

*Digital Signal Processing and Communications Laboratory
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**Challenging the compositional paradigm in horizontal gene transfer
prediction: a comparative genomics approach.**

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I will present an evaluation to the compositional paradigm for horizontal gene transfer (HGT) prediction, which posits that foreign genes display mainly atypical codon usage (CU) within the recipient genome immediately upon introgression. In our approach we first applied several criteria, including phylogenetic validation, to identify pairs of imported-exported genes that still preserve the compositional footprint of the donor DNA. Then, we estimated the number of genes showing poor, typical and rich CU in the host genome. Contrasting with the compositional paradigm, our results indicate that most alien genes exhibit predominantly typical CU in the host genome at the moment of acquisition, suggesting that such CU compatibility between foreign genes and acceptor genomes is a prerequisite to assess the selective advantage of imported functions. Thus, atypical (poor) CU may represent a strong barrier against successful integration and utilization of acquired genes. Furthermore, if the CU of alien genes is compatible with the genomic context of the new host, then, the role of amelioration has been overemphasized since it would happen in a small fraction of the genes that successfully jump across species boundaries.

Another important implication of the results is that typical CU defines a safety of tolerance zone, wherein foreign genes can be efficiently translated --presumably due to their compatibility with the translational machinery of the recipient organism. I will discuss additional evidences supporting this hypothesis.

Reference:

Medrano-Soto A, Moreno-Hagelsieb G, Vinuesa P, Christen JA, Collado-Vides J. Successful lateral transfer requires codon usage compatibility between foreign genes and recipient genomes. (2004) *Mol. Biol. Evol.* 21(10):1884-1894.

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