

Successful lateral transfer requires codon usage compatibility between foreign genes and recipient genomes

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Abstract

Recent horizontal gene acquisitions have commonly been predicted in prokaryotes by assuming that foreign genes display mainly atypical codon usage (CU). However, by looking at the CU levels (poor, typical or rich) exhibited by xenologs still resembling their original CU, we found evidence showing that most alien genes predominantly display typical CU within the recipient genome immediately upon introgression. Recent horizontal gene transfer (HGT) events were detected by first searching pairs of candidate xenologs that display about the same CU bias from the perspective of the donor and/or recipient genomes, and then predictions were subjected to phylogenetic validation. After the study of 75 available prokaryotic genomes, we conclude that CU compatibility between foreign genes and recipient genomes is an important prerequisite to assess the selective advantage of imported functions, and thus to establish successful horizontal

gene transfer (HGT) events. This suggests that CU amelioration plays a minimal role in HGT as most foreign genes already arrive to the recipient genome as ready-to-use genes.