

**Poster session I Poster #119****In silico approach to identify odor metric using odor descriptions**Anne Tromelin<sup>1</sup>, Claire Chabanet<sup>1</sup>, Karine Audouze<sup>2</sup> and Elisabeth Guichard<sup>1</sup><sup>1</sup>INRA, Centre des Sciences du Goût et de l'Alimentation, UMR1324 INRA, UMR6265 CNRS, Bourgogne University, F-21000 Dijon, France<sup>2</sup>Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark, DK-2800 Lyngby, Denmark  
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The first step of odor detection and discrimination of myriads of structurally diverse odorants depends on their interactions with olfactory receptors<sup>1</sup>, whereas the perception of odors quality results from a combinatorial coding<sup>3</sup>, whose deciphering remains now a major challenge.

Haddad *et al.* pointed out the lack of odor metrics, *i.e.* rules describing olfactory perceptual space, as an obstacle to understand olfactory coding, and proposed two physicochemical metrics<sup>2</sup>. More recently, a descriptive analysis was performed of the FlavorBase 2010 (FB2010; <http://www.leffingwell.com>), putting forward that the odor description can be successfully analyzed using a metric approach<sup>4</sup>.

FB2010 is one of the largest collections of natural and synthetic odorant molecules (4184 entries), whose flavor and odor descriptions are based on bibliographic documents.

We performed a computational analysis using odorant descriptions of the molecules present in FB2010. First, we identified 740 odorant descriptors, 200 of them are present in at least 10 molecules. These 200 descriptors have been used to create a matrix containing the 4184 odorant molecules. According to previous studies, each element of the matrix was converted into binary values<sup>5,6</sup>.

Four statistical analysis approaches based on odor descriptions of the molecules were applied: classical multidimensional scaling, correspondence analysis of odor descriptors, hierarchical clustering and Kohonen Self-Organizing Maps.

The obtained results highlight subsets of molecules sharing close odor descriptors, suggesting an interesting and promising way of using computational approaches to help to decipher olfactory coding.

- 1 L. Buck and R. Axel *Cell* 65 (1991) 175-187
- 2 R. Haddad *et al.* *Curr. Opin. Neurobiol.* 18 (2008) 438-444
- 3 B. Malnic *et al.* *Cell* 96 (1999) 713-723
- 4 K. Martinez-Mayorga *et al.* *J. Chemometr.* 25 (2011) 550-560
- 5 H. Sagae *et al.* *Chem. Senses* 36 (2011) E39-E40
- 6 A. Tromelin *et al.* *Chem. Senses* 36 (2010) E40-E40

**Poster session II Poster #72****Neuroethological analysis reveals localization of pheromone-plant odor interaction in the moth antennal lobes**Federica Trona<sup>1,2</sup>, Gianfranco Anfora<sup>2</sup>, Anna Balkenius<sup>1</sup>, Alan Knight<sup>3</sup>, Marco Tasin<sup>2</sup>, Peter Witzgall<sup>1</sup>, Rickard Ignell<sup>1</sup><sup>1</sup>SLU, Division of Chemical Ecology, Department of Plant Protection Biology, Alnarp, Sweden<sup>2</sup>Fondazione Edmund Mach, IASMA Research and Innovation Centre, San Michele all'Adige, Italy<sup>3</sup>USDA, Yakima Agricultural Research Laboratory, WA, USA  
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An outstanding challenge in olfactory neurobiology is to reveal the mechanisms that underline the discrimination of behaviourally relevant odours, including the mechanisms regulating the interaction between social and environmental cues. We have studied how binary blends of the main sex pheromone and host-plant cues affect odor processing and ensuing behavior in a worldwide insect pest, the codling moth *Cydia pomonella*. We show that the presence of ecologically relevant plant volatiles increases the attraction of males to a threshold dose of codlemone: in wind tunnel bioassays, a higher proportion of moths made close upwind flights and contact with the source of blends of pheromone

and plant volatiles than to the single compounds alone. Through an integrated analysis, we demonstrate that the high level of behavioral interaction between sex pheromone and host compounds is mirrored at the neurophysiological level. Calcium imaging of the primary olfactory centre, the antennal lobe (AL) showed that the presence of plant volatiles enhanced the response to a sub-threshold dose of codlemone in the Cu, the largest glomerulus of the macroglomerular complex (MGC), while suppressive interactions were observed in other parts of the AL. Intracellular recordings from AL projection neurons confirmed that synergistic responses were confined to the Cu and other glomeruli in the MGC. Our physiological analysis demonstrates that the coding of odor signals from conspecifics and plants is highly integrated in the central nervous system. This highlights the role of host plant cues in premating sexual communication and underscores that, in nature, sex signals and habitat cues are always perceived as an ensemble.

### Contributed talks I “Modulation of the olfactory system (Linnaeus Symposium)” Monday 25 June

#### **Sensory input regulates the dendritic development of specific neuronal subtypes in the mouse olfactory bulb**

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Sensory input has been shown to regulate development in a variety of species and in various structures, including the retina, cortex and olfactory bulb (OB). Within the mammalian OB specifically, the development of dendrites in mitral/tufted cells is well known to be odor-evoked activity-dependent. However, little is known about the developmental role of sensory input in the other major OB population of the GABAergic interneurons, such as granule cells and periglomerular cells. Here, we identified, with DNA microarray and in situ hybridization screenings, a glycoprotein gene 5T4 and a transcription factor gene Npas4, whose expression in the OB interneurons are dependent on sensory input. 5T4 is a transmembrane protein, whose extracellular domain contains seven leucine-rich repeats, and a short cytoplasmic domain. 5T4 overexpression in the newborn OB granule cells facilitated their dendritic branching even under the sensory input-deprived condition. By contrast, both 5T4 knockdown with RNAi and 5T4 knockout with mice resulted in a significant reduction in the dendritic branching of OB granule cells. Further, we identified the amino-acid sequence in the 5T4 cytoplasmic domain that is necessary and sufficient for the sensory input-dependent dendritic shaping of specific neuronal subtypes in the OB. Npas4 is a neuronal Per-Arnt-Sim (PAS) domain protein 4, whose N-terminal region contains a basic helix-loop-helix domain for DNA binding and two PAS domains involving in the adaptation of cellular stresses and environmental factors. Npas4 overexpression in the newborn OB granule cells facilitated their dendritic spine formation, while its translational fusion with the engrailed repressor domain showed a significant reduction of the dendritic spine formation. Thus, these results demonstrate that 5T4 and Npas4 contribute to regulate the activity-dependent dendritic development of interneurons and the formation of functional neural circuitry in the OB.

### Poster session I Poster #315

#### **Perception of pungent, taste and odor stimuli in the patients with congenital insensitivity to pain with anhidrosis (CIPA)**

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CIPA is a severe autosomal recessive disorder caused by mutations in the *NTRK1* gene coding for the tyrosine kinase receptor A. Since this disease is characterized by loss of pain sensitivity and peripheral unmyelinated and small myelinated nerve fibers, it raises the possibility that oral sensation such as burning sensation and taste may be affected. In addition, ability of smell could be affected because some of the patients have mental retardation. Thus, we investigated