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Program

Satellite Symposium of the DFG Schwerpunktprogramm (SPP 1392) “Integrative Analysis of Olfaction”

at the 12th Göttingen Meeting of the German Neuroscience Society
on March 21, 2017, at the ZHG, Georg-August-Universität Göttingen

Deutsche Forschungsgemeinschaft

Program

12:00 Welcome coffee, lunch snacks and poster presentations

13:00-13:10 Opening Remarks
Giovanni Galizia, University of Konstanz

Session 1: SPP project presentations (13:10-15:40), Open for all participants
Chair: **Elisa Schuh**, Max Planck Institute for Chemical Ecology, Jena

13:10-13:45 Reception and coding of pheromone signals in insects
Jürgen Krieger, Martin Luther University, Halle-Wittenberg
Silke Sachse, Max Planck Institute for Chemical Ecology, Jena

13:45-14:20 Integrative analysis of multiple pathways in the honeybee olfactory system
Wolfgang Rössler, University of Würzburg
Giovanni Galizia, University of Konstanz

14:20-14:40 Morphological and transcriptomic analysis of a beetle chemosensory system reveals a gnathal Olfactory center
Stefan Dippel, Georg August University, Göttingen

14:40-15:00 Turning olfactory memory into action
Bertram Gerber, LIN - Leibniz Institute of Neurobiology, Magdeburg

15:00-15:20 Odor discrimination learning in Drosophila: from behavior to neural circuits
André Fiala, Georg-August-University, Göttingen

15:20-15:40 Functional role of the insect odorant coreceptor
Monika Stengl, University of Kassel

15:40-16:30 Discussions, coffee and poster presentations

Session 2: SPP project presentations (16:30-19:25), Open for all participants
Chair: **Georg Raiser**, University of Konstanz

16:30-17:05 Olfaction during vertebrate evolution: the water-to-land transition
Sigrun Korsching, University of Cologne
Ivan Manzini, Georg-August-University, Göttingen

17:05-17:25 Behavioral, genetic and neuronal mechanisms of olfactory imprinting in zebrafish
Gabriele Gerlach, University of Oldenburg

17:25-17:45 New insights into the subsystem organization of the mammalian sense of smell
Frank Zufall, University of Saarland School of Medicine

17:45-18:05 Signaling mechanisms in the accessory olfactory system
Marc Spehr, RWTH, Aachen

18:05-18:25 Exploring chemical neighbourhoods in the olfactory bulb
Michael Schmuker, University of Hertfordshire, England

18:25-18:45 The rodent olfactory bulb granule cell: an alliance of numerous inhibitory mini-neurons
Veronica Egger, University of Regensburg

18:45-19:20 Odor information processing along an OR-specific neuronal pathway
Jörg Strotmann, University of Hohenheim
Anton Sirota, Ludwig-Maximilians-University, München

19:20 Closing Comments
Giovanni Galizia

Final session (19:25-19:40): Open for SPP "Olfaction" members only
7 years SPP "Integrative Analysis of Olfaction": A retrospection
Mihaela Mihaylova, University of Konstanz

20:00 Dinner at Restaurant Mazzoni (Hermann-Rein-Str. 2, Göttingen)

Please note that on 22nd of March, 14:30-16:30 there will be
another symposium on Olfaction
at the 12th Göttingen meeting of the German Neuroscience Society:
Olfactory processing and behavior across the vertebrate/insect divide: communalities and differences
Chairs: Giovanni Galizia (Konstanz), Sigrun Korsching (Cologne)

Reception and coding of pheromone signals in insects

Jürgen Krieger[1,3], Monika Zielonka[3], Elisa Badeke[2], Pablo Pregitzer[3], Ewald Große-Wilde[2] and Silke Sachse[2]

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Many insects release pheromones to elicit distinct behaviors in conspecifics. In moths, mate finding highly depends on female-released sex pheromones that are detected by the males with high accuracy and sensitivity. Data we have accumulated for the moth *Heliothis virescens* indicate that the sensitive and accurate recognition of pheromone molecules is based on an interplay of pheromone receptors (PRs) in the dendrites of pheromone-responsive olfactory sensory neurons (OSNs), and pheromone-binding proteins (PBPs) in the lymph of hair-like sensilla housing the OSNs. In this process “sensory neuron membrane proteins” (SNMPs), appears also to play a crucial role by operating as co-receptor for docking PBP/pheromone complexes and/or by contributing to the transfer of pheromones to PRs.

