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Olfactory receptors: GPCRs and beyond

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Abstract

Sensing the chemical environment is critical for all organisms. Diverse animals from insects to mammals utilize highly organized olfactory system to detect, encode, and process chemostimuli that may carry important information critical for health, survival, social interactions and reproduction. Therefore, for animals to properly interpret and react to their environment it is imperative that the olfactory system recognizes chemical stimuli with appropriate selectivity and sensitivity. Because olfactory receptor proteins play such an essential role in the specific recognition of diverse stimuli, understanding how they interact with and transduce their cognate ligands is a high priority. In the nearly two decades since the discovery that the mammalian odorant receptor (OR) gene family constitutes the largest group of G protein-coupled receptor (GPCR) genes, much attention has been focused on the roles of GPCRs in vertebrate and invertebrate olfaction. However, it has become clear that the “family” of olfactory receptors is highly diverse, with roles for enzymes and ligand-gated ion channels as well as GPCRs in the primary detection of olfactory stimuli.

Introduction

The discovery by Buck and Axel nearly two decades ago of a family of odorant receptors (ORs) in rodents (Buck & Axel 1991) was a watershed event for understanding olfactory function. Knowledge of these proteins, which are members of the superfamily of G protein-coupled receptors (GPCRs), not only provided invaluable tools for elucidating the function and organization of the main olfactory system, but they served as a template for identifying other chemosensory receptors in mammals, other vertebrates and invertebrates (Mombaerts 2004a, Imai & Sakano 2008, Keller & Vosshall 2008, Touhara & Vosshall 2009). However, a number of recent reports have greatly expanded the types of receptors implicated in the detection of chemosensory cues by olfactory systems, revealing a structural and functional diversity that was not anticipated even a few years ago.

Animals must detect and respond to a large number of structurally diverse chemical cues in their environment. These chemosignals can convey important information critical for health, survival and reproduction: the type and quality of foods or the existence of toxins; the presence and characteristics of predators, prey, competitors, or potential mates; or social

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signals that impact stereotyped behaviors or hormonal responses. Animals employ distinct molecular, cellular and neural mechanisms to detect, discriminate and react to these varied stimuli (Munger *et al.* 2009, Chandrashekar *et al.* 2006, Jordt *et al.* 2003). For example, it has become clear that the olfactory system contains numerous subsystems that can be distinguished by the chemostimuli to which they respond, the chemosensory receptors and other signaling proteins that they express, and their connections to the brain (Munger *et al.* 2009, Ma 2007, Breer *et al.* 2006) (Figure 1). With this newfound appreciation of the diversity of olfactory subsystems comes the recognition of surprising differences in receptor structure and function that confer an important degree of stimulus selectivity for each subsystem. In this review, we will consider the rapidly expanding repertoire of chemosensory receptor families employed by vertebrate and insect olfactory systems. In particular, we will highlight recent findings in rodents and *Drosophila* indicating that not all olfactory receptors are members of the GPCR superfamily. The reader interested in more comprehensive reviews of the main or accessory olfactory systems, olfactory transduction mechanisms, the roles of olfactory receptors in olfactory development, or insights into the contributions of chemosensory receptors outside the olfactory system can consult any of a number of informative reviews [e.g., (Munger *et al.* 2009, Tirindelli *et al.* 1998, Firestein 2001, Zufall & Munger 2001, Mombaerts 2004a, Brennan & Zufall 2006, Zufall & Leinders-Zufall 2007, Buck 2000, Gold 1999, Dulac & Torello 2003, Dulac & Wagner 2006, Ache & Young 2005, Imai & Sakano 2008, Keller & Vosshall 2008, Spehr *et al.* 2006, Bargmann 2006)].

