Concurrent session 9: Evolution of Regulatory Traits

Program/Abstract # 62
Co-option of an anteroposterior head axis gene network for proximodistal patterning of appendages in early bilaterian evolution
William McGinniss¹, Jens H. Fritztenwanke⁶, John Gerhart⁷, Christopher J. Lowe⁸, Derek Lemons⁵
¹Dept of Cell & Dev Biol, University of California, San Diego, CA, USA
²Dept of Organismal Biol and Anatomy, University of Chicago, IL, USA
³Dept of Molec and Cell Biol, University of California, Berkeley, CA, USA

The enormous diversity of extant animal forms is a testament to the power of evolution, and much of this diversity has been achieved through the emergence of novel morphological traits. The origin of novel morphological traits is an extremely important issue in biology, and a frequent source of this novelty is co-option of pre-existing gene networks for new purposes. Appendages, such as limbs, fins and antennae, are structures common to many animal body plans which must have arisen at least once, and probably multiple times, in lineages which lacked appendages. We provide evidence that appendage proximodistal patterning genes are expressed in similar registers in the anterior embryonic neurectoderm of Drosophila melanogaster and Saccoglossus kowalevskii (a hemichordate). These results, in concert with existing expression data from a variety of other animals suggest that a pre-existing gene network for anterior head patterning was co-opted for patterning of the proximodistal axis of appendages in bilaterian animal evolution.

doi:10.1016/j.ydbio.2010.05.097

Program/Abstract # 64
Opposite sex-determining roles of PUF proteins in convergently evolved hermaphrodites are mediated by a conserved target mRNA
Qinwen Liua, Craig Stumpfb, Marvin Wickensb, Eric Haaga
aDepartment of Biology, University of Maryland, College Park, USA
bDepartment of Biochemistry, University of Wisconsin, Madison, USA

Repetitive evolution of hermaphroditism in Caenorhabditis required major changes in germline sex determination. In C. elegans the PUF family proteins FBF-1/2 promote germline proliferation and female sexual fate. Here, we examine PUF homologs in C. briggsae, another self-fertile Caenorhabditis species. Phylogenetic analysis of the PUF family from five Caenorhabditis species shows that C. briggsae puf-2/12 and C. elegans fbfs belong to two distinct but related PUF sub-families. Simultaneous dsRNA knockdown of Ch-puf-2/12 feminizes the germ line, in contrast with the masculinization phenotype of the fbfs in C. elegans. gld-1 has opposite germline sex determination phenotypes in these two species and is an important direct target of regulation by FBF in C. elegans. Genetic and biochemical assays show Ch-puf-2/12 repress Cb-GLD-1 expression by directly binding to Cb-gld-1 3′UTR through a conserved element. The mRNA sequence element bound by C. briggsae PUF-2/12 and C. elegans FBF is conserved through yeast three-hybrid interaction assays. This suggests that the feminization caused by knockdown of Ch-puf-2/12 can be explained by conserved PUF repression of gld-1 in C. briggsae. We also provide evidence suggesting the ancestral function of the puf-2/12 and fbf sub-family proteins was promotion of germline maintenance, and that Ch-puf-2/12 were recruited into the germline sex determination pathway in the C. briggsae lineage.

doi:10.1016/j.ydbio.2010.05.099