

Parallel Evolution of Alleles, Genes, Chromosomes, and Taxa

Our understanding of genome and chromosome evolution can be significantly improved if patterns of such evolution can be discovered across taxonomic groups and species with varied complexity. In the first study, we demonstrated that variation observed for the length of different chromosomes in 68 eukaryotic genomes can be modeled by a common distribution. The conserved boundary of chromosome-size variation indicates that cellular, molecular, and evolutionary mechanisms confine the chromosome lengths around a species-specific average chromosome length. In the second study, we uncovered a clear separation pattern of base-composition values calculated across polymorphic sites between basal and derived populations separated by a bottleneck event. DNA repair genes were found to be significantly enriched within genomic regions underlying the divergence of this genome phenotype. Parallelism at the allele and gene level was again demonstrated in the third study where one gene's "shattering" effect was identified in different crop species. Our findings highlighted the need for global analysis of genomic data and the need for integration of molecular mechanisms and evolution.