

Developmental constraints versus flexibility in morphological evolution

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Developmental mechanisms could possibly constrain the direction of evolutionary change since certain morphological features are more frequently generated than others. One attractive system to analyse such constrained morphological evolution had been the study of the amazing diversity in formation of the wing patterns in butterflies. This paper reports a study of ‘eyespot’ in the wings of butterfly *Bicyclus anynana*, under the artificial selection pressure over 25 generations divided into three consecutive phases. The authors concluded in favour of natural selection over internal constraints.

The earliest known eutherian mammal

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Evolutionary lineage of placental (eutherian) mammals include all living and extinct mammals that are closer to the extant placental (e.g. human) than to the extant marsupials (e.g. kangaroos). This new discovery of the skeleton and fossilized hairs of a eutherian mammal, identified as *Eomaia scansoria* gen. et sp. nov., from the lower Cretaceous Yixian Formation of Northeastern China. The limbs and foot of this animal resemble locomotory features suitable for climbing and tree-living, as opposed to the running features of other eutherians of the Cretaceous era. Such evidence suggests that the earliest Cretaceous eutherians had scansorial and arboreal adaptations. The estimated age of the fossil is about 125 million years, placing this new fossil at the root of the phylogenetic tree as the earliest known eutherian mammal.

Evolutionary rate in the protein interaction network

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A protein’s rate of evolution is believed to be influenced by two of its functional properties: its dispensability, and the maximum number of potential changes in the primary sequence tolerated to keep the function intact. Authors here describe the correlation between the evolutionary distance and the number of protein–protein interactions that are important for the function of one particular protein. From a list of 3541 interactions between 445 different proteins in yeast *Saccharomyces cerevisiae*, their evolutionary rates were estimated by comparing putative orthologous sequences *S. cerevisiae* and nematode *Caenorhabditis elegans*. For 164 yeast proteins, an estimate of the number of potential interactions, and a well-conserved ortholog in *C. elegans* were obtained. Analysis of this correlation led to the conclusion that connectivity of well-conserved proteins is inversely related to their rates of evolution. Results also confirm that interacting proteins co-evolve at comparable rates.

Fighting fruit flies: A model system for the study of aggression

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Aggression is a typical behaviour found in many animals, including the humans, during acquisitions or defense of scarce resources. This paper reports aggressive behaviour (fighting) in *Drosophila melanogaster* males induced by competition for food. Several parameters, including presence of a female and quality of food, were varied to induce ‘fighting’. The behavioural patterns were classified into nine offensive actions (approach, low-level fencing, wing threat, high-level fencing, chasing, lunging, holding, boxing and tussling) and four defensive actions (walk away, defensive wing threat, run away/being chased, fly away). This work paves the way for detailed quantitative examination of aggressive behaviour by using mutant strains.

Eukaryotic genes in *Mycobacterium tuberculosis* could have a role in pathogenesis and immunomodulation

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Mycobacterium tuberculosis, a Gram positive bacterium, that can be called the most successful human pathogen, primarily infects the lung tissues causing pulmonary tuberculosis. In addition, *M. tuberculosis* has also been cited to be ‘most successful’ in retaining the highest number of eukaryotic-prokaryotic inter-kingdom gene fusions. A total of 19 eukaryotic genes were found in the mycobacterial genome and they were grouped under four functional classes, namely those involved in steroid metabolism, lipid metabolism, signal transduction and in other functions. These findings suggest a sequential co-opting of eukaryotic gene into mycobacterial genome and perhaps such acquisitions are important in the success of the organism as a pathogen.

GAGA can mediate enhancer function in *trans* by linking two separate DNA molecules

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It is believed that the transcription factor GAGA activates RNA polymerase II transcription, and is required for the normal expression of homeotic genes, heat shock genes and histone genes. Enhancers had been traditionally defined as *cis*-regulatory DNA element that can activate transcription of genes in a location-independent and orientation-independent manner. Experiments described in this paper demonstrate that GAGA can form a protein link between two different DNA elements, such bridges requires its POZ domain. GAGA activated transcription in cultured cells, as well as, transcription experiments reconstituted *in vitro*. It was concluded that GAGA links two separate DNA molecules to mediate enhancer function in *trans*.