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Similarities in the Embryonic Development of Various Animal Species Are Also Found at Molecular Level

The astonishing similarity in the appearance of embryos from different animal species was observed as far back as the 19th century by scientists such as Karl von Baer, Charles Darwin and Ernst Haeckel. Such observations prompted the hypothesis that the individual development of an organism reflects its evolutionary history or phylogeny. Two groups of scientists, including researchers at the Max Planck Institute of Molecular Genetics in Dresden and the Max Planck Institute for Evolutionary Biology in Plön, have now succeeded in demonstrating, for the first time, that parallels exist between individual development and phylogeny on the level of gene expression.

The research is published in the journal Nature (Dec. 9, 2010).

Whether fish or flies -- at a certain stage in their development, the embryos of different animal species within a phylum are almost impossible to distinguish on the basis of their appearance. The greatest similarity arises in the middle of embryonic development, during the "phylotypic stage"; species-specific differences predominate before and after this stage. This observation is illustrated by the hourglass model. The question as to how this extensive morphological similarity -- the "waist" of the hourglass -- arises is one that has long preoccupied researchers. The extent to which the individual development of an organism (ontogeny) and that of a phylum (phylogeny) are linked was also previously unclear.

For the first time, scientists have now demonstrated that the hourglass motif arises in organisms as diverse as the fruit fly and zebrafish, not only at morphological level but also at molecular level -- a finding that suggests that parallels do, indeed, exist between ontogeny and phylogeny. In a study, carried out on six fruit fly species (*Drosophila* sp.), the research group working with Pavel Tomancak at the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden discovered that the similarities not only in morphology, but also in the expression pattern of the genes are greatest during the phylotypic stage; before and after this phase, the differences between the species are greater. Moreover, the scientists also observed that the expression pattern of key genes reflects the hourglass model most faithfully. Meanwhile, Tomislav Domazet-Lošo and Diethard

Tautz, researchers at the Max Planck Institute for Evolutionary Biology in Plön, demonstrated with zebrafish (*Danio rerio*) that the phylogenetically oldest genes are active during the phylotypic stage and that, before and after this stage, the most active genes are those that arose later in evolutionary history. The Plön-based evolutionary biologists also made another astonishing discovery: they observed that in adult zebrafish progressively older genes are also activated with the increasing age of the animals. The same conclusion was reached in comparative analyses carried out on *Drosophila*, mosquitoes of the genus *Anopheles* and threadworms.

These two studies throw new light on an age-old biological conundrum: that of the link between ontogeny and phylogeny. "Our discovery confirms the earlier anatomical studies and broadens our understanding of how development and evolution are linked at molecular level," explains Alex T. Kalinka, a researcher from the Dresden group. "The results show that the similarity between different animal species in the middle of their embryonic development is shaped by selection," adds Casey Bergmann, a Co-author from the University of Manchester. Their findings explain how the "waist" in the hourglass arises.

Fruit flies are one of the most thoroughly researched model organisms and offer unique possibilities for the study of the molecular mechanisms that underlie embryonic development. The discovery of the hourglass pattern in different species makes it possible for evolutionary biologists to travel back in time to the earliest days of evolution when the differences

between organisms arose. "We hope to gain insight into the processes that led to the variety of forms in the animal kingdom," explains Pavel Tomancak.

For their study on zebrafish, another model organism widely used in evolutionary biology, the researchers from Plön also developed a new method: the Transcriptome Age Index (TAI). This method enables the measurement of the phylogenetic age of active genes. Domazet-Lošo and Tautz used this new tool to trace the development of the zebrafish from the fertilised egg to the adult organism. "The TAI profile faithfully reproduces the hourglass model and therefore demonstrates that parallels exist between ontogeny and phylogeny," reports Diethard Tautz. The scientists explain

the observation that the phylogenetically oldest genes are active in older zebrafish with the fact that animals which have passed reproductive age are "overlooked" by selection.

These studies show that naturalists like Karl von Baer, Charles Darwin and Ernst Haeckel were basically correct in their hypothesis that embryonic development is a reflection of phylogeny. "It will be very exciting to extend our approach to other species with different blueprints and life-cycle strategies," says Domazet-Lošo.

Tomislav Domazet-Lošo, Diethard Tautz. A phylogenetically based transcriptome age index mirrors ontogenetic divergence patterns. *Nature*, 2010; 468 (7325): 815 DOI: 10.1038/nature09632