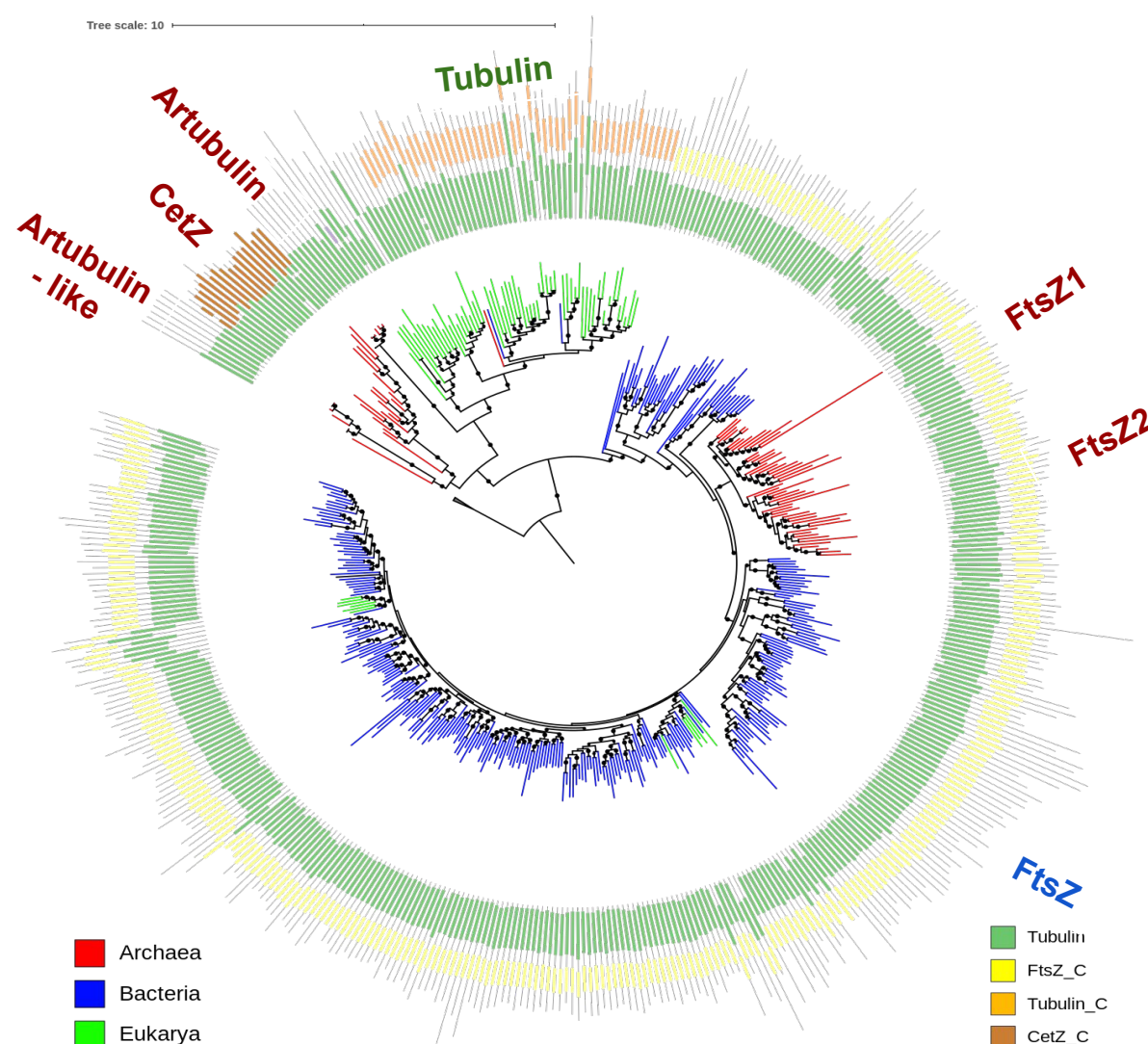


Figure 1. Phylogenetic analysis of the FtsZ/Tubulin superfamily and representative Pfam domains proteins.