The mammalian olfactory system is composed of several subsystems

The mammalian olfactory system contains a number of distinct subsystems that can be differentiated based on a number of molecular, functional and anatomical criteria (Munger *et al.* 2009, Ma 2007, Breer *et al.* 2006). However, the most fundamental division is between the main and accessory olfactory systems (Munger *et al.* 2009, Ma 2007, Breer *et al.* 2006). Olfactory sensory neurons (OSNs) of the main olfactory system are located in the main olfactory epithelium (MOE) and send their axons to synapse with second order neurons in the main olfactory bulb (Munger *et al.* 2009, Firestein 2001). In contrast, sensory neurons in the accessory system are found within the vomeronasal organ (VNO, which lies above the hard palate and at the base of the nasal septum); axons of these vomeronasal sensory neurons (VSNs) project to the accessory olfactory bulb (Munger *et al.* 2009, Brennan & Zufall 2006). Anatomical and genetic evidence indicates that a functional accessory olfactory system is not maintained in higher primates, including humans (Brennan & Zufall 2006).

These two divisions of the mammalian olfactory system are not homogeneous (Munger *et al.* 2009). The MOE contains a number of sensory neuron subpopulations that respond to distinct types of chemosensory stimuli, express different receptors and/or utilize different transduction cascades. Similarly, the vomeronasal organ contains at least two different groups of chemosensory neurons that vary in stimulus selectivity and mechanisms of chemosensory transduction. In the next section we will discuss the diversity of mammalian olfactory receptors in the context of these different subsystems.

GPCRs and the detection of olfactory stimuli in mammals

ORs: the canonical odorant receptors

Prior to the discovery of mammalian ORs, several studies supported a G protein-coupled, cAMP-mediated transduction mechanism for odor detection in the main olfactory system (Pace *et al.* 1985, Pace & Lancet 1986, Sklar *et al.* 1986, Anholt *et al.* 1987, Nakamura & Gold 1987). These findings strongly suggested that mammalian odorant receptors would be members of the GPCR superfamily. In addition, the large repertoire of odorous molecules recognized by the main olfactory system implicated a multigene family of odorant receptors. Based on these criteria, Buck and Axel devised a successful cloning strategy to isolate novel cDNAs exhibiting GPCR homology from the MOE of rats (Buck & Axel 1991). The identified transcripts encoded proteins with key hallmarks of GPCRs, including seven putative membrane-spanning helices, three putative intracellular and three putative extracellular loops connecting these helices, and a conserved DRY amino acid motif (a hallmark of GPCRs) within the second intracellular loop (Buck & Axel 1991, Mombaerts 2004a). The encoded proteins also contain hypervariable regions that likely contribute to selective binding of different odorants (Buck & Axel 1991, Katada *et al.* 2005, Bozza *et al.* 2002, Zhao *et al.* 1998, Krautwurst *et al.* 1998, Abaffy *et al.* 2006, Shirokova *et al.* 2005).

Genome sequencing has confirmed Buck and Axel's initial findings that the ORs are part of a large, multigene family: it is estimated that humans express ~350 functional ORs, while rodents express over 1000 (Buck & Axel 1991, Glusman *et al.* 2001, Zozulya *et al.* 2001, Young *et al.* 2002, Zhang & Firestein 2002, Niimura & Nei 2003)! However, ORs are not restricted to mammals; they are expressed in the OSNs of both terrestrial and aquatic vertebrates (Mombaerts 2004a), including the primitive lamprey (Freitag *et al.* 1999). OR genes can be divided into two primary phylogenetic classes: mammals contain both Class I and Class II OR genes, while the genomes of jawed fishes contain only the more ancient Class I OR genes (Mombaerts 2004a).

Consistent with a role in odor recognition, most OR genes are expressed in OSNs (Buck & Axel 1991, Mombaerts 2004a, Zhang *et al.* 2004, Zhang *et al.* 2007, Feldmesser *et al.* 2006). Individual OSNs each seem to express only a single OR protein, and thus individual OR genes are expressed in only a subset of OSNs (Mombaerts 2004b). While the choice of which OR gene to express appears to be largely stochastic, monogenic (indeed, monoallelic) OR gene expression is regulated in OSNs through a negative feedback mechanism mediated by the OR proteins themselves (Serizawa *et al.* 2003, Lewcock & Reed 2004). Though those OSNs expressing the same OR intermingle with OSNs expressing other ORs, the OSN cohort expressing any one OR is restricted to one of several anatomical zones within the MOE (Mombaerts 2004a). The functional relevance of these OR-expression zones remains unknown.

