## SFB 680 MOLECULAR BASIS OF EVOLUTIONARY INNOVATIONS

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## Phylogenetic patterns of gene emergence in vertebrate genomes

Gene emergence has been assumed to be mostly driven by duplication and divergence of existing genes. The possibility that entirely new genes could emerge out of the non-coding genomic background was long thought to be almost negligible. With the increasing availability of fully sequenced genomes across broad scales of phylogeny, it has become possible to systematically study the origin of new genes over time and thus revisit this question.

Using phylostratigraphy to assess trends of gene evolution, and the annotation power of the mouse genome as a reference, we find several general trends and confirm them for three other vertebrate genomes (humans, zebrafish and stickleback). Younger genes are shorter, both with respect to gene length, as well as to open reading frame length. They contain also fewer exons and have fewer recognizable domains. Average exon length, on the other hand, does not change much over time. Only the most recently evolved genes have longer exons and they are often associated with active promotor regions, i.e. are part of bidirectional promotors. Which leads us to think in a transcription-based model of gene emergence.

We have also revisited the possibility that de novo evolution of genes could occur even within existing genes, by making use of an alternative reading frame (also known as overprinting or dual-coding genes). We suggest that the overall trends of gene emergence are more compatible with a de novo evolution model for orphan genes than a general duplication-divergence model. Hence, de novo evolution of genes appears to have occurred continuously throughout evolutionary time and should therefore be considered as a general mechanism for the emergence of new gene functions.

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Institute for Genetics, Zülpicher Str. 47a, Seminar Room, 4th Floor

Host: Thomas Wiehe

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