

The Linkage Between Olfactory Receptor Genes and Major Histocompatibility Complex

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ABSTRACT

One of the most considered functions of MHC molecules is utilized to bind to peptide fragments originated from pathogens and display them on the cell surface for later recognition by the appropriate T-cells. The olfactory system also called sense of smell is the part of the sensory system used for smelling (olfaction). Many reports revealed that olfactory receptors (ORs) are encoded by the largest multigene family in mammals. Moreover, several researches 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 understanding about the activation mechanisms of the immune system to later apply to improve the life quality as well as to develop some better strategies in the livestock industry. Although, the results from this report show the linkage which is not strong between Olfactory receptor clusters and Major Histocompatibility Complex region, they still have large number of OR genes located on the same chromosome with MHC regions, such as 77 and 253 OR genes on MHC chromosomes of cattle and porcine, respectively.

INTRODUCTION

The immune system could be divided into two including innate and acquired immune system, and the major histocompatibility complex (MHC) belongs to the acquired immune system with a set of proteins on their cell surfaces needed to recognize foreign molecules in vertebrates. So, it turns out that this system will determine the histocompatibility. Several studies carried out on inbred mice and rats proved that products from MHC genes influence individual-specific odors which could play an essential role in the process of mating choice (Yamazaki et al., 1979, Brown et al., 1987, Singh et al., 1987) (Yamazaki et al., 1976, Brown et al., 1989, Potts et al., 1991, Penn and Potts, 1998a, b, Penn and Potts, 1998c). Several researches had been confirmed that OR proteins are encoded by the largest gene superfamily in the mammalian genome, and with the emerging of sequencing technologies and the availability of genome sequences, many studies have been performed to decode the complexity of Olfactory receptor gene family in several species such as humans (Glusman et al., 2001, Zozulya et al., 2001, Niimura and Nei, 2003, Malnic et al., 2004), Bovine (Lee et al., 2013), Pigs (Nguyen et al., 2012), dogs and rats (Olender et al., 2004, Quignon et al., 2005, Niimura and Nei, 2007), mice (Young et al., 2002, Zhang and Firestein, 2002, Godfrey et al., 2004, Zhang et al., 2004), other vertebrates (Freitag et al., 1995, Freitag et al., 1998, Niimura and Nei, 2005, 2007), and fish species (Ngai et al., 1993, Barth et al., 1997, Cao et al., 1998, Freitag et al., 1999, Sun et al., 1999, Dugas and Ngai, 2001, Kondo et al., 2002, Alioto and Ngai, 2005). 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 (Freitag et al., 1995). In this study, we try to perform the relationship between OR clusters and MHC region within six species.

PROCESS TO RETRIEVE OLFACTORY RECEPTOR GENES

The process with three steps as described below is the common procedure that has been widely used by several scientists previously to measure the physical distance among loci. (Nguyen et al., 2012, Lee et al., 2013).

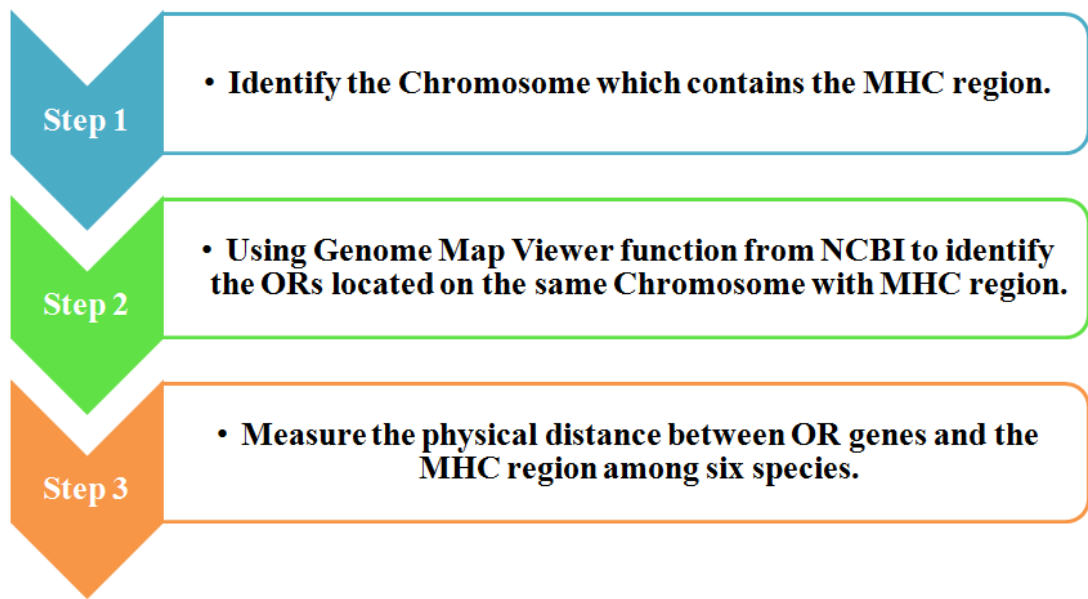


Figure 1. The process to measure physical distance between OR genes and the MHC region.