A number of genes are classified as ORs based on sequence similarity but are expressed outside the MOE, including in the vomeronasal epithelium (Levai *et al.* 2006) and in non-olfactory tissues (Zhang *et al.* 2007, Feldmesser *et al.* 2006, Zhang *et al.* 2004, Tian & Ma 2004, Fleischer *et al.* 2006). While ORs expressed in chemosensory organs like the VNO and the septal organ of Masera (Tian & Ma 2004), part of an olfactory subsystem that shares

many functional and molecular biological features with the MOE, likely serve a chemosensory role, other “ectopically-expressed” ORs may have additional chemosensory functions in the body (Spehr *et al.* 2004) or may not function to detect odors at all (De la Cruz *et al.* 2008).

A chemosensory role for many ORs has been confirmed through both *in vitro* and *in vivo* functional studies. ORs confer selective odor responsiveness on either OSNs [e.g., (Zhao *et al.* 1998, Bozza *et al.* 2002, Grosmaître *et al.* 2006, Touhara *et al.* 1999)] or heterologous cells [e.g., (Krautwurst *et al.* 1998, Abaffy *et al.* 2006, Kajiya *et al.* 2001, Wetzel *et al.* 1999, Saito *et al.* 2009)]; thus, the OR dictates the stimulus tuning of the OSN. All of the ORs deorphaned to date respond to volatile odorants of diverse chemical classes, and most ORs are broadly tuned to multiple stimuli (Zhao *et al.* 1998, Krautwurst *et al.* 1998, Mombaerts 2004a, Abaffy *et al.* 2006). In addition, multiple ORs can respond to the same odorant, though usually with different efficacies (Malnic *et al.* 1999, Mombaerts 2004a). This is consistent with the observation that most OSNs recognize multiple odorants (Firestein 2001). Thus, odors are encoded using a combinatorial strategy employing multiple ORs of overlapping stimulus selectivity (Malnic *et al.* 1999, Buck 2000). Interestingly, some odors are OR antagonists (Shirokova *et al.* 2005, Spehr *et al.* 2003, Oka *et al.* 2004) and could therefore increase the complexity of odor coding.

Trace amine-associated receptors (TAARs)

The MOE is responsive to diverse chemostimuli, including both general odors (e.g., food odors) and semiochemicals (e.g., pheromones) (Munger *et al.* 2009, Spehr *et al.* 2006). This stimulus diversity suggested that canonical ORs (Buck & Axel 1991) might not be the only members of the GPCR family serving as chemosensory receptors in the main olfactory system. A screen of OSN-enriched cDNA isolated from mice provided evidence of other GPCRs (Liberles & Buck 2006). These included all but one member of the trace amine-associated receptor (TAAR) family, which are related to other aminergic GPCRs such as metabotropic serotonin and dopamine receptors (Borowsky *et al.* 2001) but which had no established physiological function. The expression of TAARs in small subpopulations of mouse OSNs (Liberles & Buck 2006) suggests an olfactory role.

TAARs are expressed in sparse, nonoverlapping subsets of OSNs within the MOE (Liberles & Buck 2006). Furthermore, although TAAR-expressing OSNs appear to use a similar cAMP-mediated odor transduction cascade to that employed by OR-expressing (i.e., canonical) OSNs, it seems that the expression of these two types of olfactory receptor is mutually exclusive: OSNs expressing both an OR and a TAAR have not been identified (Liberles & Buck 2006). Reminiscent of the distribution of OSNs expressing the same OR, OSNs expressing the same TAAR are restricted within epithelial zones but randomly distributed within those zones (Liberles & Buck 2006).

