

Dr. John H. Postlethwait
3-25-05 MBF Seminar Series-OHH Sponsored Speaker

Talk: “**Genome duplication and the origin of fish diversity.**”

Abstract:

A whole genome duplication event appears to have preceded the diversification of teleost fish lineages, and thereby affects 25,000 species of fish, half of all vertebrate species. This event provided teleosts with duplicate copies of many human genes. Subsequent evolution of these gene duplicates affects the biology of teleosts today. Gene duplicate evolution often involved the process of subfunction partitioning, in which complementary gene subfunctions were independently and reciprocally lost from each member of a duplicate gene pair. Such subfunctions might be regulatory, controlling the amount, timing, or spatial distribution of transcripts, or they might be structural, involving complementary domains of the encoded polypeptide. Subfunction partitioning occurring differently in different populations can speed lineage divergence and may have contributed to the enormous explosion of teleost biodiversity. In addition, subfunction partitioning can facilitate the analysis of gene function. For mammalian genes with many independent subfunctions, including many important developmental regulatory genes, pleiotropy can hinder the discovery of gene function. For example, if a gene has both early and late essential functions, a null activity allele might block development early; as a consequence, later functions would not become apparent in a mutant phenotype because the appropriate cell types would not form or the embryo might die. If, however, different subfunctions partitioned to different duplicated gene copies, then null mutations (or morpholino treatments) can reveal both functions. Because of lineage-specific subfunction partitioning, the analysis of different teleost species is necessary to reveal a wide variety of ancestral gene functions otherwise obscured by pleiotropy in tetrapods.