Unexpectedly, recent studies have indicated that also the larvae of moth respond to female sex pheromones and suggested a role of pheromone components in food source selection. Moreover, also female moths were shown to “autodetect” sex pheromone components released from conspecifics, which is thought to trigger behavior reducing the competition between females for ecological resources. To elucidate the molecular basis for the larval and female responsiveness to pheromones, we examined their antenna for molecular elements that are involved in pheromone detection by adult males, namely PRs, PBPs and SNMP1. The results indicate that the responses of *H. virescens* larvae and females to distinct sex pheromones components are based on the same molecular machinery as in the antennae of adult males.

Since certain plants odorants that coexist in the natural environment of males inhibit the electrophysiological response of their sex pheromone-specific OSNs and the pheromone-induced activity in the brain, we assessed the molecular targets for this inhibitory effect and found that the pheromone receptors but not PBPs were affected. Moreover, we tested if plant odorants effect pheromone-guided flight behavior in males. Together, the results revealed that pheromone-plant interactions in *H. virescens* might be an effect of stimulation with supra-natural plant odor concentrations, whereas under more natural conditions the olfactory system of the male moth appears to be well adapted to follow the female pheromone plume.

This work was supported by research grants from the Deutsche Forschungsgemeinschaft (SPP 1392, KR1786/4-2 and SA 909/3-2).

Integrative analysis of multiple pathways in the honeybee olfactory system

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Honeybees are excellent model systems to study olfactory processing via parallel information streams. We focused on two sets of anatomically isolated projection neurons (PNs) that form a dual olfactory pathway connecting glomeruli from two antennal-lobe hemilobes via a lateral and medial tract in opposite sequence with higher order olfactory centers - the mushroom bodies (MBs) and lateral horn.

Imaging studies had shown that glomeruli in both hemilobes receive largely redundant sensory input. Using simultaneous multi-electrode recordings from output neurons of both tracts, we found that both PN populations respond to similar odorants, but with different physiological properties further supporting the concept of parallel olfactory processing. Whereas lateral-tract PNs respond fast with broad odor tuning, medial-tract PNs respond with more narrow odorant tuning and with longer response latencies.

Interestingly, lateral-tract and medial-tract PNs form anatomical trajectories reminiscent of delay-line like neuronal circuits. To investigate the role of temporal coding, we analyzed levels of PN spike coincidences. Odor driven coincidences were present in PNs within and between tracts with highest levels in medial-tract PNs. Correlation of PN coincidence levels with odor tuning revealed a clear difference with low correlation levels in lateral-tract and high levels in medial-tract PNs.

Comparison of ionic-currents in lateral and medial tract PNs with those in postsynaptic MB Kenyon cells (KCs) using *in-situ* patch clamp recordings combined with live-labeling identification revealed similar properties of typical spiking neurons in both PN classes. This suggests that the different physiological properties in the two PN classes are caused by the differential sensory input we found for example for *Sensilla basiconica* and/or different synaptic interaction in local antennal-lobe circuits. In contrast to PNs, KCs exhibited very prominent K^+ currents promoting temporally sparse (phasic) responses that are well suited for coincidence detection from convergent PN input.

Additionally, Kenyon cells respond rapidly to changing olfactory stimuli. We tested the capacity of brain neurons to follow the fluctuations in concentration of a varying olfactory stimulus. LFP recordings from the MB vertical lobe revealed a pulse following capability of up to at least 60 Hz. This indicates that information about a stimulus' temporal structure is relayed to a higher order olfactory processing center, as well as demonstrating a temporal precision required for temporal coding schemes. We propose that fast processes contribute to the capacity of the honeybee olfactory system to deal with a diverse and temporally complex olfactory environment.

The results suggest that the dual olfactory system of the honeybee employs both parallel processing and coincidence coding, which integrates well into our current understanding of synaptic integration and memory-related plasticity at the level of MB KCs.

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Morphological and transcriptomic analysis of a beetle chemosensory system reveals a gnathal olfactory center

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The red flour beetle *Tribolium castaneum*, is an emerging insect model organism representing the largest insect order, Coleoptera, which encompasses several serious agricultural and forest pests. Despite the ecological and economic importance of beetles, most insect olfaction studies have so far focused on dipteran, lepidopteran, or hymenopteran systems.