As predicted (Borowsky *et al.* 2001), many mouse TAARs respond to biogenic amines including isoamylamine, β -phenylethylamine and trimethylamine (ligands for the mouse TAAR3, TAAR4 and TAAR5 proteins, respectively). TAAR5 also responds to adult male mouse urine (Liberles & Buck 2006), consistent with a role in the detection of conspecific olfactory signals. Other chemosensory receptors implicated in the detection of conspecific

olfactory signals (e.g., vomeronasal receptors and the receptor guanylyl cyclase GC-D; see below) are largely pseudogenized in humans and other higher primates (Young *et al.* 2005, Young *et al.* 2007). In contrast, numerous intact TAAR genes are found in diverse vertebrate genomes, including the zebrafish, chicken, platypus and human genomes (Liberles & Buck 2006, Gloriam *et al.* 2005, Mueller *et al.* 2008, Grus & Zhang 2008). The maintenance of apparently functional TAAR genes across such diverse species suggests a common olfactory role.

Vomeronasal type 1 receptors (V1Rs)

After identification of the OR multigene family (Buck & Axel 1991), initial attempts to uncover putative VNO-specific chemoreceptor genes based on homology with ORs were unsuccessful. In 1995, Dulac and Axel (Dulac & Axel 1995) employed a different approach. Based on the hypothesis that individual VSNs express a single or a neuron-specific subset of receptors, single rat VSN cDNA libraries were differentially screened for putative GPCRs. This elegant experimental strategy led to the discovery of the *V1r* multigene family (Dulac & Axel 1995); in mouse, this family contains over 130 members with uninterrupted, full-length open reading frames as well as over 150 likely pseudogenes (Rodriguez *et al.* 2002). *In situ* hybridization studies revealed a punctate, non-overlapping expression pattern restricted to the apical layer of the VNO sensory epithelium (Dulac & Axel 1995). V1R-expressing VSNs also express the G protein subunit G α_{i2} (Halpern *et al.* 1995, Berghard & Buck 1996), which has been hypothesized to play a role in sensory transduction in these cells (Mombaerts 2004a). Although ORs and V1Rs share no significant sequence homology, both are Class-A (i.e., rhodopsin-like) GPCRs. Further common features include an intron-free coding region, a scattered, largely clustered chromosomal organization (Rodriguez *et al.* 2002), tightly controlled monogenic (Rodriguez *et al.* 1999) and monoallelic (Roppolo *et al.* 2007) expression, and a punctuate tissue expression pattern consistent with the 'one neuron – one (or a few) receptor(s)' hypothesis (Mombaerts 2004b).

A hallmark of the V1R superfamily is its unusual diversity: within each of the 12 extremely isolated gene subfamilies/clades (each containing between one and 30 members) sequence identity is at least 40%, but interfamilial homology is less than 15%. Conserved sequence motifs are largely missing. This interfamilial divergence is in sharp contrast to the smooth continuum in OR sequence variability (Dulac & Wagner 2006). Intact *V1r* genes are found in species ranging from teleost fish to man (Dulac & Wagner 2006, Rodriguez & Mombaerts 2002, Shi & Zhang 2007, Pfister & Rodriguez 2005, Saraiva & Korsching 2007). While *V1r*-like genes in different teleost species appear highly conserved, mammals display high across-species variability in both total *V1r* gene count and primary sequence (Grus *et al.* 2005, Grus *et al.* 2007). Primates, including humans, appear to have experienced the most substantial degeneration of the functional *V1r* repertoire. For example, among ~200 identified human *V1r*-like sequences, only five retain an intact open reading frame (Rodriguez & Mombaerts 2002). Although one human receptor, V1RL1, is expressed in human olfactory epithelium (Rodriguez *et al.* 2000), it remains unclear whether human V1Rs simply represent non-functional remnants of a massively decayed V1R repertoire (Mombaerts 2004a).

Gene targeting of one *V1r* gene, *V1rb2* (previously designated VR_{i2}) (Rodriguez *et al.* 1999), has been useful in understanding the monoallelic expression of V1r genes, the axonal wiring and convergence patterns of V1R-expressing VSNs, and the stimulus tuning of individual V1Rs. For example, Ca²⁺ imaging and patch-clamp recordings from GFP-tagged V1Rb2-expressing VSNs identified 2-heptanone – a urinary constituent shown to extend the length of female estrous cycles (Brennan & Zufall 2006, Novotny 2003) – as an *in-situ* ligand for V1Rb2 (Boschat *et al.* 2002). Recently, the same mouse strain was employed for a comprehensive biophysical characterization of the ionic properties of a defined subpopulation of apical VSNs (Ukhanov *et al.* 2007). All other vertebrate V1Rs remain orphan receptors whose putative chemosensory function can only indirectly be inferred from their expression in VSNs and their influence on stereotyped behaviors. For example, the deletion of 16 V1R genes in a single cluster on mouse chromosome 6 resulted in specific deficits in mating behavior and maternal aggression (Del Punta *et al.* 2002).

