

Phylogenomics of Asgard archaea reveals a unique blend of prokaryotic-like horizontal transfer and eukaryotic-like gene duplication

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BACKGROUND

Asgard archaea are the **closest prokaryotic relatives of eukaryotes**, and therefore key to our understanding of eukaryogenesis. Asgard archaea have a markedly larger genome size than other archaea; however, we know little about how **genome content** has been shaped across asgard evolution, in particular the role of **inter-domain HGT**.

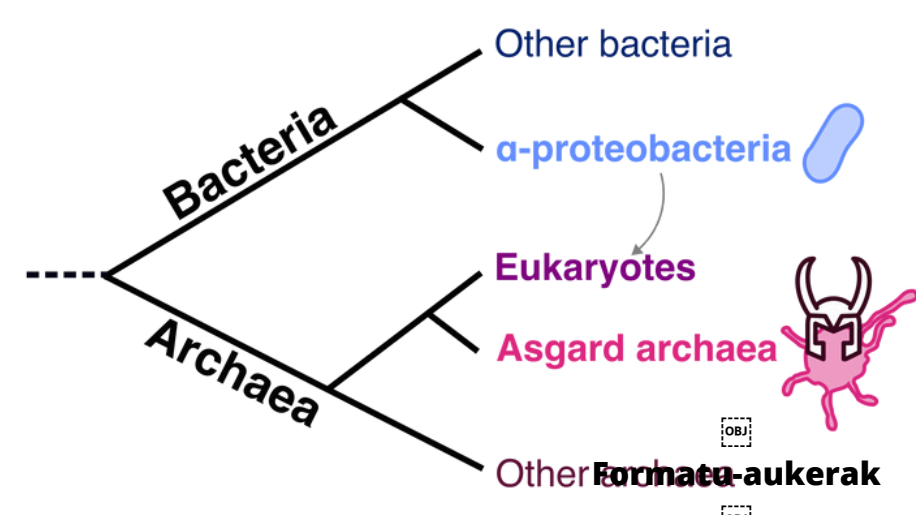


Fig. 1: Schematic view of eukaryogenesis.

METHODOLOGY

- **Seed proteomes: 31 sequenced asgard species**, spanning all **11 major lineages**, the 2 cultured isolates. **Two alternative species tree** topologies.
- **Duplication/Transfer/Loss assessment: species-overlap** (metaphylome approach) and reconciliation (**AleRax**) against backbone of prokaryotic species.
- **In-depth analysis of inter-domain HGT**: screening with **HGTector** and a **phylogenetic approach**.

