

Bos taurus Olfactory Receptor

Katie Davis^{1,2} and Sandra Rodriguez-Zas¹

¹ Department of Animal Sciences, University of Illinois Urbana-Champaign, ² ACES James Scholar Honors Program

Introduction

- Mammals have a very complex system from sensing environmental stimuli. Odorant molecules, in particular, are capable of providing a variety of information about the environment.
- Olfactory receptors (OR) detect and identify a wide range of odors and chemosensory stimuli through the binding of and activation of the minimum of one olfactory receptor.
- A large multigene family of olfactory receptor genes mediates odor perception in mammals. The amount of these genes varies between species.
- A significant amount of homology exists between the genes coding for OR in *Mus musculus*, *Homo sapiens* and *Canis lupus familiaris*
- M. musculus* has approximately 1200 genes that code for OR, *H. sapiens* to have around 900 OR genes and *C. lupus familiaris* is estimated to have 800 OR genes.
- By 2007 only 29 OR genes were reported in *Bos taurus*.

Hypotheses

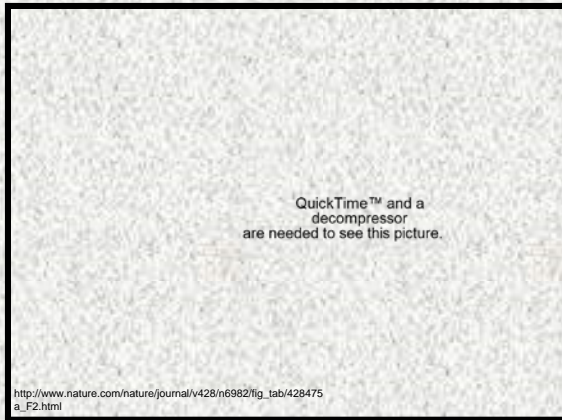
- Based off the level of homology, a similar number of genes coding for OR should exist in *Bos taurus*
- The homology between the species can be used to locate the remaining OR in *Bos taurus*.

Objectives and Activities

- The HomoloGene database <http://www.ncbi.nlm.nih.gov/homologene> automatically detects homologs that exist within the eukaryotic genomes that have been completely sequenced. This database was used to detect the homologs that exist within the olfactory receptors of the completely sequenced eukaryotic genomes.
- A compilation of the known OR genes of *M. musculus*, *H. sapiens* and *C. lupus familiaris* and their related proteins was made using the Homologene, Protein, Nucleotide, and Gene databases in the NCBI GenBank <http://www.ncbi.nlm.nih.gov/genbank/>. This information was used to locate similar sequences in the *B. taurus* genome. Matches were identified based on a high percentage of sequence identities and similarities, a low number of gaps and the location of the matches in the genome. Matches between *M. musculus* sequences to fragments in the *B. taurus* genome were further investigated to

Results

Figure 1. Phylogenetic Tree, Figure 2. Sample Homologene Cattle Blast Match Table



Homologene Number	79418
Mus musculus	Olfr1490
Mus musculus Protein ID	NP_001011832
Homo sapiens	OR10W1
Homo sapiens Protein ID	NP_997257
Canis lupus familiaris	LOC6100022
Canis lupus familiaris Protein ID	XP_852500
Blast Bos taurus Genome	8.00E-122
Features	59062 bp at 5' side: similar to olfactory receptor, family 1, subfamily S, member 1; 25158 bp at 3' side: similar to olfactory receptor 1487
Score	Identities= 215/288 (74%), Positives=242/288 (84%), Gaps= 0/288 (0%), Frame=-2
Status	New

Figure 3. Table of OR genes studied

Genus species	Olfactory Receptor Genes Studied with Homologene	Olfactory Receptor Genes Discovered Using Cattle Blast
<i>Mus musculus</i>	491	N/A
<i>Homo Sapiens</i>	328	N/A
<i>Canis lupus familiaris</i>	309	N/A
<i>Bos taurus</i>	465	111

Conclusions

- The known olfactory receptor for *Mus musculus*, *Homo sapiens* and *Canis lupus familiaris* were successfully extrapolated upon to locate new OR genes in the known *Bos taurus* genome.
- The three-step process was a successful and time effective method for locating previously unknown olfactory receptor genes in the cattle genome.
- The process also resulted in the compilation of data relating to all four species and their olfactory receptors. - Insight into distinguishing factors of the *B. taurus* olfactory receptor has the potential to positively impact the effectiveness of cattle production practices, and the overall well being of cattle in production settings.

Acknowledgements

ACES James Scholar Honors Program