What stimuli activate V1Rs? The role of the VNO in mediating several stereotyped responses in mice (e.g., male aggression, puberty acceleration or estrus synchronization) suggests that semiochemicals are good candidates (Brennan & Zufall 2006). Indeed, studies combining functional single cell imaging and cell-attached patch-clamp recordings observed specific and highly sensitive sensory responses to seven putative mouse pheromones, including compounds isolated from mouse urine or glandular secretions (Novotny 2003), in non-overlapping VSN subpopulations (Leinders-Zufall *et al.* 2000). Although recent experimental results suggest that urine-dependent sensory signals in the VNO are predominantly generated by apical (i.e., Gα_{i2}/V1R-expressing) VSNs neurons (Holekamp *et al.* 2008) and that sulfated steroids represent a major source of this urinary activity (Nodari *et al.* 2008), other data show robust sensory activation in basal (i.e., Gα_o-expressing) VSNs as well (Kelliher *et al.* 2006, Leinders-Zufall *et al.* 2004b, He *et al.* 2008).

Vomer nasal type 2 receptors (V2Rs)

The topographically restricted expression of V1Rs in the apical, Gα_{i2}-expressing layer of the VNO neuroepithelium (Dulac & Axel 1995) strongly suggested that one or more additional families of vomeronasal receptors are expressed in the VNO, likely in the basal neurons that express Gα_o. Indeed, three different groups simultaneously reported the identification of a second multigene family of VNO-specific GPCRs (Herrada & Dulac 1997, Matsunami & Buck 1997, Ryba & Tirindelli 1997). Exclusively expressed in Gα_o-positive VSNs, these receptors were named V2Rs. The Buck and Dulac groups both employed a differential screening approach in which they compared gene expression profiles of single VNO neurons from mouse (Matsunami & Buck 1997) or rat (Herrada & Dulac 1997). Ryba and Tirindelli (Ryba & Tirindelli 1997), on the other hand, used a degenerate rat OR probes to search for novel vomeronasal receptors (a single V2R cDNA was identified serendipitously by this approach even though V2Rs share no significant sequence homology with ORs). Approximately 120 intact *V2r* genes (and an additional ~160 apparent pseudogenes) are present in the mouse genome (Young & Trask 2007).

As with other Class C GPCRs including metabotropic glutamate receptors, Ca²⁺-sensing receptors, and sweet/umami-sensing taste receptors, V2Rs have a large hydrophobic amino

(N)-terminal extracellular domain and a seven transmembrane domain, joined by a cysteine-rich linker domain (Mombaerts 2004a, Pin *et al.* 2003). Although this N-terminal domain is the primary site of ligand binding to most Class C GPCRs, allosteric interactions of some ligands with the transmembrane domain have been reported (Lagerstrom & Schiöth 2008, Vignes *et al.* 2008).

As with genes encoding the ORs and V1Rs, *V2rs* are found in clusters on most chromosomes and can be grouped into distinct subfamilies [family-A, -B, -D, and -C (synonymously named *V2r2* family)] (Young & Trask 2007, Silvotti *et al.* 2007). With over 100 members, family-A represents approximately 80% of all *V2r* genes (Young & Trask 2007, Yang *et al.* 2005). On the other extreme, family-D includes only 4 members (Silvotti *et al.* 2007). The *V2r* gene repertoire is relatively large in teleosts (Shi & Zhang 2007). The intact *V1r*:*V2r* ratio, however, is dramatically increased in tetrapods, paralleling the simultaneous evolutionary jump in the class II : class I ratio of vertebrate OR genes. In some mammalian species (including human, chimpanzee, macaque, cow and dog), *V2r* repertoires have completely degenerated (Young & Trask 2007).

