

# Evolution of biology



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Evolutionary Development of the Fibroblast Growth Factor The article, “ Evolution of FGF Gene Family” by Oulion, Bertrand and Escriva was published in the International Journal of Evolutionary Biology in the year 2012. The article reflects on the evolutionary development and progression of the Fibroblast Growth Factor (FGF) family over the years. The FGF family is involved in the normal developmental and physiological processes of human biology. The research observes the FGF family evolution in the chordates and the eumetazoan family which helps in understanding the evolution of the FGF family brought about by the successive genetic alterations.

On the basis of the FGF amino acid sequences found in the metazoan lineages, it has been exhibited that the evolutionary scenarios in the metazoan lineages are associated with the FGF gene content. Two hypotheses have been proposed on the basis of the evolutionary progression in the metazoan lineage. The first hypothesis states that the eight FGF subfamilies are chordae-specific and the second hypothesis states that the eight subfamilies were ancestral to all eumetazoans. The study results showed that the chordates possessed two gene copies of the FGF gene and duplications occurred generating the current diversity. The metazoan lineage, on the other hand, exhibits high degree of gene losses during their evolution. Therefore, a total of eight gene families were present in the eumetazoan ancestors, out of which there were six gene losses in cnidarians, five in ambulacrarians and five in protostomes.

For phylogenetic analysis of vertebrae FGFs, the amino acids were aligned and maximum likelihood tree was built. For the nonvertebrae FGF phylogenetic analyses, the obtained FGF sequences were aligned with the already known FGF sequences from the metazoan lineages. Maximum

likelihood tree for this group was also generated. The methodology focuses on comparing the FGF subfamilies from the vertebrae and non-vertebrae groups to understand the genetic evolutionary process. The approach of the methods used by the research was focused on supporting the hypothesis and different sequences were compared so that an understanding of the variations in the genetics of FGF family could be compared. The data is exhibited through easy to understand diagrams and chromosomal maps. For exhibiting the evolutionary progression of the FGF family the comparison of the amino acid sequences is crucial so that the duplications or losses could be understood.

The hypothesis is supported successfully by the results of the data which represents that the FGF family specific in the chordae was a result of various gene duplications and the ancestral eumetazoan had at least a set of two genes of the FGF family from the current FGF family seen in the metazoan lineage. However, the research focuses only on the genetic evolution of the FGF family and the morphological and functional evolution of the FGF family is not discussed, hence the functional evolution of the signal should also be discussed. The process of diversification in the chordae as well as the metazoan lineage is consistent with the current understanding of the evolutionary genetics changes an organism has to undergo over several generations for its survival and progress.

#### References

Oulion, Silvan, Stephanie Bertrand and Hector Escriva. " Evolution of FGF Gene Family." International Journal of Evolutionary Biology. 2012. Web. 11 Mar. 2014. <http://www.hindawi.com/journals/ijeb/2012/298147/>