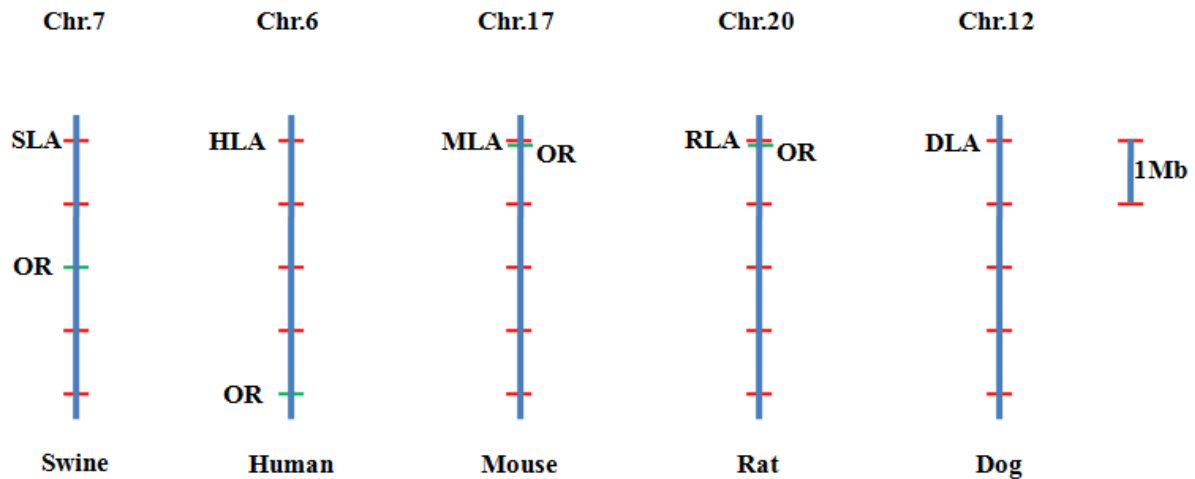


Figure 2. The physical distance between OR clusters and the MHC region. SLA, Swine Leukocyte Antigen; HLA, Human Leukocyte Antigen; MLA, Mouse Leukocyte Antigen; RLA, Rat Leukocyte Antigen; DLA and Dog Leukocyte Antigen. OR, Olfactory receptors. Data were from Niimura and Nei (Niimura and Nei, 2006), Nguyen *et al.* (Nguyen *et al.*, 2012), (Olender *et al.*, 2004, Quignon *et al.*, 2005, Niimura and Nei, 2007), (Glusman *et al.*, 2001, Zozulya *et al.*, 2001, Niimura and Nei, 2003, Malnic *et al.*, 2004) and Lee *et al.* (Lee *et al.*, 2013).

DISCUSSION

MHC haplotypes and olfaction have been suspected to be related (Younger et al., 2001, Santos et al., 2010). Therefore, we determined the number of OR genes that were located on the same chromosome as the MHC region in humans, dogs, mice, rats, pigs and cows. Although, the number of OR genes on chromosome 23, which contains the MHC region in cows (Lee et al., 2013), was 77 much lower than in pigs (n=253) (Nguyen et al., 2012), their distribution was still higher than other species with the MHC containing chromosomes (data not shown). Moreover, we found that the distribution of OR genes on the chromosome 23 and BoLA (bovine leukocyte antigen) regions are nearby together. Further evaluation of the physical distance between OR genes and the MHC region among six species also showed that these clusters were not always physically proximal to each other, showing that the physical linkage between OR clusters and MHC regions is not strong.

However, 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 (Jahromi, 2012).

CONCLUSIONS

Our report provides the preliminary observation about the physical linkage between OR genes and MHC regions. Although in theory there is no strong linkage among them, some practical experiments should be further carried out to confirm the significant effects of OR gene variations on MHC activity.

COMPETING INTERESTS

The authors declare that they have no competing interests.

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