Here, we present the first detailed morphological description of a coleopteran olfactory pathway in combination with genome-wide expression analysis of the relevant gene families involved in chemoreception. Our study revealed that besides the antennae also the mouthparts are highly involved in olfaction and that their respective contribution is processed separately. In *T. castaneum*, olfactory sensory neurons from the mouthparts are projecting to the lobus glomerulatus, a structure so far only being characterized in hemimetabolous insects, as well as to a so far non-described unpaired glomerularly organized olfactory neuropil in the gnathal ganglion, we term gnathal olfactory center. The high number of functional odorant receptor genes expressed in the mouthparts also supports the importance of the maxillary and labial palps in olfaction of this beetle. Moreover, gustatory perception seems equally distributed between antenna and mouthparts, since the amount of expressed gustatory receptors is similar for both organs.

Turning olfactory memory into action

Bertram Gerber, LIN - Leibniz Institute of Neurobiology, Magdeburg, Germany

Brains organize behavior. This involves the integration of present sensory input, past experience, and future behavior. I will argue that the insect mushroom body is a paradigmatic case of a central-brain structure bringing about such triadic integration.

The focus will be on the behavioral architecture of the mushroom body input and output neurons, and their role in the association of odor with taste reward as a biologically meaningful learning process. I will argue that a reasonably satisfying account of associative odor-taste memory trace formation seems within reach. However, we lack a comparable understanding as to how sensory and motor formats of processing are centrally integrated, and how adaptive, outcome-oriented action comes about. Such an understanding will pave the way to also understand the motivating factors of behavior, i.e. the systems that make Drosophila do what Drosophila ’s got to do.

Odor discrimination learning in *Drosophila*: from behavior to neural circuits

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Drosophila represents a favorable model organism to dissect neuronal circuits underlying behavior. We investigate those neuronal structures that mediate associative learning and encode complex associative memories. Fruit flies can learn to avoid an odor temporally paired with an electric shock punishment. The genetic techniques available in this organism allow one to selectively manipulate distinct neuronal populations. Moreover, optical imaging using genetically encoded fluorescence sensors enables one to monitor neuronal activity in response to the trained stimuli. Thereby, those neuronal subsets underlying associative learning can be determined. We have analyzed two aspects of aversive associative olfactory learning in detail.

First, we performed associative conditioning experiments using chemically similar odorants that evoke overlapping neuronal activity in the fly's antennal lobes and highly correlated activity in mushroom body lobes. We compared the animals' performance in discriminating between these odors after subjecting them to one of two types of training: either absolute conditioning, in which only one odor is reinforced, or differential conditioning, in which one odor is reinforced and a second odor is explicitly not reinforced. We show that differential conditioning decreases behavioral generalization of similar odorants in a choice situation. The mushroom body represents a site of convergence between the punitive, reinforcing stimulus and the neuronal representation of the odor stimulus. We show that differential, but not absolute, training causes decorrelation of odor representations in the mushroom body. In conclusion, differential training with similar odors ultimately induces a behaviorally expressed contrast enhancement between the two similar stimuli that facilitates fine discrimination of odors.

Second, we addressed the question whether the neuronal activity of the mushroom body's intrinsic neurons, the Kenyon cells, in coincidence with a punitive stimulus is sufficient to acquire and store an aversive associative odor memory. We experimentally bypassed olfactory sensory input and thermogenetically activated sparse and random ensembles of Kenyon cells directly. We found that if the artificial activation of Kenyon cell ensembles coincides with a salient, aversive stimulus, learning was induced. The animals adjusted their behavior in a subsequent test situation and actively avoided reactivation of these Kenyon cells. Our results show that Kenyon cell activity in coincidence with a salient aversive stimulus can suffice to form an associative memory. Associative short-term memory retrieval is characterized by a closed feedback loop between a behavioral action and the avoidance to re-activate sparse ensembles of Kenyon cells.