Most V2Rs show a punctate expression pattern in the VNO, likely generated by stochastic selection and subsequent negative feedback on the expression of other family members (mutual and allelic exclusion). An exception is the V2R2 (family-C) receptors, which are expressed in most, if not all, G α_o -positive VSNs (Martini *et al.* 2001), though individual V2R2 members appear to be expressed in segregated non-overlapping VSN subsets (Silvotti *et al.* 2007). In mammalian species marked by substantial *V2r* degeneration, a single *V2r2* orthologue is commonly found. Few inactivating mutations indicate a relatively recent pseudogenization process and, thus, a likely conserved function across species (Young & Trask 2007). The unusual characteristics of *V2r2* genes are reminiscent of the atypical insect odorant receptor (OR83b in *Drosophila* (Larsson *et al.* 2004)) that acts as a heterodimeric partner to other insect ORs (see discussion of *Drosophila* ORs below). Or83b and its orthologues are required for proper membrane targeting and function of coexpressed ORs, thus suggesting an analogous role for V2R2 proteins in vomeronasal chemoreception. Individual V2R-expressing basal VSNs also express one of nine members of a family of nonclassical class Ib major histocompatibility complex (MHC) genes (Loconto *et al.* 2003, Ishii *et al.* 2003). The proteins encoded by these *H2-Mv* genes, in complex with $\beta 2$ -microglobulin, have been implicated in V2R trafficking and surface expression (Dulac & Torello 2003). However, it appears that a substantial fraction of basal VSNs tolerate absence of MHC Ib escort molecule for proper V2R membrane targeting (Ishii & Mombaerts 2008, Silvotti *et al.* 2007). Moreover, it has recently become apparent that the *H2-Mv* family is restricted to rodents (Shi & Zhang 2007).

As is the case for V1Rs, direct functional information for V2R receptor-ligand interactions is sparse. One popular model hypothesizes that the anatomical and molecular dichotomy of the vomeronasal system is reflected by distinct chemical properties of V1R- and V2R-specific ligands (Dulac & Torello 2003, Brennan & Zufall 2006) such that V1Rs respond to small, relatively volatile molecules while V2Rs are activated by peptides or proteins. Major urinary proteins (MUPs, which are members of the lipocalin family) have long been intriguing candidates as VSN stimuli (Cheetham *et al.* 2007, Sherborne *et al.* 2007, Dulac &

Torello 2003), but whether they function as carriers of small organic ligands or as receptor ligands themselves has been a longstanding question. A recent functional imaging study revealed that purified MUPs alone are sufficient to activate dissociated G_{α_o} -positive VSNs and trigger robust male–male territorial aggression (Chamero *et al.* 2007). Other mammalian species, however, possess only a single intact MUP gene, challenging the general applicability of these findings.

Other potential V2R receptor ligands identified thus far are either genetically encoded or metabolically processed peptides. For example, exocrine gland-secreting peptide 1 (ESP1) stimulates basal V2R-expressing VSNs as measured by c-Fos immunohistochemistry and field potential recordings at the epithelial surface of the VNO (Kimoto *et al.* 2005, Kimchi *et al.* 2007). The product of one of 24 related genes in mouse, this peptide is secreted from the male extraorbital lacrimal gland (Kimoto *et al.* 2005). Intriguingly, some ESPs appear to be expressed in a sexually dimorphic pattern. There are only ten putative ESP genes in rat, possibly one in opossum, and none in human (Kimoto *et al.* 2007), suggesting species-specific functions for these proteins.

It has long been recognized that mice are able to both discriminate the body odors of conspecifics that differ genetically only in their MHC haplotypes and to translate this olfactory individuality code into ethologically relevant information (Beauchamp *et al.* 1985, Yamazaki *et al.* 1983, Penn & Potts 1998, Restrepo *et al.* 2006). These observations suggested that MHC class I peptides, small peptides that are bound to and presented by MHC proteins at the cell surface, could represent one molecular component of this MHC ‘odor’ (Leinders-Zufall *et al.* 2004a). MHC class I peptides, indeed, activate V2R-expressing VSNs *in-situ* and are also able to generate a robust olfactory memory sufficient to trigger pregnancy failure (the Bruce effect) (Leinders-Zufall *et al.* 2004a, Brennan & Zufall 2006). In this scenario, however, both volatile compounds and MHC peptides most likely play complementary roles (Restrepo *et al.* 2006).

