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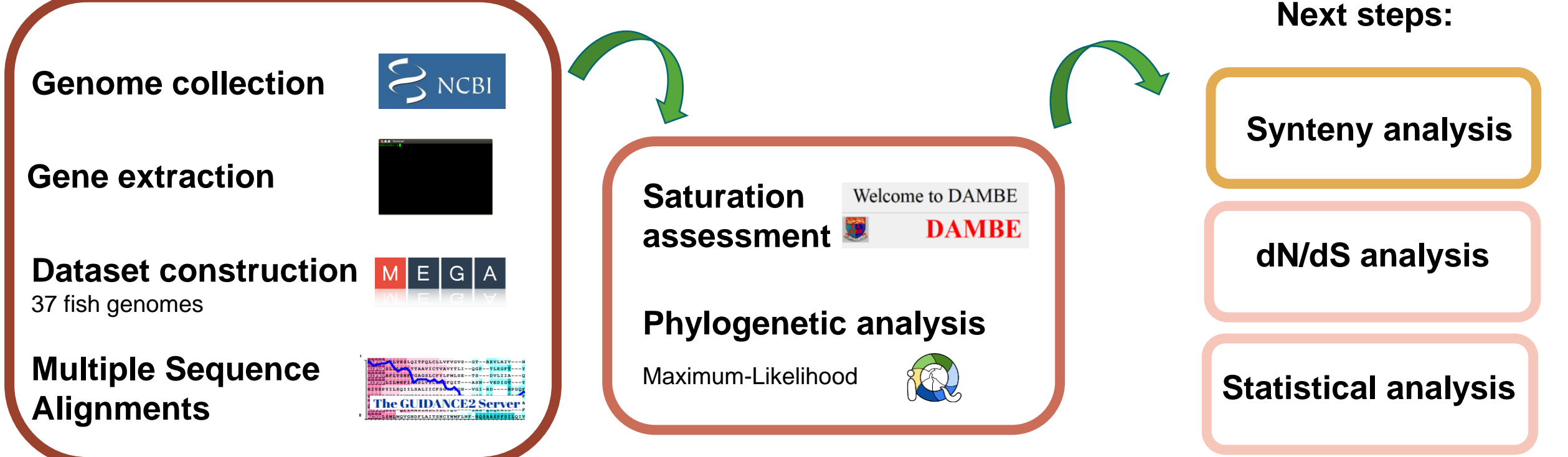
Introduction

Recognition of odors is extremely important for intra/interspecific communication and species survival. Olfactory receptors (ORs) perform a major role in detecting odors. The several ORs classification systems available are full of ambiguities mainly related with existence of a gene repertoire highly diverse across vertebrate species (the presence of few intact genes in elephant sharks compared to the more than 1,000 genes in some mammalian species)¹. In Actinopterygii lineage, the OR family was characterized in some punctual species but little is known about the gene repertoire and molecular evolution in most fish. Thus, the aim was to explore the diversity of OR genes among fish lineages.

Objectives

- Access the full OR repertoire in a sample of Cyclostomata, Chondrichthyes, Actinopterygii and Sarcopterygii species.
- Evaluate the diverse classification systems and homogenize them.
- Evaluate the molecular evolution of ORs across fish lineages.

Material and Methods



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Initial results

- We extract the full OR repertoire in the 37 fish of Cyclostomata, Chondrichthyes, Actinopterygii and Sarcopterygii lineages.
- The range of OR repertoire varies between less than 10 to more than 400 copies in some species.
- The phylogenetic approach leads us to conclude that the previously reported classification systems^{2,3,4} are complementary but they need a new refinement due to inclusion, by the first-time, of some fish lineages.