Functional role of the insect odorant coreceptor

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Insect odor transduction is still not resolved, since contradictory results and competing functional hypotheses coexist in the current literature. Insect odorant receptors (ORs) belong to a new family of 7 transmembrane receptors with internal N-terminus, different from vertebrate ORs. Insect ORs colocalize with a larger, very conserved molecule, termed olfactory receptor coreceptor (Orco). Orco locates and maintains ORs in the ciliary membrane of olfactory receptor neurons (ORNs). Based upon this generally accepted property, Orco was coined as “chaperon”. In addition, Orco serves as Ca^{2+}-permeable ion channel that controls spontaneous activity. Thus, we introduced the term “pacemaker channel” for this generally accepted property of Orco. However, it is still not resolved whether and how Orco affects the primary processes of insect odor/pheromone transduction *in vivo,* in addition to its functions as chaperon and pacemaker channel.

With patch clamp and Ca^{2+} imaging in HEK cells and primary cell cultures of ORNs from the hawkmoth *Manduca sexta,* as well as extracellular tip-recordings from pheromone-sensitive antennal sensilla of intact hawkmoths, we examined Orco function pharmacologically. The general Orco agonist VUAA1 activated *M.* sexta-specific Orco in heterologous expression systems, in primary cell cultures, and *in vivo* tip-recordings. Application of VUAA1 increased spontaneous activity of pheromone-sensitive ORNs and boosted the pheromone-response to the main sex-pheromone bombykal within seconds to minutes after pheromone application (= late-long-lasting pheromone response). However, VUAA1 did not alter phasic bombykal responses within the first 100 ms of the pheromone response. Accordingly, the general Orco antagonist OLC15 did not affect primary events of bombykal transduction within the first 100 ms, while it decreased spontaneous activity and late-long-lasting pheromone responses at a later time window of pheromone transduction.

Therefore, our data do not support a role for OR-Orco heteromers as ionotropic pheromone receptors. In contrast, they are consistent with a role of Orco as chaperon and pacemaker channel, controlling odor responses via ciliary membrane localization of ORs and via setting of the resting potential of ORNs. We suggest that Orco is activated voltage- and second messenger-dependently after metabotropic opening of Ca^{2+}-permeable pheromone-dependent ion channels in hawkmoths.
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Olfaction during vertebrate evolution: the water-to-land transition

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In contrast to the single sensory surface present in teleost fishes, the mammalian olfactory system is defined by spatially segregated subsystems with distinct molecular and functional characteristics, chief among them the main olfactory epithelium expressing ORs and TAARs, and the vomeronasal organ expressing V1Rs and V2Rs. The semi-aquatic lifestyle of amphibians represents a unique opportunity to study the molecular driving forces involved in this transition of aquatic to terrestrial olfaction in vertebrates. Most amphibians also have anatomically segregated main and vomeronasal olfactory systems, but at the cellular and molecular level the segregation differs from that found in mammals. We have characterized expression patterns of four different olfactory receptor gene families in the secondarily aquatic pipid frog *Xenopus laevis*, and concomitantly have analysed odor-evoked neuronal activity in olfactory epithelium and olfactory bulb for four main odor classes of amphibians. We show a high degree of correlation between expression of *taar* genes and amine responses and between expression of 'ancient' *v2r* genes and amino acid responses. We report that the signal transduction cascade for amino acid responses involves PLC, DAG, and TRPC2. During metamorphosis extensive cell death and mitosis events lead to a remodelling of the larval main olfactory epithelium (detecting aquatic odors) into the adult 'air nose', with concomitant formation of a novel olfactory organ, the so-called 'water nose'. We report here that both olfactory receptor expression patterns and corresponding odor responses faithfully relocate from larval main olfactory epithelium to adult water nose.

Behavioral and neuronal mechanisms of olfactory imprinting in zebrafish

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Olfactory imprinting on environmental, population- and kin-specific cues is a form of life-long memory. Gathering with kin can prompt increased growth and reduced aggression. This suggests that selection should favor the capability of recognizing kin. One mechanism to discriminate between kin and non-kin is based on phenotype matching, when an individual learns a template of itself or of its kin and can later use this template to recognize even unfamiliar kin.

We could show that in zebrafish olfactory kin recognition depends on an imprinting process that requires a two-step learning process of olfactory as well as visual cues of kin. If larvae are exposed to visual cues of kin at day 5 and chemical cues of kin at day 6 post fertilization, zebrafish will recognize kin throughout life. Surprisingly, exposure to non-kin during the sensitive phase of development did not result in imprinting on cues of unrelated individuals, suggesting a genetic predisposition to kin signals. Through this combined imprinting process larvae can avoid false imprinting on unrelated individuals.

