

# The Review for Olfactory Receptor Genes

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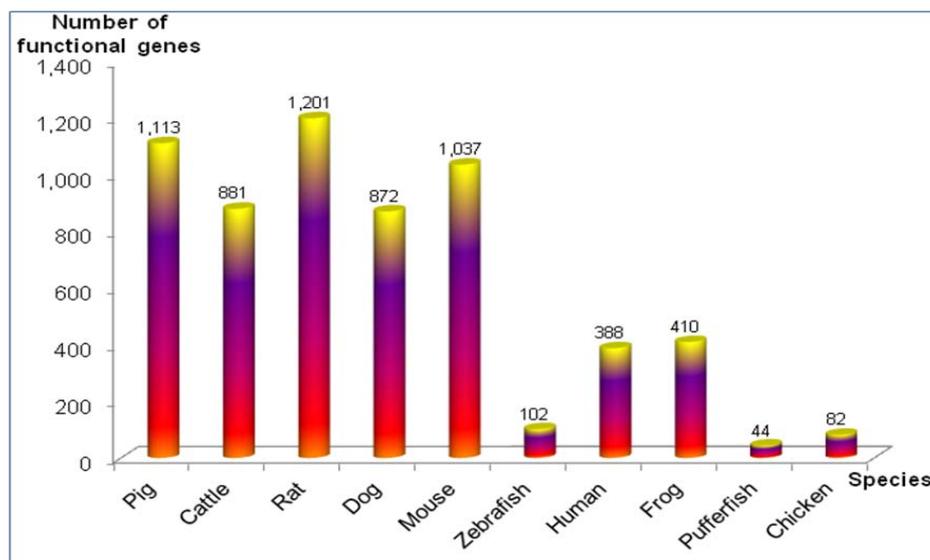
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## **ABSTRACT**

Mammals use the olfactory system as one of the basic instincts to avoid dangers and search for food. Many researches showed olfactory receptors (ORs) in mammals are encoded by the largest multigene family. Beside it has been suggested that the activation of ORs also have the links to reproductive and immune systems. Understanding the operation mechanism of OR system could lead to the way to improve the human's life quality as well as to develop some better strategies in the livestock industry. Our report here revealed the almost complete data sets of the current OR genes from NCBI database. Although the number of functional OR genes in pigs (1,113) and cows (881) are lower than rats (1,201) and mice (1,037) as well, they are still relatively high and should be highly considered for further application in the livestock industry, especially in the process to produce the best and suitable food for them. The most important aspect is this data could contribute as the available data to get more understanding in the evolutionary process of species through the environment condition changed.

