Analysis of the lincRNA transcriptome in the accessory olfactory system

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The olfactory system is a sensory system capable of detecting environmental chemical cues, leading to the sensation of an odor and/or behavioral and endocrine changes. In order to perform these functions, this system comprises two olfactory organs in manmals, the main olfactory epithelium (MOE) and the vomeronasal organ (VNO), found in the nasal cavity. The VNO is responsible for detecting intra and inter-species stimuli and for initiating inate behaviour, such as sexual, agressive and social. Recently, a huge variety of long non-coding RNA (lncRNAs) has been discovered in several tissues, playing roles in the regulation of gene expression and development. Given the unique properties of the process by which genes coding for vomeronasal receptors are expressed in the VNO sensory neurons, we hypothesize that lncRNAs might be involved in such regulation. In order to unveil intergenic long non-coding RNAs (lincRNAs) that could be participating in the process of VNO neurons differentiation, we developed a bioinformatics pipeline to identify and functionally annotate lincRNAs preferentially expressed in this organ. Using public RNA-Seq libraries from eight tissues, including the VNO and MOE, we constructed a transcriptome atlas of mice using differential gene and transcript expression analysis based on the mouse Ensembl reference genome that is being utilized for searching lincRNAs. Bioinformatics tools are being used for predicting the coding potential of a transcript using information about the nucleotide composition, evolutionary pattern, ORF length and similarity against known proteins and protein domains. Non-coding transcripts that are differentially expressed in the VNO will be selected to further inspection, both *in silico* and *in vitro*. We will predict the secondary structure of these lincRNAs as well as their possible interactions with proteins and other RNA molecules in order to try to infer their functional role in the tissue. Wet lab experiments, such as real-time PCR and *in situ* hybridization, will provide more information concerning the levels of expression and the spatial localization of the selected transcripts in the VNO. We expect to discover lincRNAs that participate in VNO neuron differentiation, contributing to their unique gene expression and physiological properties, ultimately resulting in the generation of innatebbehaviours in mice.