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Ohnologs: Why do basal bony fish hold‘em but crown groups fold‘em?

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S19-03 Streptophyta): Quantitative morphometrics at the cellular level

Neustupa, Jiri (Charles University in Prague, CZE)

Morphological symmetry of cellular shapes is an omnipresent feature in protists and different types of complex symmetry are particularly exhibited in freshwater microalgae, such as the desmids (Desmidiaceae). Their cells are typically composed of two bilaterally symmetric semicells arranged according to two perpendicular axes of symmetry. New semicells develop after mitotic division so that each cell is composed of two unequally old, bilaterally symmetric parts. The peculiar morphological patterns of the desmids were used for addressing several questions regarding their environmentally induced plasticity and shape allometry. Mapping morphological diversification of the *Micrasterias* lineage on the molecular phylogenetic trees revealed an accelerated rate of morphological evolution, including acquisition or loss of the complex symmetric parts. Plasticity and development of the symmetric structures of *Micrasterias* cells were found to be associated with key environmental factors, such as temperature or pH. In addition, positive allometric scaling of cell volumes and surfaces revealed that evolution of the intricate morphological patterns of the desmid cells can be related to the selection pressure for maximizing the exchange surface areas.

S19-04 Developmental canalization in the vertebrate cranium: A morphometric approach

Mitteroecker, Philipp (University of Vienna, AUT)

Canalization against internal and environmental fluctuations is a key property of non-pathological development. The underlying mechanisms and molecular components, however, are still poorly understood. I present one formalization of developmental canalization, which allows for the statistical mapping of the strength and pattern of canalization throughout an investigated time period. C. H. Waddington's metaphor of the epigenetic landscape thus turns into an actual estimable statistical property of development. By applications to the vertebrate cranium, I show how different cranial shape features differ fundamentally in the generation and canalization of developmental variance. Functionally relevant features appear to be more tightly canalized than other traits.

09.00 – 10.40 Symposium S20: Less is more: Loss of gene functions as a driving force of developmental evolution**ROOM C1***Organizers:* Cristian Cañestro and Ingo Braasch*Chairs:* Cristian Cañestro and Ingo Braasch**S20-01 Dynamic gain and loss of genes in animal evolution**

Holland, Peter (University of Oxford, GBR); Quah, Shan (University of Oxford, GBR); Maeso, Ignacio (University of Oxford, GBR); Marletaz, Ferdinand (University of Oxford, GBR); Paps, Jordi (University of Oxford, GBR); Olson, Peter (Natural History Museum, London, GBR); Martin, Kyle (University of Oxford, GBR); Hui, Jerome (The Chinese University of Hong Kong, CHN)

Gene duplication and gene loss are complementary processes. Using examples from mammals, insects and other animals, including homeobox and miRNA genes, I will discuss how gain of genes can occur through a dynamic evolutionary process, balanced by equally rapid gene loss. The net result of such balance would be stasis. In rare cases, new genes get incorporated more deeply into developmental pathways and subsequently less prone to loss. However, on occasion even conserved and ancient genes will be lost, presumably in association with restructuring of developmental pathways.

S20-02 Ohnologs: Why do basal bony fish hold'em but crown groups fold'em?

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Multiple paralogs in vertebrate genomes likely arose from whole genome duplication (WGD) events at the base of the vertebrate radiation. Some have thought that these genome expansion events provided opportunities for variation in genetic information that allowed vertebrates to invent themselves. Recent genome sequencing of coelacanth (a basally diverging lobe-finned fish), and spotted gar (a basally diverging ray-finned fish), shows that these ancient lineages retain a fuller set of ohnologs (i.e., WGD-derived paralogs) than their respective crown groups, the tetrapods and the teleosts. This raises the hypothesis that selective ohnolog loss is associated with innovations derived in crown group evolution. Informed by the coelacanth and spotted gar genomes, we will explore the types of ohnologs gone missing from tetrapods, from teleosts, and from both taxa to help understand how less is more.