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# Dynamics and adaptive benefits of emergence and modular rearrangements of protein domains

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Modularity is a characteristic of molecular evolution as it helps reuse autonomous module in different context and thus expedite evolutionary innovation. Protein domains are the evolutionary units of proteins and their rearrangements generate a rich molecular variety on which selection can act. These rearrangement processes can be well studied using HMM-based methods -- which are readily implemented in many custom databases such as PFAM or SUPERFAMILY -- because HMMs have a high accuracy and domain rearrangements occur relatively rarely compared to site based mutations. Accordingly, rearrangement events become amenable to study using the ever growing wealth of available genomes. So far, we used insect and plant genomes for comparative studies as they are well resolved and diverse taxonomic groups. We find high diversity in domain arrangements in even very closely related organisms and provide -- to the best of our knowledge for the first time -- branch specific rates for domain gain and loss and fusion and fission. We find a dramatic loss of domains along every lineage which is offset by a large number of fusion, fission and rearrangements. The majority of all new domain arrangements can be explained by just one step of modular rearrangement events but frequency of fission and terminal deletions increase over time. We find a particularly high rate of rearrangements in signaling molecules. Furthermore, newly emerging domains are predominantly single domain and have a high degree of disorder probability. They thus most likely result from neighbouring genomic regions. Most strikingly, and remniscent of the tenet that paralogs evolve fastest shortly ofter creation, we also find that novel domains establish higher copy numbers within their genomes than older domains did and are predominantly associated with environmental adaptation such as biotic defence, abiotic stress response, reproduction and development. These results also demonstrate how easily domain based analyses can analyse adaptive changes and complement other, more established methods such as site based methods or gene family growth. Current research compares signals of domain rearrangements across clades and explores methods to resolve phylogenies using domain based events instead of site based analyses.

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