

[POSTER] Post-HGT compensatory evolution: codon usage amelioration and tRNA gene copy number variation in *Pseudomonas aeruginosa*.

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Abstract. Prokaryote genome evolution is characterized by the frequent gain of genes through horizontal gene transfer (HGT). When a gene is transferred from one species to another, it arrives in a genomic context different from its original one. Consequently, efficient expression and integration of this new gene can be limited due to mismatch between the transferred gene and the expression machinery and network of the receiving organism. Mismatch in codon usage between the transferred gene and the receiving genome is known to impair efficient gene expression after HGT. Because of the redundant nature of the genetic code, the same amino acid can be coded by different codons, and it is commonly observed that different species use their own preferred subset of codons, giving rise to species-specific codon usage preferences (CUP). When the CUP of a transferred gene strongly diverges from the CUP of the receiving organism, the speed and accuracy of protein translation can be strongly affected. One mechanism to compensate for this is codon usage amelioration, whereby the transferred gene evolves towards a CUP similar to that of the receiving organism. We are investigating codon usage amelioration on a phylogenetic timescale in *Pseudomonas aeruginosa*. To obtain estimates of the timing of HGT events, we use a reconciliation approach to place gene trees of genes from the dispensable genome on a core genome based strain phylogeny. This allows us to investigate the relation between the residence time of a gene within the species and its CUP, which could give us clues about the magnitude of amelioration processes in post-HGT evolution. Furthermore, CUP is known to be related to the gene copy number of tRNA's matching specific codons. We are therefore also investigating the importance of tRNA gene pool evolution in *P. aeruginosa* as an alternative way of providing post-HGT compensatory evolution.

Keywords: Horizontal gene transfer, Codon usage amelioration, Compensatory evolution