Despite its ecological significance, natural chemicals for olfactory imprinting have not been identified yet. Urine-born chemical imprinting signals are transcribed by genes expressed by polymorphic genes of the immune system - the major histocompatibility complex MHC genes – which are important messengers carrying information about ‘self’ and ‘other’. We show that MHC peptides function as chemical signals for olfactory imprinting in zebrafish. MHC peptides consisting of nine amino acids elicit olfactory imprinting and subsequent kin recognition depending on the MHC genotype of the fish. In vivo calcium imaging shows that some olfactory bulb neurons are highly sensitive to MHC peptides with a detection threshold at 1 pM or lower, indicating that MHC peptides are potent olfactory stimuli. Responses to MHC peptides overlapped spatially with responses to kin odor but not food odor, consistent with the hypothesis that MHC peptides are natural signals for olfactory imprinting.

The zebrafish olfactory epithelium harbors ciliated Olfactory sensory neurons(OSNs) expressing OR and TAAR gene family receptors (mammals: main olfactory epithelium) and microvillous OSNs with V1R and V2R gene family receptors (mammals: vomeronasal organ). In addition to these two main OSN types, teleosts exhibit crypt cells, bearing cilia and microvilli and expressing apparently only a single olfactory receptor, the V1R-related ORA4 and kappe neurons possessing only

microvilli. To investigate which Olfactory sensory neurons (OSN) is/are involved in detection of kin odor we used the activity marker pERK (phosphorylated extracellular signal regulated kinase) and stimulated imprinted and non-imprinted 9 day old zebrafish larvae with kin odor. We provide the first evidence that crypt cells, and likely a subpopulation of microvillous OSNs play a role in detecting a kin odor related signal. In addition, we show a lower activation of olfactory bulb neurons in non-imprinted than in imprinted zebrafish larvae after exposure to kin-odor, especially at the level of the medial dorsal glomerulus 2, the only glomerulus in which crypt cells project their axon.

New insights into the subsystem organization of the mammalian sense of smell

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Recent years have witnessed tremendous progress in our understanding of the subsystem organisation of the mammalian sense of smell. This lecture will present new developments in this field and summarize our most recent results. Specifically, I will focus on a subset of sensory in the mouse main olfactory system that express the soluble guanylate cyclase Gucy1b2 and the cation channel Trpc2: type B cells. We have recently reported the first sensory stimulus for type B cells, a reduced level of environmental oxygen. Low oxygen induces calcium influx in these neurons, and Gucy1b2 and Trpc2 are both required for these cellular responses. In vivo exposure of a mouse to low environmental oxygen causes Gucy1b2-dependent activation of postsynaptic olfactory bulb neurons in close vicinity to the glomeruli formed by axons of Gucy1b2-expressing sensory neurons. Low environmental oxygen also induces conditioned place aversion, for which Gucy1b2 and Trpc2 are required. We propose that this chemosensory function enables a mouse to assess rapidly the oxygen level in the external environment. This is the first report of an oxygen sensor in the mammalian olfactory system and the first evidence for a physiological and biological function for Trpc2 outside vomeronasal sensory neurons.

(1) Munger SD, Leinders-Zufall T, Zufall F (2009). *Annu Rev Physiol* 71, 115-140.

(2) Bleymehl K, Pérez-Gómez A, Omura M, Moreno-Pérez A, Macías D, Bai Z, Johnson RS, Leinders-Zufall T, Zufall F, Mombaerts P (2016). *Neuron* 92: 1-8.