GAIN-LOSS DYNAMICS

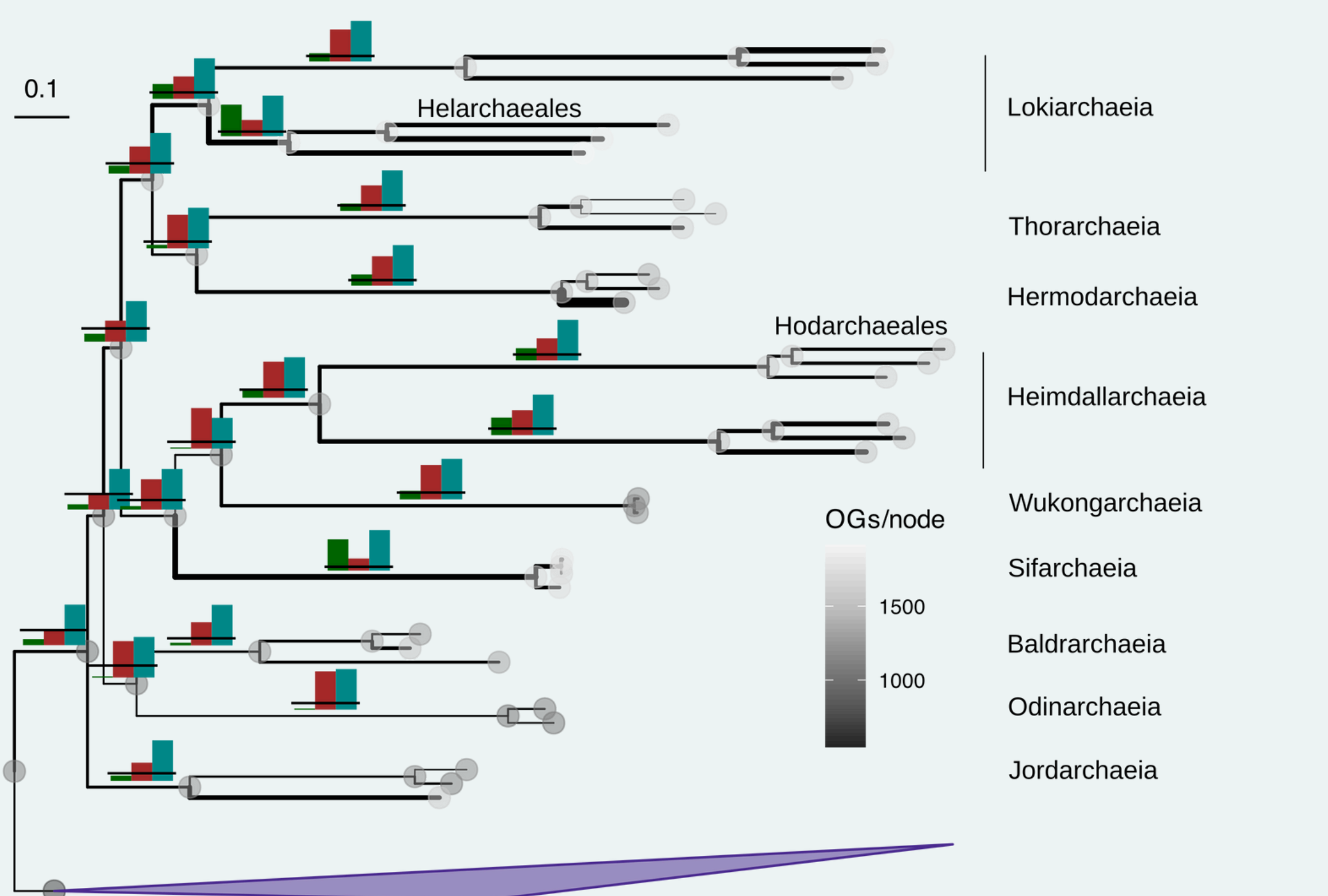


Fig. 4: Duplication, transfer and loss dynamics across the Asgard Tree of Life and their impact on inferred proteome size. Gains depicted in green, losses depicted in red, transfers depicted in blue. Line thickness is proportional to duplication rate.

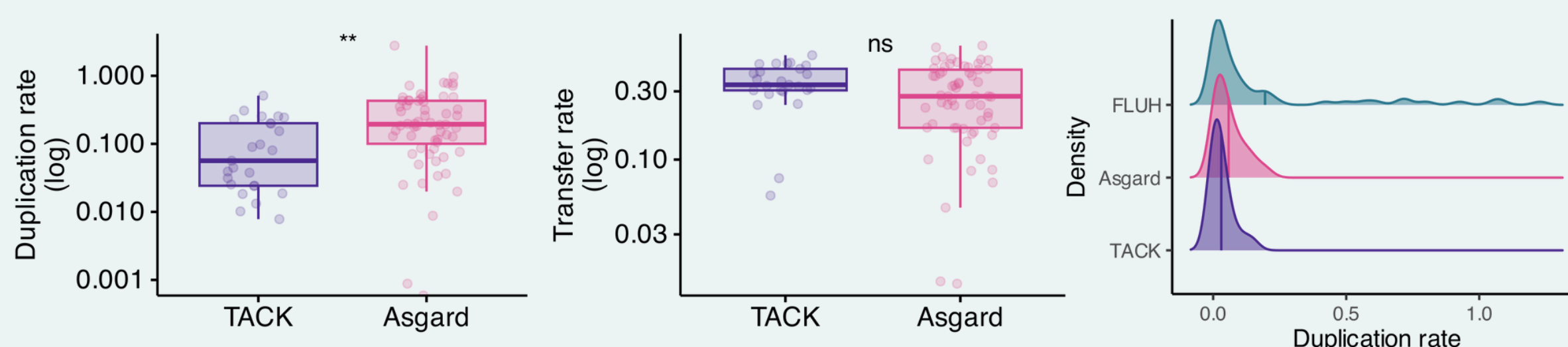


Fig. 5: Duplication rate (left) and transfer rate (center) for TACK and Asgard. Duplication rate for TACK, Asgard, and Free-living Unicellular Heterotrophic eukaryotes (FLUHs).