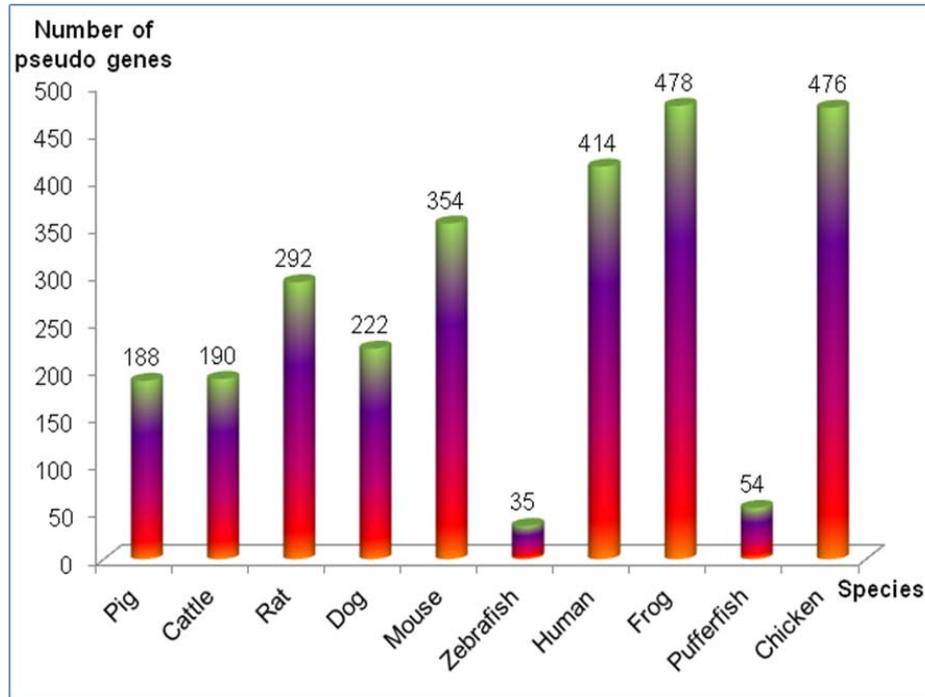
## INTRODUCTION

About two decades ago, the studies about olfactory receptors had been started in order to support scientists to clarify the mechanisms in insects and animals that how they can detect and recognize exactly thousands of chemical odorants from the environment around them [1]. From the preliminary results, the structures which contributed into this process are proteins having seven transmembrane domains, and many researches later confirmed that they are belonging to the G-protein-coupled receptor superfamily. To start the smelling processes, the volatile odorant molecules have to bind specifically to dedicated ORs expressed by olfactory sensory neurons (OSNs) in the olfactory epithelium then the electrical signals will be transmitted to the olfactory bulb [2,3,4,5]. It has been known that OR proteins are encoded by the largest gene superfamily in the mammalian genome. Took the advantage from the emerging of sequencing technologies and utilized the available genome sequences, many reports have been performed to decode the complexity of Olfactory receptor gene family in several species such as humans [6,7,8,9], Bovine [10], Pigs [11], dogs and rats [12,13,14], mice [15,16,17,18], other vertebrates [12,19,20,21], and fish species [22,23,24,25,26,27,28,29]. Basically, there are two classes of OR gene families including the fish-like Class I ORs consisting of 17 families and the tetrapod-specific Class II ORs consisting of 14 families [20]. The Figures 1, 2 and 3 show that there is extremely high diversity in the number of functional as well as pseudo OR genes. Interestingly, in spite of the large number of genes that make up the OR subgenome, most OR neurons express a single genes and in fact they expressed even just a single allele [1,30].

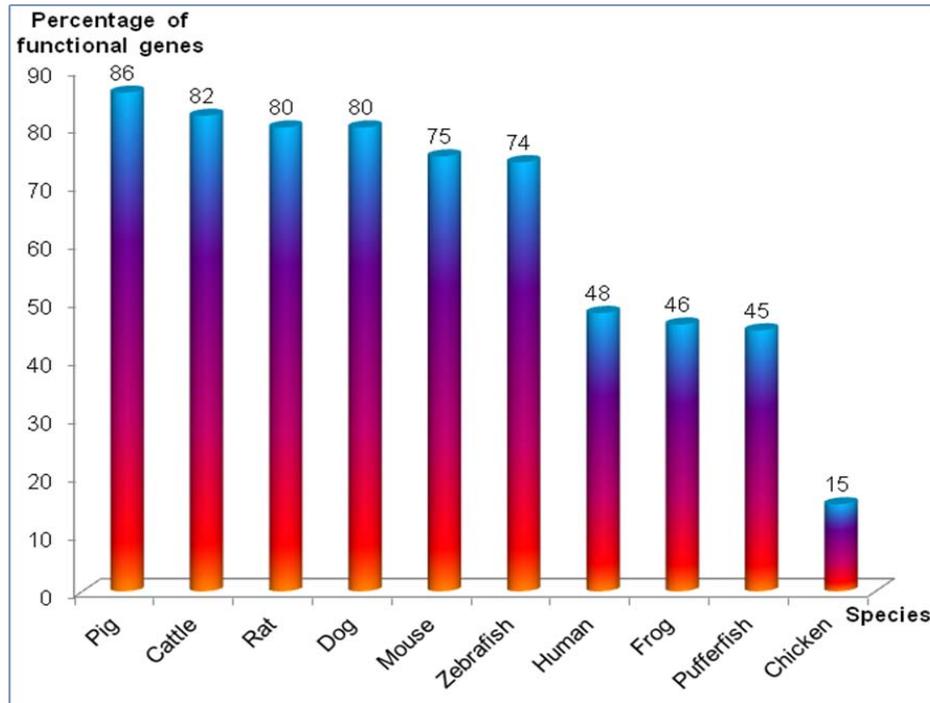


**Figure 1.** Differences in the number of functional OR genes among different species.

Comparison in the number of functional OR gene among pigs, cattle, rats, dogs, mice, zebrafish, humans, frogs, pufferfish and chickens. The Y-axis shows the number of functional OR genes of each species. The X-axis indicates ten species (pigs, cattle, rats, dogs, mice, zebrafish, humans, frogs, pufferfish and chickens) used in this report. Data were from Niimura and Nei [31], Nguyen *et al.* [11] and Lee *et al.* [10].



