Integration of European eel transcriptome into the PHYLOFISH project, a high throughput phylogenomic analysis designed to study teleost gene evolution after whole genome duplication

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HAL Id: hal-02743789
https://hal.inrae.fr/hal-02743789

Submitted on 3 Jun 2020

Oral presentation

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Investigation of gene evolution after whole genome duplications is crucial to better understand the mechanisms by which genomes evolved and drive the development and physiology of vertebrates. The PHYLOFISH project will take advantage of the additional whole genome duplication rounds of teleost to address this question. In addition, a special attention has been paid to species presenting a key taxonomic position in the teleost tree of life, including the European eel as a basal teleost. Using next generation sequencing, this project has already provided original information on the transcript repertoires of 24 fish species, including European eel. The eel RNA libraries have been produced from 10 organs, including ovary, testis, brain and liver, in addition to a leptocephalus larva. The number of sequenced reads per libraries were comprised between 35 million to 83 million and enabled to reconstruct more than 60 thousand contigs. The totality of the generated datasets will be released and accessible through a web browser providing multiple and comparative information on the transcript repertoires of the 24 investigated species.

This evolutionary-relevant sequence dataset has then been used as a basis for the development of a high throughput analysis combining gene phylogenies, synteny information, and expression profiling. As we have investigated a wide range of teleost species, including basal species such as European eel, the results of this project should provide high resolution and genome-wide answers concerning the fate of paralogous genes after genome duplication events in teleosts. The project will provide new insight into the influence of sub- and neo-functionalization process on teleost gene diversity. In addition, and because these gene duplications also have a major impact on the quality of gene annotation in teleosts, the PHYLOFISH project will propose a phylogenetically-supported refinement of teleost gene nomenclature. This will link gene information across many vertebrate species, allowing to bridge functional information from conventional model species to emergent model species.