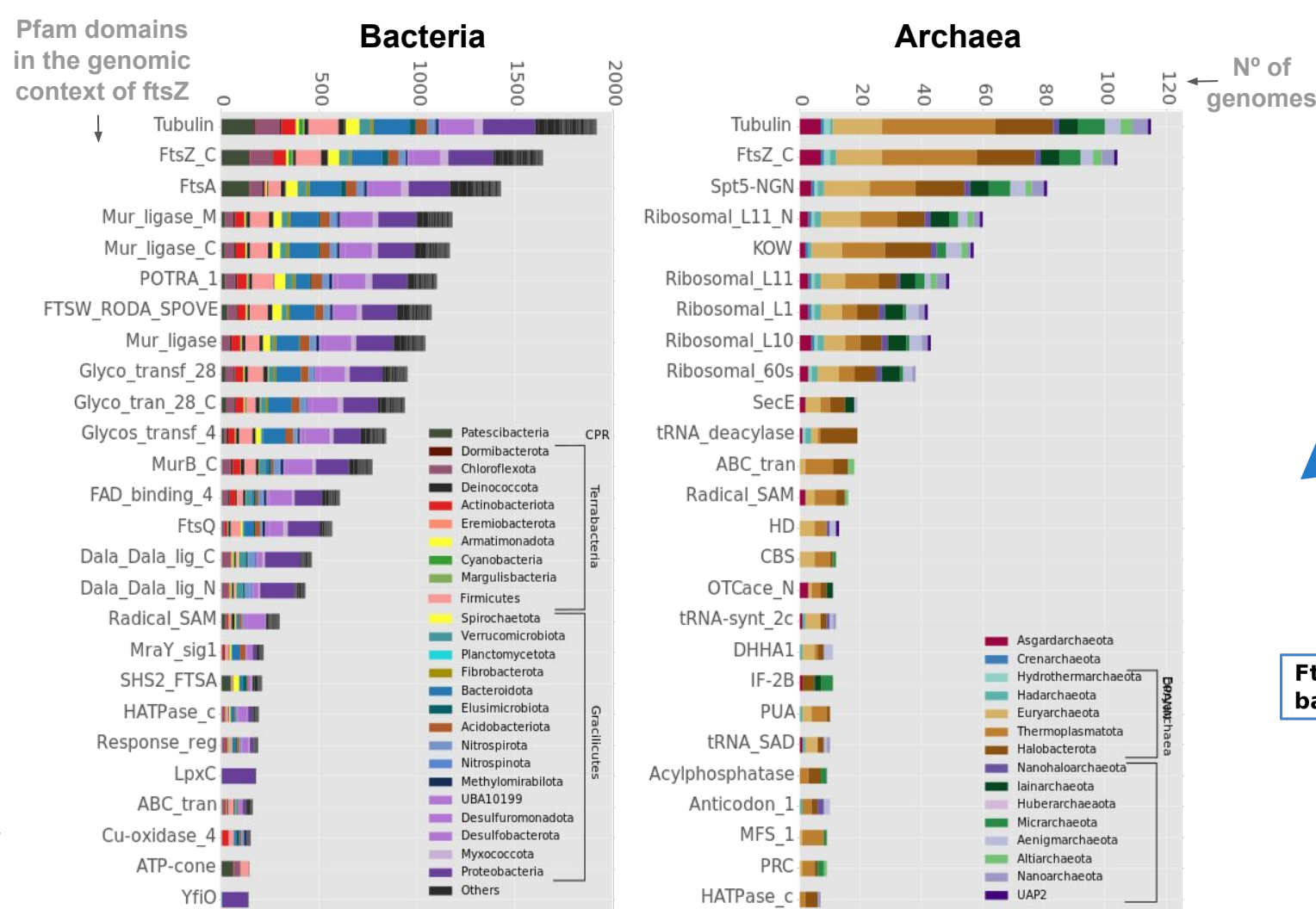


Figure 2. Genome context analysis of the bacteria FtsZ and archaea FtsZ1 (FtsZ2 not shown).

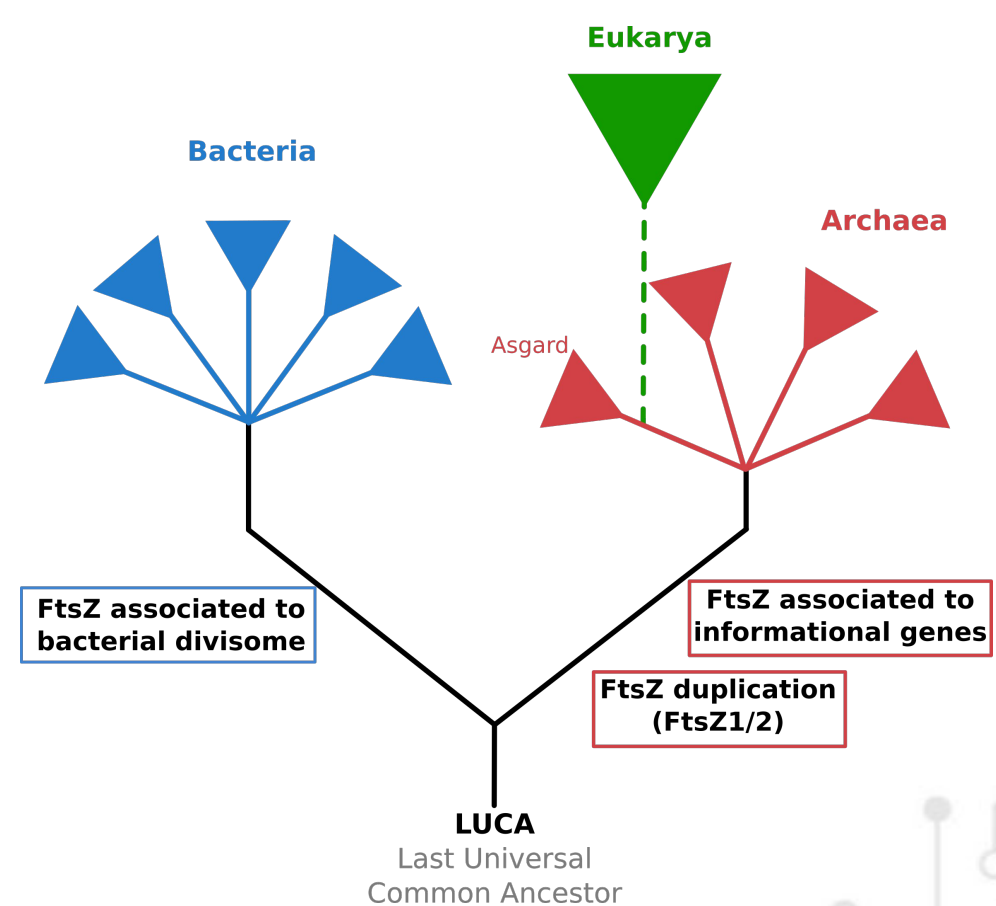


Figure 3. Early evolutionary history of FtsZ and the three domains of life.