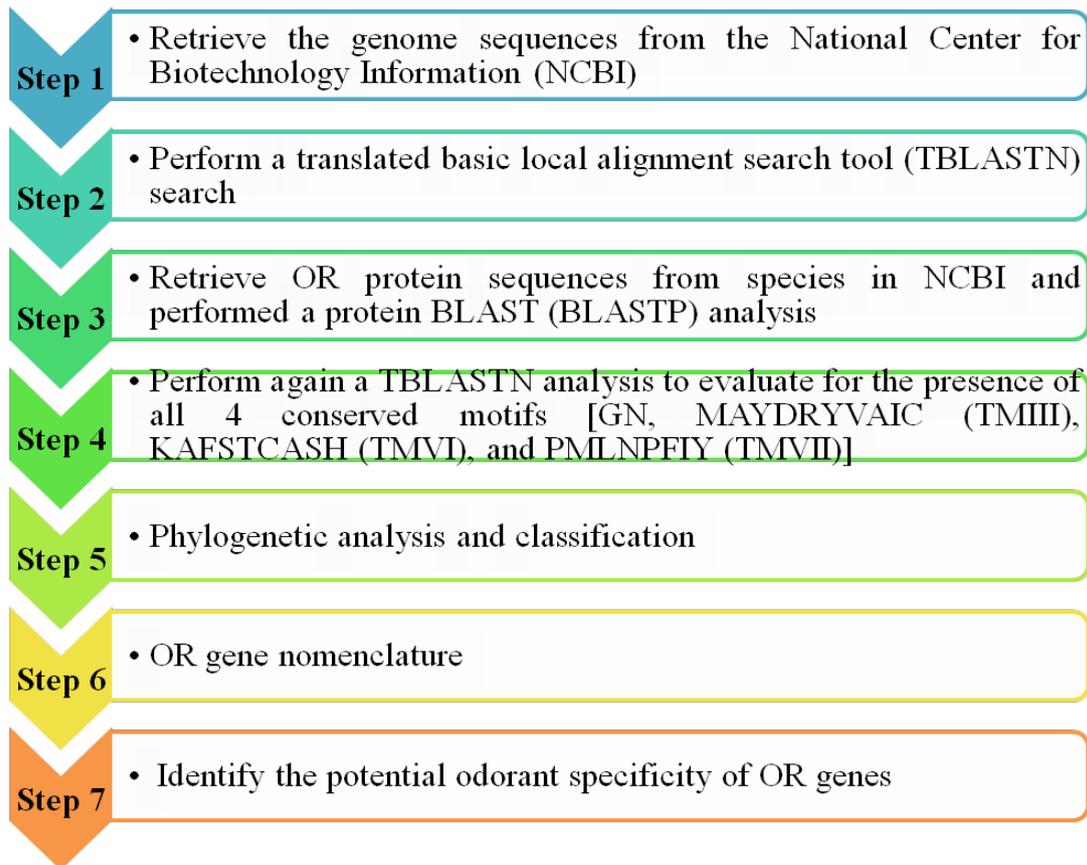
**Figure 2.** Differences in the number of pseudo OR genes among different species. Comparison in the number of pseudo OR gene among pigs, cattle, rats, dogs, mice, zebrafish, humans, frogs, pufferfish and chickens. The Y-axis shows the number of pseudo OR genes of each species. The X-axis indicates ten species (pigs, cattle, rats, dogs, mice, zebrafish, humans, frogs, pufferfish and chickens) used in this report. Data were from Niimura and Nei [31], Nguyen *et al.* [11] and Lee *et al.* [10].



**Figure 3.** Differences in the percentage of functional OR genes among different species. Comparison in the percentage of functional OR gene among pig, cattle, rat, dogs, mice, zebrafishes, humans, frogs, pufferfishes and chickens. The Y-axis shows the percentage of functional OR genes of each species. The X-axis indicates ten species (pigs, cattle, rats, dogs, mice, zebrafish, humans, frogs, pufferfish and chickens) used in this report. Data were from Niimura and Nei [31], Nguyen *et al.* [11] and Lee *et al.* [10].

## PROCESS TO RETRIEVE OLFACTORY RECEPTOR GENES

The process with seven steps as described below is the common procedure that has been widely used by several scientists previously to search for OR genes in several species [9,10,11,18].



