

Abstract

The purpose of this project was to research the Functional Development of the Olfactory System in Zebrafish. By comparing the olfactory function which includes the number of Trace amine-associated receptor (TAAR) genes that functions in the olfactory system and the pseudogene ratio between zebrafish and four other vertebrates such as amphibians, jawless vertebrates, birds, and mammals to demonstrate the olfactory function development. The method that applies to the pseudogene determination is through the SMS ORF finder to detect the incomplete OR gene sequence. After filtering out the pseudogene and inputting the functional FASTA sequences into the MAFFT server in order to translate the sequence alignment to the phylogenetic tree which can be used to determine clusters and gene families. In addition, the TAAR amount of each species is according to Science Direct article, Hashiguchi (2016). Based on the analysis, it was found that there was a negative relationship between pseudogenes and TARR genes. As pseudogenes increased, TARR genes decreased. The zebrafish had more TARR genes which have higher sensitivity on zebrafish's olfactory system compared to the other vertebrates. In addition, the gene family consists of the gene that has high related, same transcription orientation and identity. Therefore, the number of zebrafish OR gene families can be determined by applying the amino acid identity percentage in the gene family cluster tree.

Gene Family Cluster Tree

The data analysis of the FASTA gene of zebrafish represents the total number of a pseudogene is 12 and the total number of function genes is 148 which has a less pseudogene percentage than other species. Applying the pseudogene fraction of zebrafish as evidence can indicate that zebrafish’s variation during the evolution nearly retains the original function and DNA sequence. Figure 3, Cluster analysis presents the percentage of amino acids identity in our study, there exist 8 clusters that are greater than 40%. According to Alioto and Ngai (2005) “OR (Olfactory receptor) Gene family members need to share an average 40% amino acid identity”. Therefore, the 8 gene families in our study are family 6 (OR 6.1, OR 6.2, OR 6.3, OR 6.4), family 4 (OR 4.0, OR4.1, OR 4.2), family 8 (OR 8.0), family 5 (OR 5.5), family 3 (OR 3.0), family 9 (OR 9.0, OR 9.1, OR 9.2, OR 9.3, OR 9.4, OR 9.5), family 7.1 and family 7.0. The gene family consists of the gene that has high related, same transcription orientation and identity. However, family 7.1 and family 7.0 are not in the same cluster due to their different identity.

Methods

The study investigated the relationship of 5 vertebrates pseudogene fraction with each species TAAR gene amount including human, sea lamprey, chicken, frog, and zebrafish. According to Niimura (2009), vertebrate animals and insects both have receptors for detecting odor molecules in the environment. By comparing the pseudogene fraction of 5 vertebrates to each species TAAR gene amount including mammals, jawless vertebrates, amphibians, fish, and birds, the negative correlation will be present between pseudogenes and TAAR genes, which are more pseudogene will lead to less TAAR gene, and vice versa. In Figures 1 and 2, the zebrafish has more TAAR genes and less pseudogene compared to other species. The pseudogene will increase through the variation of the evolution process based on the mutation, a stop codon misplacement during the duplication which suggests the number of pseudogenes in zebrafish will be relatively lower due to its less evolution. In the research of Dugas and Ngai (2001), the species that have less reliance on the olfactory system will accumulate more OR pseudogenes due to the inactivation. Therefore, zebrafish will have less OR pseudogenes than other species based on their high dependence on the olfactory system. Olfaction is an important organ for fish to perceive the external environment and participate in foraging, avoiding enemies, and reproductive migration.

Results/Data

In Figures 1 and 2, the zebrafish has more TAAR gene and less pseudogene compared to other species such as mammals, reptiles, amphibians, and birds. The pseudogene will increase through the variation of the evolution process based on the mutation, a stop codon misplacement during the duplication. Such as the pseudogene in humans will increase throughout the high evolution, also the pseudogene in zebrafish will be relatively lower due to its less evolution.

