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PHEROMONE SIGNALLING IN THE MOUSE: ROLE OF URINARY PROTEINS AND VOMERONASAL ORGAN

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INTRODUCTION

Pheromone signalling in the mouse is characterized by a special chemosensory organ, the vomeronasal organ, and a high concentration of proteins binding and releasing volatile pheromones in male mouse urine. The endocrine effects primed by male mouse urine reported to require both the vomeronasal organ and the urinary proteins are the acceleration of female puberty onset, the pregnancy block and the estrus acceleration/synchronization. This association is challenging and outlines a system which, while sharing some of the properties of the sense of smell, is profoundly different as to the biology, the transduction mechanism, the stimulus/receptor interaction and the adequate stimulus. The study is at an early stage and only rudimentary or suggestive evidence is available today. This presentation intends to highlight some of the problems for investigations to come.

The Lipocalins

In nature, molecules can be used as chemical labels or tags for the signalling and the recognition of individuals, sexes, strains and species. The Major Histocompatibility Group, for example, contributes to single out a haplotype (40) and is recognized by the immune system in order to sort out the alien from the self. Another example are insect pheromones, species-specific molecules that trigger precise reactions in conspecifics (22, 32). In mammals, it is now clearer and clearer that lipocalins are a third class of label molecules used as complex chemosignals (17). In the animal kingdom, lipocalins are a large, disparate and diverse group of small proteins, molecular weight about 20 kDa, many of which are extracellular and display binding with high selectivity and affinity for small hydrophobic molecules. Beta-lactoglobulin is the first lipocalin crystallized from cow's whey in the 1930s (1), and more than thirty proteins are classified as lipocalins today (18). All lipocalins share a common structure. The common structure is a central 8-stranded beta-barrel with simple forth and back repeated topology lining a hydrophobic cavity, an N-terminal helical turn and a long C-terminal helix. The overall sequence homology between different lipocalins is low, typically about 20%, despite the presence of three well-defined and highly conseved motifs. At variance with

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