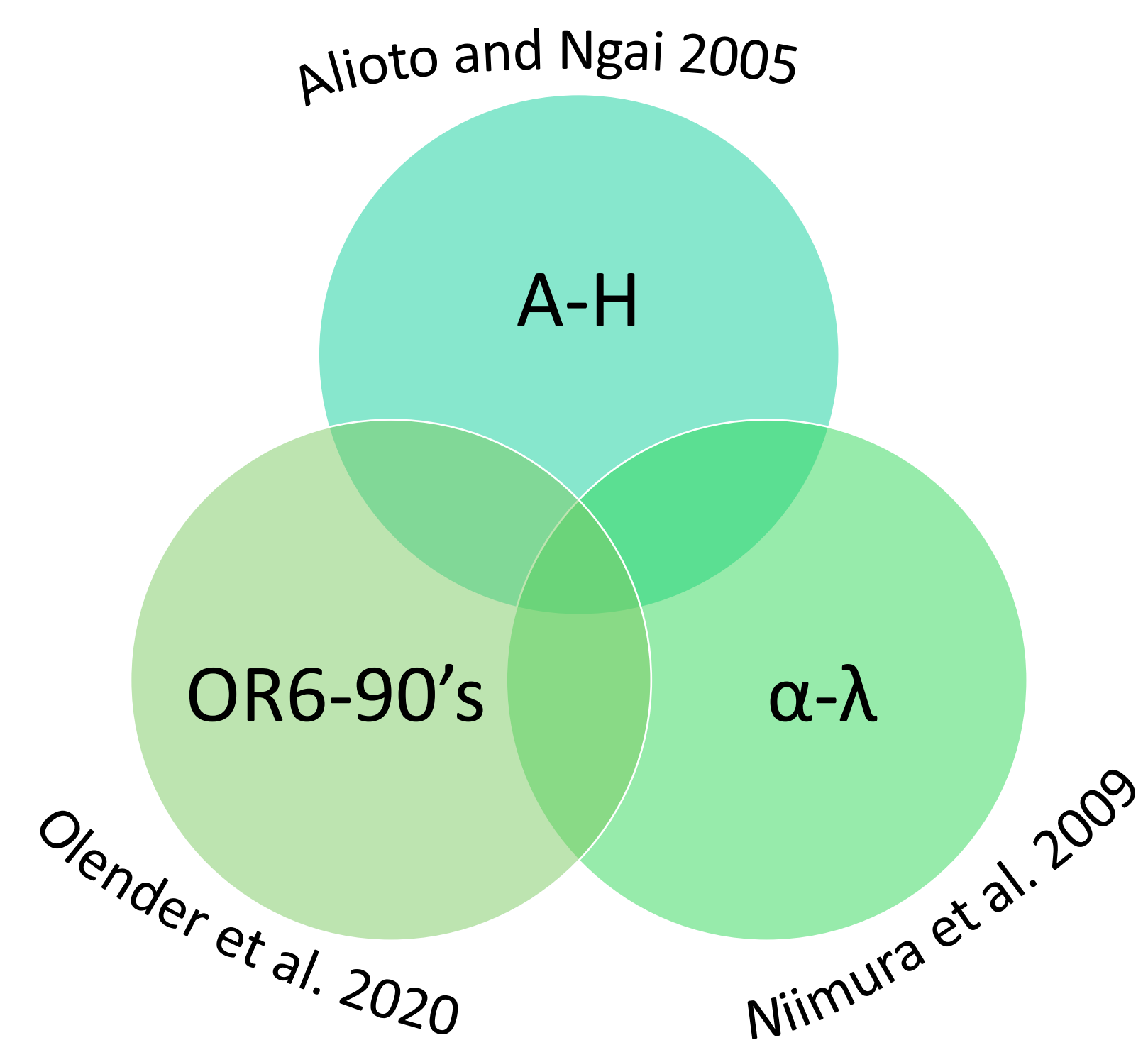


Figure 1 – The available classification systems share common points but they do not reach all putative families identified in our phylogenetic reconstruction.

