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

Ingo Braasch, Peter Batzel, Angel Amores, Allyse Ferrara, Quenton Fontenot, Julien Bobe, John H. Postlethwait, Yann Guiguen

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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 (Desmidiales). Their cells are typically composed of two bilaterally symmetric semicells arranged according to two perpendicular axes of symmetry. New semi-cells 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 mor-phological evolution, including acquisition or loss of the complex sym-metric 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 in-tricate 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 mecha-nisms 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 cana-lization throughout an investigated time period. C. H. Waddington's metaphor of the epigenetic landscape thus turns into an actual estima-ble statistical property of development. By applications to the vertebra-te cranium, I show how different cranial shape features differ funda-mentally 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 (Universi-ty 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 oc-cur 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 con-served 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 geno-me duplication (WGD) events at the base of the vertebrate radiation. Some have thought that these genome expansion events provided op-portunities for variation in genetic information that allowed vertebrates to invent themselves. Recent genome sequencing of coelacanth (a ba-sally diverging lobefin fish), and spotted gar (a basally diverging rayfin 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.