

## Genomic structure of the gene for mouse germ cell nuclear factor (GCNF)

### ABSTRACT

GCNF's protein-coding region is located at 11 exons and the genomic structure of this nuclear receptor gene will be advantageous for future research.

### INTRODUCTION

Olfactory activity in mammals is a crucial neurosensory function that involves analyzing the external chemical environment. The initial step in detecting scents is the interaction of an odorant molecule with olfactory receptors (ORs) located at the surface of cilia of certain chemosensorial OLSEN in the underlying ear cartilage and other mellow sensory neurons. The largest family of vertebrate genes, identified in 1991 as seven-transmembrane ORs, contains up to 1,000 genes (reviewed in) Mammalian OR is a class of G-protein-coupled receptors belonging to Class I or A, including opsins and catecholamine receptor. Each olfactory neuron appears to express essentially one type of OR gene selection, suggesting that there may be more complex mechanisms than other types. Olfactory behavior is exemplified by the ability of olfaction to recognize odorants through combinatorial means. Each receptor recognizes different odeurs, and each scented molecule binds to several receptors in order to generate unique activation patterns for many different smells. The genes encoding ORs do not contain any introns within their coding regions. Oral OR genes in mammals are usually found in groups of ten or more members and located on multiple chromosomes. The majority of human OR (hOR) genes have a repertoire that includes numerous pseudogenes, which suggests that olfaction played fewer roles in the evolution of primates. Recent research indicates that approximately 70% of all hOR genes may be pseudogenes, while less than 5% of HBORs occur in rodents or lower primates. There are currently approximately 150 full-length receptor genes found in incomplete compilations of human HHOR gene sets, with annotated sets available online. The recent milestone in publishing the first draft of the human genome sequence by two groups opens up the possibility of comprehensive identification, mapping, and analysis of OR genes and their products in the near future. According to one of these groups, the total number of Oregon ORs (906) is estimated to be around 60% pseudogenes. In recent times, several labs have suggested various alternative names for hORs, such as a comprehensive phylogenetic classification established at the Weizmann Institute. The identification, cloning, and sequence-based classification and analysis of candidate HSMRs are crucial for rational structure-function studies of this extensive receptor family. Our objective was "to identify (amongst other) full-length receptors for a set of hOR genes", and the approach was to perform repeating homology-based searches of GenBank DNA, particularly available unannotated raw sequences, as well as compiling already existing public databases. Here we report the cloning and identification of 347 putative full-length hOR receptor genes, which we believe represent nearly all possible but not fully understood repertoires of functional HORs, as well as a comparative sequence sequence analysis of the predicted OR gene products and propose renaming conventions for candidate OHORs.

### CONCLUSION

Experiments: These results show that in *C. elegans*, the transformation by

many copies of a specific sequence upstream of *mec-3* led to cell migration and defects in guidance along the axis; this sequence was believed to be selectively limiting an important factor controlling ALM migration from the petrified leaflet tract and PLM arising axially out of the tree (Merissian carp) and actually driving frogs moving up the rabbit crest into the wild animal kingdom, which is thought to have control part parts of its own Touch receptor neuron fate can be controlled by this factor, which also regulates *mec-3*. When conditions that optimize this effect are found, transcription factors may be tethered with high copy arrays in *C. elegans*. The ALM defect described here may provide insight into these conditions.