## DISCUSSION

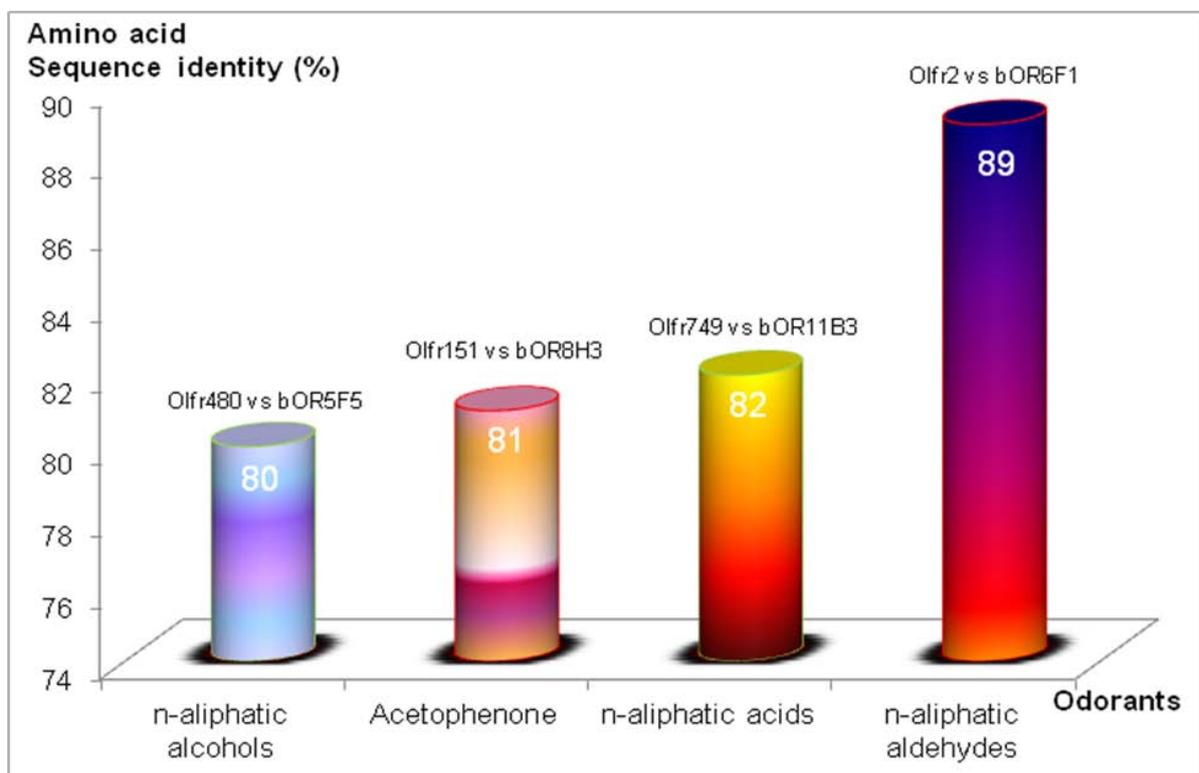
It has been shown that in mammals, olfactory receptors are encoded by a gene family of hundreds to thousands of genes in the genome, which together constitute the OR subgenome [6,9,10,11,13,14,16,18,20,21]. With the availability of whole genome sequence information, several studies have been carried out to characterize the OR subgenomes of vertebrates [9,11,13,14,18,20,21,32] in the aim to better understand the underlying biology of olfaction. In this study, we tried to summarize for whole current data about olfactory receptors from diverse species.

Pseudogenes are actually described as the genes without the function. In this study, we also tried to summarize whole the percentage of OR pseudogenes in order to have the full picture about the actual size of OR repertoire within the genome of each species. Moreover, it should be considered as the factor indicating the trend and strength of evolutionary process of that.

Recently, Jahromi suggested that a single nucleotide polymorphism (SNP) in the olfactory receptor family 14, subfamily J, member 1 (OR14J1) gene, rs9257691, in the MHC

telomeric region might become a signal to identify the role of OR gene in the pathogenesis of T1D (Type 1 diabetes) in patients who are prone to diabetic complications [33]. Beside, another study in humans also showed that a polymorphism in a region on chromosome 11 containing the OR genes OR51B5 and OR51B6 was associated with fetal hemoglobin concentration. This indicates that the elements within this OR gene cluster may play a regulatory role in gamma-globin gene expression [34]. The stereotypical mating posture of an estrus female pig when exposed to a compound in the saliva of boars is also mediated by the olfactory system [35]. Further studies on OR genes and their functional importance could elucidate phenotypes other than olfaction, such as reproductive or behavioral traits, that may be associated with OR gene clusters.

Last but not least, to predict potential target specificity of olfactory receptors. This report also summarizes about one of the most important characteristics of OR genes that there are several OR sequences among different species that their similarity in amino acid sequences is extremely high. Shown in Figure 4 are four representatives of OR pairs with at least 80% identity in amino acid sequences between mice and cows OR genes in their genome sequences. This means that they might have the similar function in the process to perceive the odorants with similar chemical structures between two species.



**Figure 4.** Potential odorant specificity of representative OR sequence pairs retrieved from

mice and cows genome sequences. The Y-axis shows the amino acid sequence identity in percentage. The X-axis indicates the kinds of odorants exemplified in this report. Olfr480; Olfr151; Olfr749 and Olfr2 are mice Ors that are used to compare with cow ORs including bOR5F5; bOR8H3; bOR11B3 and bOR6F1. Data were from [10,11,36,37,38,39,40,41,42,43,44]

## CONCLUSIONS

This report is the summary about the current data of olfactory receptors in mammals as well as in insects. The results from this study more or less can be utilized as comparative and reference information for us to get more inside into the understanding about the complexity of olfactory system and the process to perceive the odorants from the world around us.

## COMPETING INTERESTS

The authors declare that they have no competing interests.

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