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An updated database and user interface for the GEISHA gene expression resource

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The GEISHA (gallus expression in situ hybridization analysis) project is an NIH-funded initiative to create and maintain a comprehensive, searchable database of whole-mount in situ hybridization images and metadata covering chicken embryo gene expression through organogenesis. An initial database and web interface developed several years ago to house and display information have been redesigned to incorporate increasing amounts of data obtained from high throughput in situ hybridization analyses in our laboratory and by others and from the published literature. The new database also integrates with, and will annotate, the chicken genome browsers. Key features of the new database include metadata allowing enhanced interactivity with various chicken genomics resources, precise mapping of all probe sequences on the genome, and updated search capabilities that allow querying by stage, anatomical location, key word and nucleotide sequence. Searches will return all current images sharing a desired feature (e.g., expression in the pancreatic precursor at stage 21, or from sequences with homology to the Ephrin family), allowing scientists to develop new hypotheses about previously unknown mRNA, microRNA or protein function. Future metadata will allow searches by gene ontology. This centralized repository for in situ hybridization gene expression information will provide a valuable and comprehensive tool for the research community. Supported by NIH R01HD044767 to PBA.

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Deciphering the molecular evolution of the ependymin protein family

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The ependymin protein was originally associated with neuroplasticity and regeneration in fishes. More recently, ependymin-related proteins (ERPs) have been identified in other vertebrates, including amphibians and mammals. Since these proteins were initially identified only in vertebrates, the ependymin protein family was classified as vertebrate-specific. Last year, we reported the identification and characterization of an ependymin gene in echinoderms, showing that there are ependymin family members in non-vertebrate deuterostomes. We have now explored multiple databases to find ERPs in different metazoan species. Using these sequences, we have performed genome mapping, molecular phylogenetic analyses and statistical tests in order to ascertain the phylogenetic relationship among the ependymin molecules. Our results demonstrate that ependymin genes are present also in protostomes. In addition, as a result of the putative fish-specific genome duplication event and posterior divergence of the gene copies, the ependymin family can be divided into three groups: (1) a brain-specific group of ependymin sequences that is unique to teleost fishes and encompasses the original ependymin; (2) a group of ependymin genes expressed in non-brain tissue in fishes; (3) a group of ependymin genes that can be found in deuterostomes and protostomes species and that probably represents the initial evolutionary origin of the ependymin molecules. These analyses and the tissue-specific expression patterns suggest that the ependymin protein family is a suitable target to test subfunctionalization in gene copies originated after gene or genome duplication events.

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