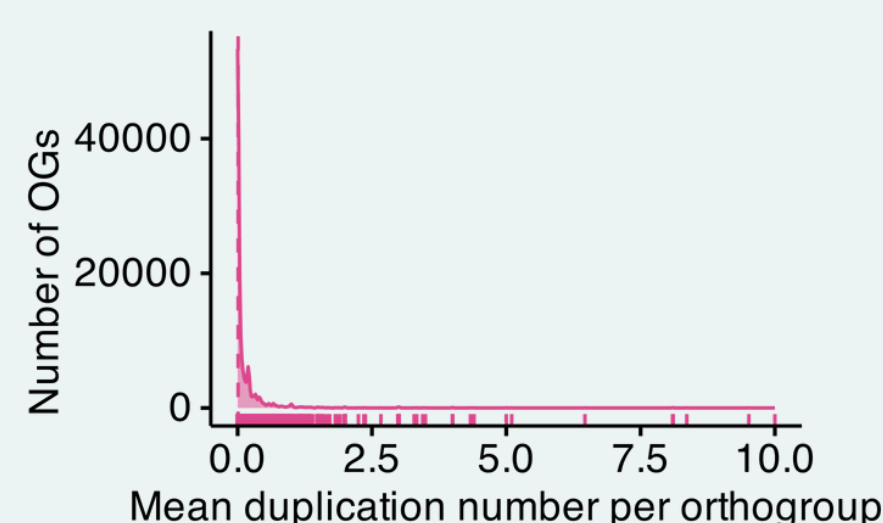


Fig. 6: Mean duplication rate per orthogroup.

Asgard archaea have lineage-dependent genome dynamics (Fig.4), but on average, significantly **higher duplication rates** than their sister clade (Fig.5 left), despite comparable rates of HGT (Fig.5 center), and seem to be an evolutionary intermediate between prokaryotic and eukaryotic duplication rates (Fig.5 right). Like in eukaryotes, the gene duplications seem to be linked to expansions of key gene families (Fig.6).

THE ASGARD PANGENOME

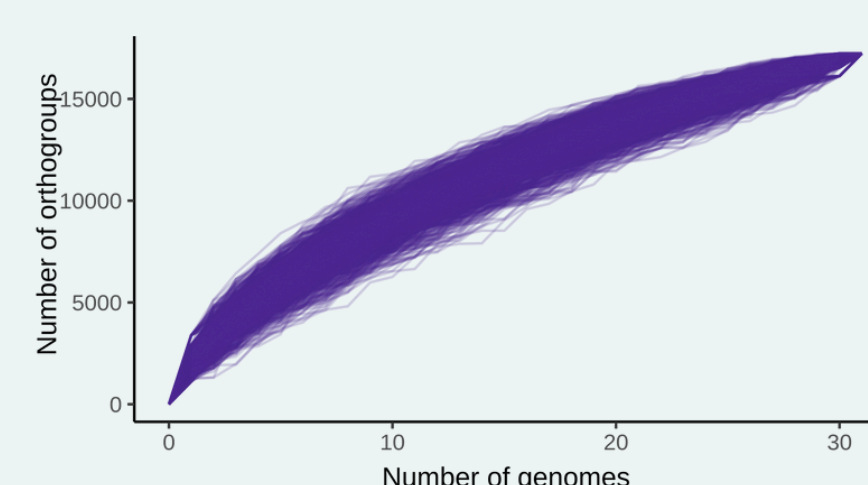


Fig. 2: Asgard archaea rarefaction curve.

Asgard archaea have an **open pangenome** (Fig.2), indicating that their total pangenome size cannot be mathematically predicted.

Asgard Signature Proteins (ASPs) are functionally interconnected (Fig.3).