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Signaling mechanisms in the accessory olfactory system

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In most mammals, conspecific chemical communication controls complex behaviors. Information about individuality, social and reproductive status is conveyed by an elusive class of chemical cues – pheromones. The highly reproducible character of pheromone responses offers a unique opportunity to uncover the neuronal basis of genetically programmed behavior. The accessory olfactory system is a key component in rodent conspecific chemical communication. However, sensory detection and coding of socially relevant chemosignals within the vomeronasal organ and downstream brain areas - the accessory olfactory bulb, the 'vomeronasal' amygdala and the hypothalamus - is poorly understood. Combining molecular, biochemical, (electro)physiological, and live-cell imaging methods, as well as behavioral techniques in wildtype and mutant mouse models, we have extended existing models of sensory signal transduction in the vomeronasal organ, analyzed aspects underlying the principle coding logic of pheromone detection, and have, thus, shed light on the physiological basis of social behavior. More recently, we have begun to address the physiological signaling mechanisms in the rodent accessory olfactory bulb. Both *in* and *ex vivo* approaches from different electrophysiological angles reveal unexpected intrinsic as well as stimulation-dependent mitral cell properties.

Exploring chemical neighbourhoods in the olfactory bulb

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While we have largely understood how primary sensory neurons in e.g. vision encode their relevant input space, the chemical receptive range of many olfactory receptors still remains elusive. We profiled the receptive range of a genetically labelled olfactory receptor (MOR18-2) using intrinsic signal imaging in anaesthesized mice. We measured its response to 214 odorants in a total of 41 animals. Using advanced image processing methods [1] we extracted the responses of neighboring glomeruli. Based on their responses to a set of 45 diagnostic odors we identified glomeruli across individuals, enabling to relate their chemical receptive ranges with their spatial position relative to MOR18-2 (Figure 1). We found that MOR18-2 is embedded in a local tunotopic response domain that shares several ligands with spatially proximal glomeruli. Furthermore, we derived a description of MOR18-2's chemical receptive range in terms of physico-chemical properties. With regard to those properties we found a weak chemotopic embedding of MOR18-2 in a lateral-posterior domain of the dorsal olfactory bulb. Our findings provide insight how the arrangement of glomeruli in the olfactory bulb reflects the structure of chemical space.

References

[1] Soelter, J., Schumacher, J., Spors, H., and Schmuker, M. (2014). Automatic segmentation of odor maps in the mouse olfactory bulb using regularized non-negative matrix factorization. *Neuroimage* 98, 279-288. doi:10.1016/j.neuroimage.2014.04.041.

