

Highly conserved regions in the 5' region of human olfactory receptor genes

H.F. Tobar^{2*}, P.A. Moreno^{2,3*} and P.E. Vélez^{1,2*}

¹Department of Biology, Universidad del Cauca, Popayán, Colombia

²Group of Molecular, Environmental, and Cancer Biology BIMAC, Universidad del Cauca, Popayán, Colombia

³School of Systems and Computer Engineering, Universidad del Valle, Santiago de Cali, Colombia

*All authors contributed equally to this study.

Corresponding author: P.E. Vélez

E-mail: pvelez@unicauca.edu.co

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ABSTRACT. Regulation of human olfactory receptor (hOR) genes is a complex process of control and signalization with various structures and functions that are not clearly understood. To date, nearly 390 functional hOR genes and 462 pseudogenes have been discovered in the human genome. Enhancer models and trans-acting elements for the regulation of different hOR genes are among the few examples of our knowledge concerning regulation of these genes. We looked for upstream control elements that might help explain these complex control mechanisms. To analyze the human olfactory gene family, we looked for functional genes and pseudogenes common to all hOR genes obtained from public databases. Subsequently, we analyzed sequences upstream of the transcription start sites with data mining and bioinformatics tools. We found two highly conserved regions, which we called HCR I and HCR II, upstream of the transcription start sites in 77 hOR genes and 87 pseudogenes. These regions showed possible enhancer functions common to both genes

and pseudogenes, an intriguing feature that may be associated with the expression of pseudogenes. Based on these HCRs, we propose a structural model of gene regulation for the olfactory gene family.

Key words: Olfactory receptor gene; Promoter region; Highly conserved region; Regulation; Enhancers