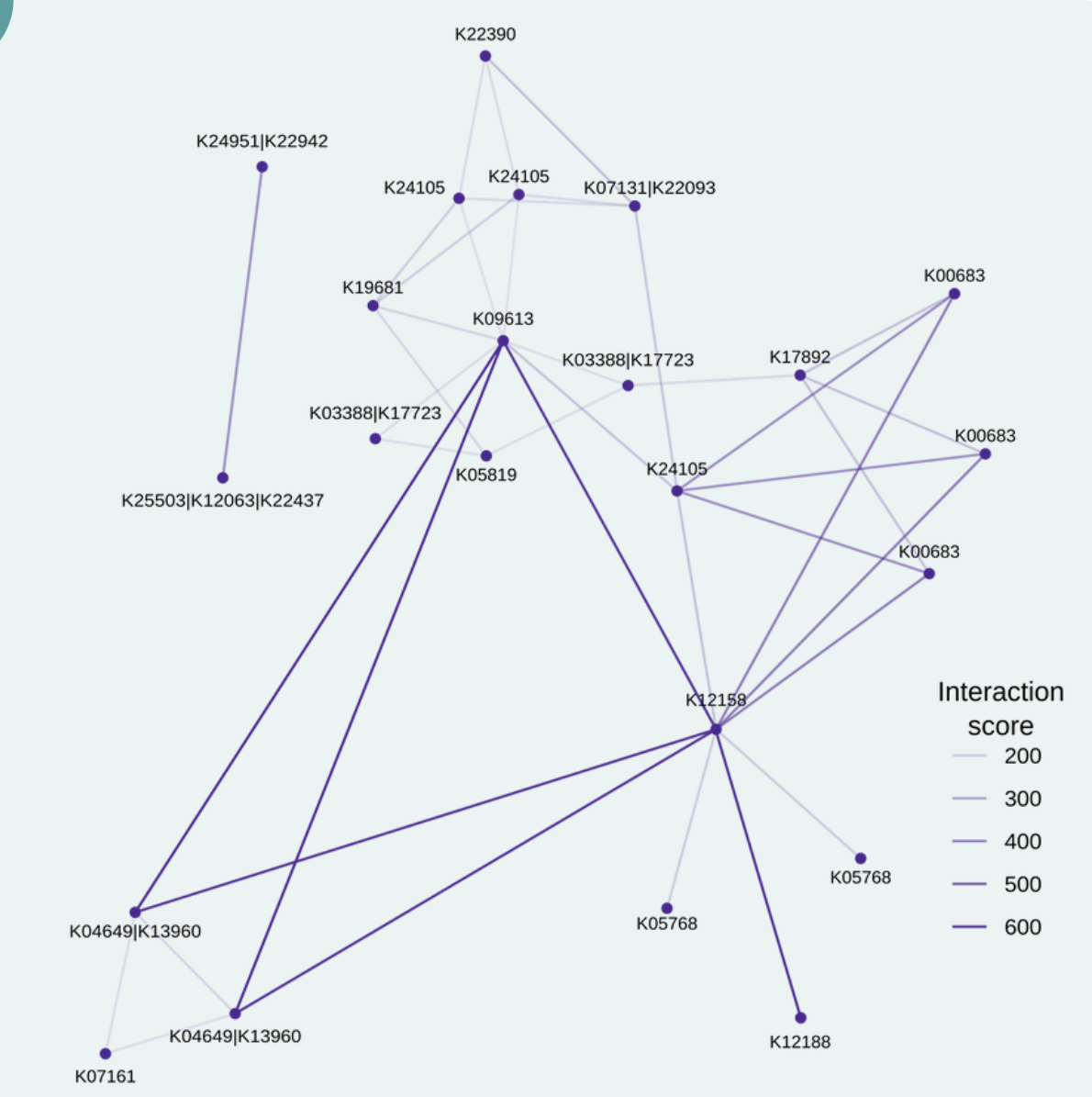
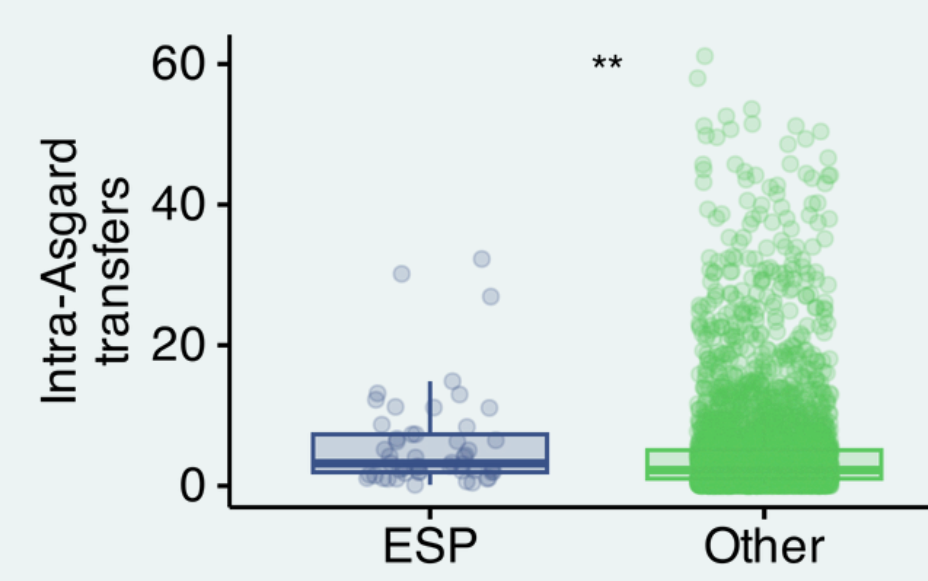