The role of non-GPCRs in the detection of olfactory stimuli

The discovery of the ORs by Buck and Axel fit nicely with the extensive biochemical and molecular biological evidence implicating a G protein-coupled, cAMP-mediated odor-transduction mechanism in mammals and other vertebrates. We have already discussed how diverse olfactory GPCRs confer an exquisite sensitivity on the main and accessory olfactory systems to a broad range of volatile and non-volatile sensory stimuli. However, findings in both rodents and insects now indicate that olfactory systems may also employ a number of non-GPCRs to detect chemosensory stimuli.

Receptor Guanylyl Cyclases

Both ORs and TAARs seem to transduce olfactory stimuli through a signaling mechanism that employs G proteins and the second messenger cAMP (Munger *et al.* 2009). Identification of an orphan receptor guanylyl cyclase (GC) expressed in a small number of OSNs (Fulle *et al.* 1995), called GC-D, suggested that the repertoire of olfactory receptors might not be restricted to GPCRs. The receptor GC family includes peptide and orphan receptors expressed in numerous species and tissues (Gibson & Garbers 2000). First isolated

from sea urchin sperm, receptor GCs have been implicated in diverse functions including invertebrate sperm chemotaxis, the regulation of natriuresis and diuresis, mammalian phototransduction and nematode chemosensation (Gibson & Garbers 2000, Kuhn 2009). These proteins share a common structure, including an extracellular receptor domain, an intracellular regulatory (kinase homology) domain, and an intracellular catalytic domain (Gibson & Garbers 2000, Kuhn 2009). In mammals, deorphaned receptor GCs respond to various natriuretic peptides (Kuhn 2009). Peptide binding to the extracellular domain leads to activation of the intracellular cyclase domain and the elevation of intracellular cGMP. The activity of some receptor GCs may also be regulated by intracellular proteins such as Ca²⁺-inhibited GCAPs (guanylyl cyclase activating proteins) (Kuhn 2009).

Until recently, little was known about the function of the GC-D protein or the olfactory role of the OSNs that express it. The observation that the gene encoding GC-D is intact in rodents, canines and some prosimians (though not in other primates) suggests a conserved function across many mammalian species (Young *et al.* 2007). GC-D-expressing OSNs contain several proteins that could participate in a cGMP-mediated cascade (including GC-D, the cGMP-stimulated phosphodiesterase PDE2 and the cGMP-gated channel subunit CNGA3) but lack many of the proteins required for cAMP-mediated odor transduction by canonical OSNs (Juilfs *et al.* 1997, Meyer *et al.* 2000, Munger *et al.* 2008, Luo 2008). GC-D-expressing OSNs, like those expressing individual OR or TAAR types, comprise a small percentage of the OSNs in the MOE and are restricted to an epithelial zone (Fulle *et al.* 1995, Juilfs *et al.* 1997, Walz *et al.* 2007). In contrast to these other OSN populations, however, GC-D-expressing OSNs are not randomly distributed throughout this zone: they can be found in clusters within the dorsal recesses of the nasal cavity or more sparsely distributed in other areas of the MOE (Fulle *et al.* 1995, Juilfs *et al.* 1997, Walz *et al.* 2007, Cockerham *et al.* 2009).