Figure 1. The species pseudogene fraction



Figure 2.The TAAR gene number of Species

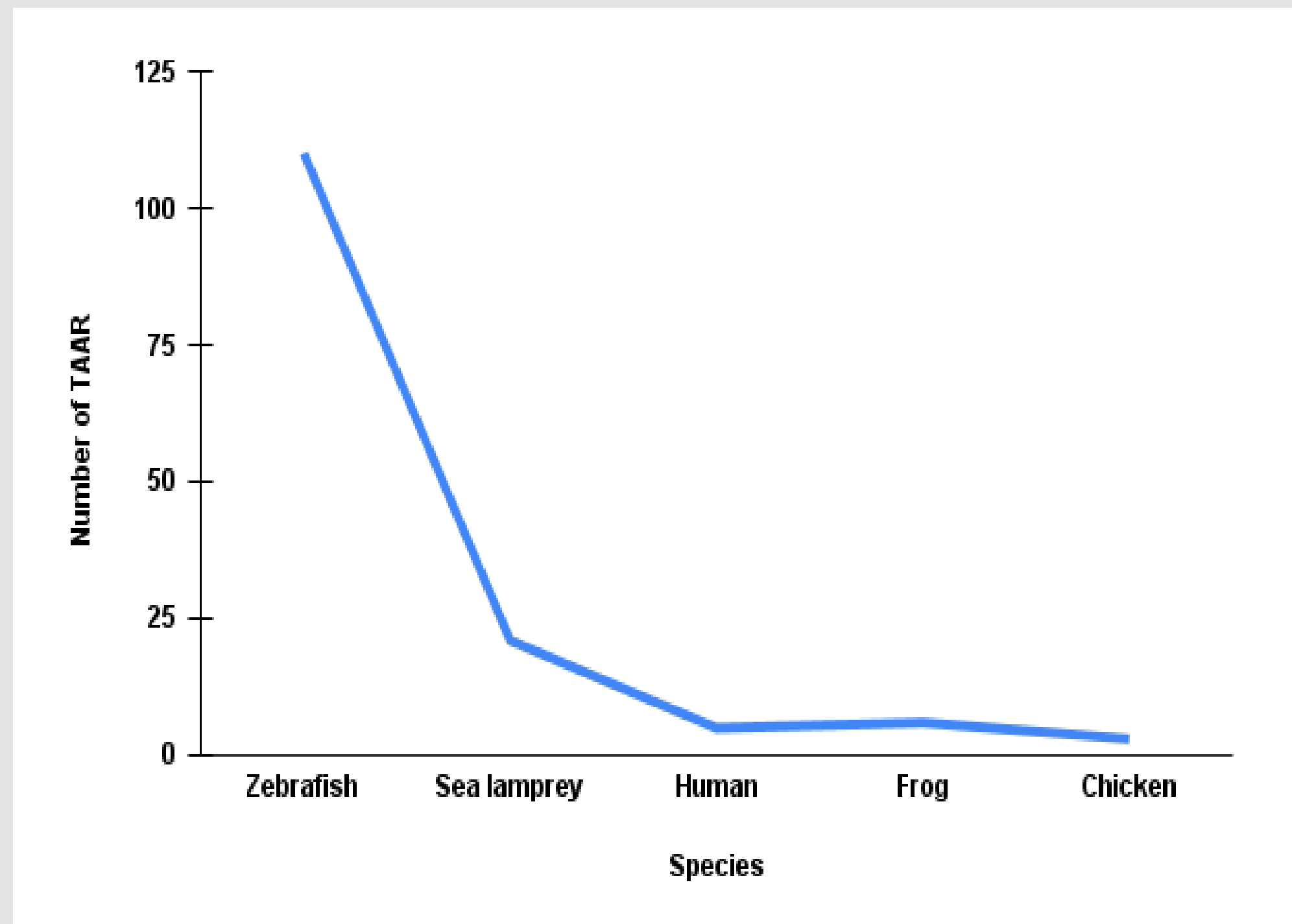
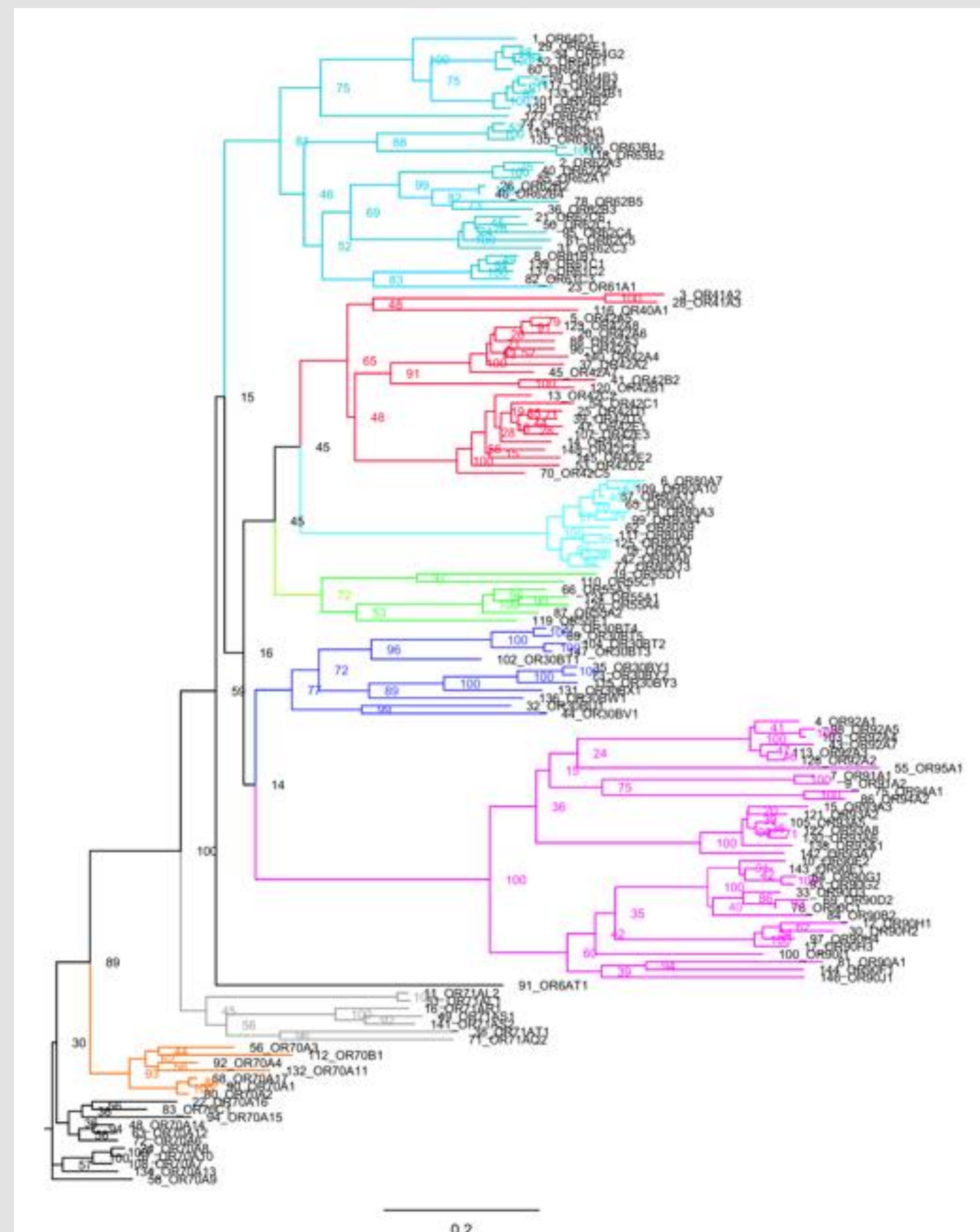


Figure 3.Cluster analysis



Discussion

The zebrafish can detect more chemical substances than other species which suggests that the fewer pseudogene and more TAAR genes will lead to higher olfactory sensitivities and a well-developed olfactory system. Gene Family Clustering tree: Our cluster information matches the zebrafish OR gene families. In addition, this information also suggests that the gene family clustering tree can be used to identify the gene families based on their identity. Unlike other mammalian families of olfactory receptor genes, zebrafish TAAR genes are more abundant than mammals. Eight of the nine OR genomes still belong to current fish species, compared with just two OR genomes for mammals, It shows how the environment changes with the species and a decreasing trend of OR genome from fish to amphibians and land mammals. The appearance of trichromatic vision and the loss of olfactory receptors suggest that mammals have reduced their dependence on olfactory sense.

Citations

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