Fig. 3: Protein-Protein Interaction Network (PPIN) of Asgard Signature Proteins.

HORIZONTAL GENE TRANSFER



ESPs have a **higher intra-Asgard transfer rate** than the rest of the proteome (Fig.7), explaining their **patchy distribution**.

Fig. 7: Intra-Asgard transfer rate of Eukaryotic Signature Proteins (ESPs)

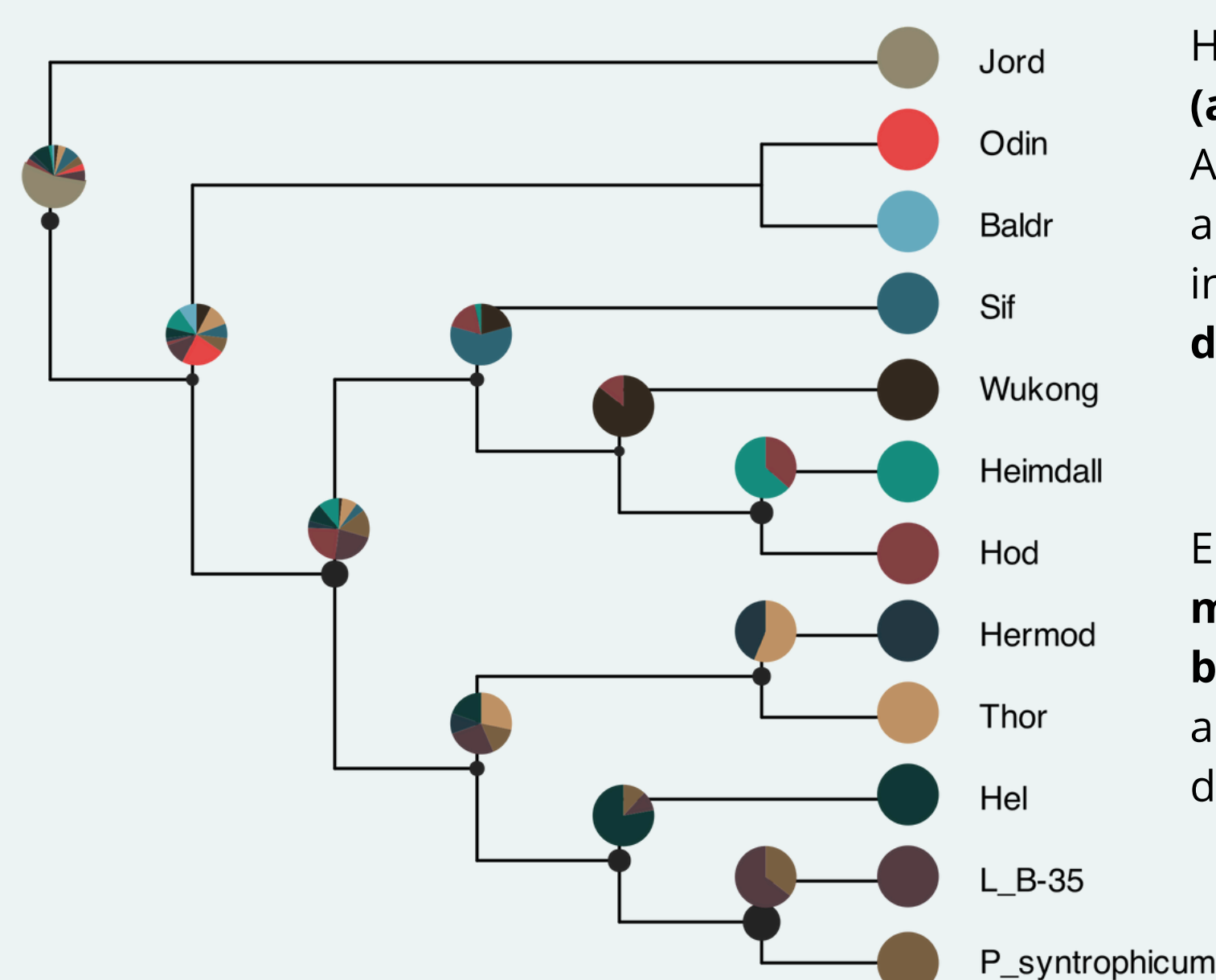


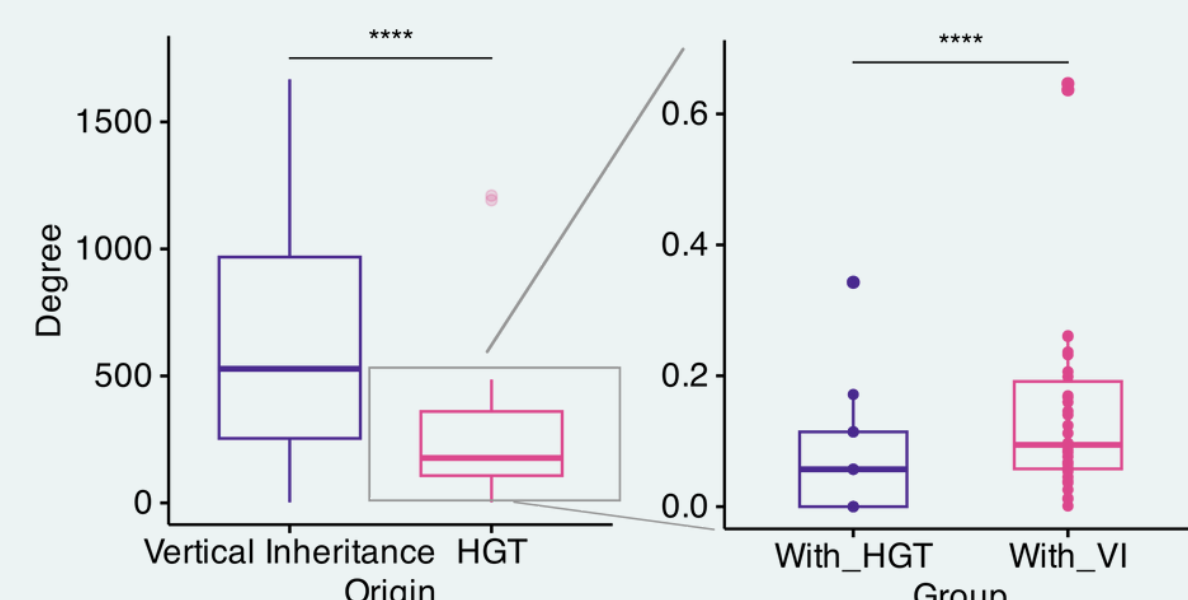
Fig. 8: Acceptors for bacterial-derived HGTs.

HGT has been a **continuous (and on-going) process** across Asgard evolution as seen by the array of acceptor clades (Fig.8), involving a **large number of donor phyla**.

Enriched functions deal with **metabolism of basic building blocks** but the specific pathways and proteins are organism-dependent.

HGT proteins are well-integrated, if **peripheral** (Fig.9) and seemingly **not modular** but stepwise additions to native pathways.

Fig. 9: Network properties of HGT proteins within the organism's interactome.



CONCLUSIONS

- Asgard genome expansion has been mainly driven by **prokaryote-like gene transfer** and an increased gene duplication rate that is intermediate between prokaryotes and eukaryotes.
- This underscores the **"stepping-stone" nature of Asgard archaea**, even in this genomic trait.
- The functions of acquired bacterial genes were highly diverse and **lineage-specific**, predominantly **metabolic**.
- Bacterial-derived proteins found to be **peripheral in protein-protein and metabolic networks**, interspersed with genes of vertical inheritance.

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