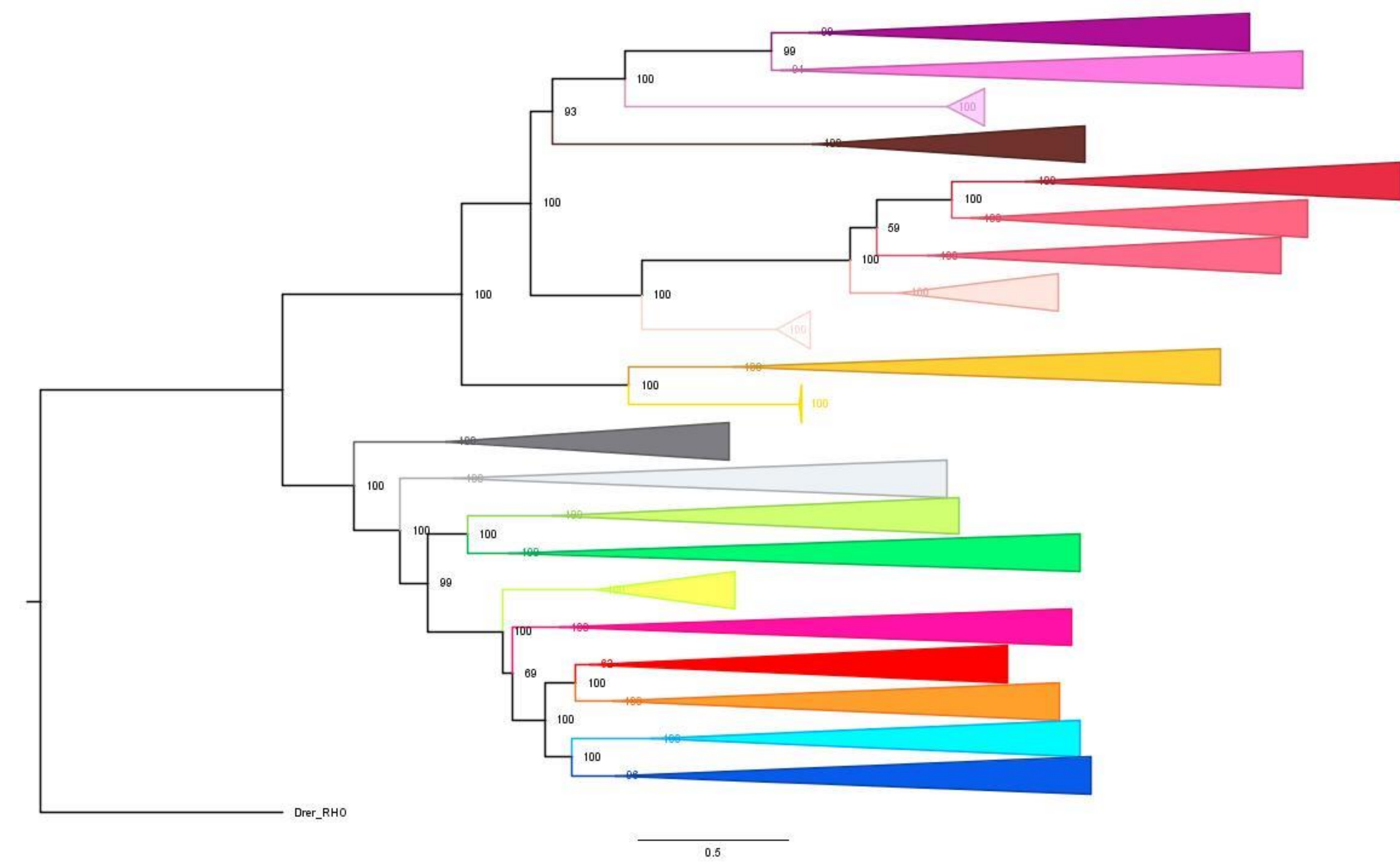


Figure 2 – Phylogenetic reconstruction of OR genes, using Rhodopsin gene of Zebrafish as outgroup. Our results, considering previously methodologies and the information of former reported classification systems¹⁻⁴, lead us to determine 21 distinct OR families represented in this phylogenetic tree.

Discussion

- ORs are a family of GPCRs responsible for odor recognition present in all classes of vertebrates.
- Fishes present a diversified repertoire of OR genes with high and heterogeneous duplication rates.
- The applied methodology helped to clarify and standardize the OR classification system at family level. However there are some current issues when we try to categorize ORs at sub-family level.

Future directions

- As future perspectives, integration of synteny will clarify the family divisions.
- Adaptive selection approaches (such as codon- and branch analyses) must be performed to demystify OR evolutionary patterns.
- Statistical analysis will be performed to support our conclusions

References

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