Characterization of odorant receptors (RproORs) in *Rhodnius prolixus* antennae

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Olfaction, an intricate signal transduction mechanism, allows insects to recognize the environment by the interpretation of odor molecules present in the air. Such mechanism involves a series of proteins among which odorant receptors (ORs) are essential for correct odor-molecule recognition. ORs are functionally active when co-expressed with another OR, called odorant receptor co-receptor (Orco). The main goal of this study was to select and characterize odorant receptors in *R. prolixus* genome. Initially, we selected 22 RproOR using bioinformatics and phylogenetic analysis, taking into account their homology with ORs previously described in other insects. Total RNA extraction, cDNA synthesis and PCR were carried out according to manufacturer’s instructions. PCR products were carried out on a 1% agarose gel stained with GelRed. *R18S* was used as a reference gene. The ORs showed a high amino acid content divergence in the 7-transmembrane regions, suggesting they are involved in different odor molecules detection. Based on a PCR profile, we selected 10 RproORs showing expression in adult antennae. Eight of them were expressed in both male and female antennae. Interestingly, *RproORM201* was found to be expressed exclusively in male antennae, suggesting this OR could be associated with the detection of male specific molecules. On the other hand, *RproORF301* was expressed exclusively in female antennae, indicating this OR should be linked to detection of particular semiochemicals by females. Quantitative PCR reinforced their high expression in antennae. These ORs constitute excellent targets for gene silencing by RNAi. Our next step, already in progress, consists in silencing these genes for function characterization according to their deficiency in the olfactory system. Based on this study, we should be able to propose traps or other forms of interfering with the behavior of search and location of the host by *R. prolixus*.

Key Words: Odorant receptor, *Rhodnius prolixus*, Chagas disease
Supported by: FAPERJ, CNPq, CNPq/INCT-EM and CAPES