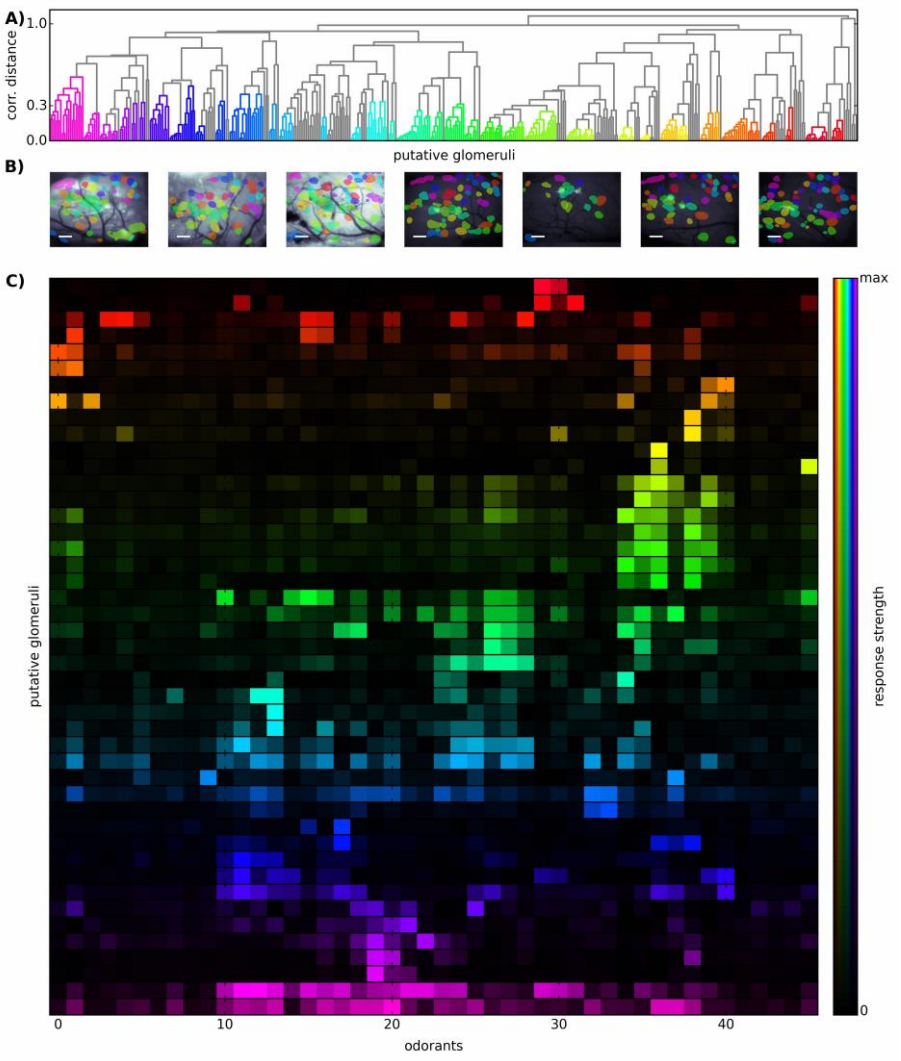

Figure 1: Response Clustering. A) Hierarchical clustering of putative glomeruli of seven mice based on the correlation between their odorant response spectra. B) Spatial location of cluster members in the olfactory bulbs of all seven mice. Colours according to cluster colouring in A). Scale bar 100 µm. C) Median odorant spectra of all putative glomeruli in each cluster.

The rodent olfactory bulb granule cell: an alliance of numerous inhibitory mini-neurons

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The vertebrate olfactory bulb processes olfactory stimuli within a two-stage network, the first located within the glomerular input layer and the second in the external plexiform layer below, which are brigded via the principal mitral and tufted cells. Both subnetworks strongly draw on dendrodendritic interactions, with the axonless inhibitory granule cells being the main players in the second stage. Granule cells are directing their sole output towards lateral dendrites of mitral and tufted cells via reciprocal dendrodendritic synapses. In spite or because of their apparently reduced anatomy, granule cells are capable of various modes of dendritic signalling, including local sodium spikes within their large reciprocal spines. I will discuss mechanisms underlying these dendritic signals and how they might influence processing in mitral and tufted cells.

Odor information processing along an OR-specific neuronal pathway

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Within the main olfactory system of mammals, a unique subsystem exists comprised of sensory neurons expressing odorant receptors of the OR37 subfamily. These receptors are exclusive for mammals and highly conserved across species. The mouse OR37 receptor subtypes A, B and C were shown to be activated by the long-chain aliphatic aldehydes penta-, hexa- and heptadecanal, respectively. The search for biological sources of these compounds now shows that bodily secretions from conspecifics activate the OR37A, B and C glomerulus. At the same time the activity of cells in a target region of projection neurons from OR37 glomeruli, the paraventricular nucleus of the hypothalamus (PVN), is reduced compared to controls (clean test box). The large number of activated cells in the PVN of mice that are placed into a clean test box are corticotropin-releasing hormone cells, indicating an induction of the stress axis due to the novel environment. The much lower number of activated cells of mice in a box enriched with bodily secretions from conspecifics indicates a reduced stress response. Since bodily secretions from conspecifics activate the OR37 system and simultaneously reduce stress-induced activation of the PVN, it was tested whether the ligands for OR37 receptors can induce this effect. Indeed, a similarly reduced activity in the PVN is found in mice kept in a clean test box and exposed to a mixture of the OR37 ligands delivered via an air stream. These data indicate that the OR37 system may play a role in mediating a phenomenon called social buffering.

This work was supported by the Deutsche Forschungsgemeinschaft (SPP1392).

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Rodent behavior expressed in body, head and sensor motor pattern is tightly coupled with internal brain dynamics, providing for active sampling of sensory information from the outside world for its optimal detection and encoding, as well as guidance of the behavior. We investigated fine-time scale olfactory system behavioral dynamics in freely moving mice and rats and it's coordination with the neural activity in the hippocampus and prefrontal cortex across wide range of behavioral states (exploration of real and virtual object, fear, sleep). We demonstrate high-resolution

pattern of head-motion coupled with the sniffing cycle that is associated with exploratory behavior, direct effect of this behavioral state on hippocampal spatial coding and characteristic behavioral-state-dependent oscillatory dynamics across brain regions coupled with respiratory dynamics. Our results suggest that in the rodent respiratory dynamics provides a generalized rhythm that coordinates large brain regions with motor output, providing a basis for a separate brain network.