



CDB SEMINAR

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14:00~15:00 Seminar Room A7F

Non-conservation of developmental 'toolkit' genes

Summary

Decades of molecular developmental studies have led to discoveries of regulatory networks governing various morphogenetic processes. Cross-species comparisons among diverse animals have revealed a high level of conservation of gene repertoires responsible for those developmental processes. A prevalent idea is that changes in regulations or functions of commonly shared genes, often termed 'toolkit' genes, have resulted in phenotypic diversity, through heterotopy, heterochrony, or co-option. This idea, which was established in the pre-genomic era, should now be verified with many genomes fully sequenced and further analyses. In particular, my team has been interested in detecting unusual small-scale losses of developmental genes of vertebrates in well-studied gene families. Our bioinformatic survey has revealed quite a few genes that mark taxon-specific gains or losses. They included the Bmp16 gene, closely related to Bmp2 and Bmp4 and missing in mammalian and bird genomes, as well as the Pax4 gene, closely related to Pax6 and missing in the currently available chicken and Xenopus genome sequences. We also scrutinized loss-prone members of the Hox clusters, Hox14 genes, missing in the genomes of all traditional model vertebrates. These data, together with results from genome-wide analyses, emphasize a more dynamic nature of developmental gene repertoires in vertebrates than documented before. The approaches employed here, based on molecular phylogenetics and genome informatics, should potentially address more questions in life science regarding the laws of genome organization and expression in model organisms as well as us humans.

Host:

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