



Universität Heidelberg

HBIGS Lecture

by

Prof. Erich Bornberg-Bauer

(Institute for Evolution and Biodiversity, University of Münster)

"How smart and efficient can molecular evolution be?"

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Abstract:

Many biological systems are highly adaptable due to the modularity of their components which are reused in different context. Proteins, the cellular workhorses encoded by genes, are composed of domains and their modular domain-wise rearrangements can create a vast molecular diversity with relatively few genetic operations. We used two clades, arthropods and viridiplantae, to study evolutionary dynamics and adaptive benefits of domain loss, emergence and rearrangements. We find a dramatic loss of protein domains along every lineage which is offset by a large number of fusion, fission and duplications of existgin domain arrangements. Novel domains occur only rarely but have a high adaptive value as they rise to high copy numbers in relatively short evolutionary time scales and can be related to environmental adaptations such as abiotic stress response, biotic defence, development and reproduction. Novel domain arrangements are foremost associated with signalling and regulation and can be related to developmental innovations such as multicellularity and environmental sensing. Our results also demonstrate the powers of domain based analyses as methodologically these signals are very reliable due to the powers of Hidden-Markov-Model based profiles and biologically they are complementary to and largely independent from functional results obtained from studies of gene family evolution and site dependent studies.