Functional studies in gene-targeted mice and in heterologous cells now indicate that GC-D, and the neurons that express it, are essential for the detection and transduction of certain peptide stimuli by the main olfactory system (Leinders-Zufall *et al.* 2007, Duda & Sharma 2008). Field potential recordings from wildtype or *Cnga2* null mice (which lack responses to general odors recognized by ORs) show that the mouse MOE responds to uroguanylin and guanylin (Leinders-Zufall *et al.* 2007), two natriuretic peptides involved in the regulation of salt and fluid balance in the gut and kidney (Forte 2004). However, they are completely abolished in the MOE of mice in which the *Gucy2d* gene (which encodes GC-D) or *Cnga3* gene has been deleted (Leinders-Zufall *et al.* 2007). Patch-clamp electrophysiological recordings and Ca²⁺-imaging from identified OSNs expressing GC-D confirmed the requirement of GC-D for uroguanylin and guanylin responses in the MOE (Leinders-Zufall *et al.* 2007). These responses are highly effective and specific: $K_{1/2}$ values were as low as 66 pM, while some other receptor GC ligands [e.g., urodilatin, heat-stable enterotoxin; (Forte 2004)] did not activate the MOE. GC-D-expressing OSNs also respond to mouse urine (Leinders-Zufall *et al.* 2007), a rich source of chemostimuli (Brennan & Zufall 2006) that contains uroguanylin (Forte 2004).

But is GC-D itself a chemosensory receptor in this subpopulation of OSNs? Several lines of evidence suggest that it is. First, other receptor GCs function as peptide receptors (Gibson &

Garbers 2000, Kuhn 2009). Second, all GC-D-expressing OSNs respond to a mixture of uroguanylin and guanylin, but OSNs that don't express GC-D (either normally or through genetic deletion) are unresponsive to these peptides (Leinders-Zufall et al. 2007). Third, guanylyl cyclase activity of the rat GC-D isoform is stimulated by uroguanylin (but not guanylin) when expressed in heterologous cells (Duda & Sharma 2008). The specificity of rat GC-D for uroguanylin alone was not wholly surprising, as GC-D-expressing OSNs in mice are differentially tuned to the two peptide stimuli: though some are activated by both peptides, others are activated by only uroguanylin or guanylin (Leinders-Zufall et al. 2007). Together, these findings suggest that stimulus tuning of the GC-D protein can be regulated (e.g., by differential splicing, posttranslational modifications, or the presence of "co-receptor" proteins). Other mammalian receptor GCs function as homodimers (Gibson & Garbers 2000, Kuhn 2009), but heterodimerization remains a possibility.

Evidence for intracellular modulation of GC-D activity is limited, but growing. Studies in heterologous cells and in rat MOE extracts from Sharma and colleagues (Duda *et al.* 2001, Duda *et al.* 2004) suggest that the Ca²⁺-binding protein neurocalcin- δ mediates a Ca²⁺-dependent stimulation of GC-D cyclase activity. These authors suggest that elevation of intracellular Ca²⁺ upon activation of OSNs by general odors will stimulate GC-D activity as part of a general transduction pathway. However, such a model assumes that GC-D is expressed in many, if not most, OSNs, and is in conflict with numerous immunohistochemical, *in situ* hybridization, gene-targeting and functional studies in mouse and rat that support the restricted expression of GC-D in just a small subpopulation of OSNs (Fulle et al. 1995, Juilfs et al. 1997, Meyer et al. 2000, Leinders-Zufall et al. 2007, Hu *et al.* 2007, Walz et al. 2007). A more likely source of intracellular Ca²⁺ is the cGMP-dependent opening of cyclic nucleotide-gated channels present in these cells (Meyer et al. 2000). Indeed, specific stimulation of GC-D neurons promotes an increase in Ca²⁺ within the dendritic knobs of these cells that is sensitive to the cyclic nucleotide-gated channel blocker l-cis-diltiazem (Leinders-Zufall et al. 2007, Hu et al. 2007).

A second mechanism for intracellular regulation of GC-D is likely. GC-D expressing neurons are also sensitive CO₂ sensors (Hu et al. 2007). CO₂ responses in GC-D-expressing OSNs are mediated by CO₂ catalyzing enzyme carbonic anhydrase type II (CAII), which is specifically expressed in this group of OSNs: CO₂ responses in GC-D-expressing neurons are blocked by a CO₂ inhibitor, while behavioral responses are perturbed in *Car2* null mice, which lack CAII (Hu et al. 2007). Sensitivity of CO₂-dependent Ca²⁺ responses in GC-D-expressing neurons to l-cis-diltiazem suggests that both CO₂ and the natriuretic peptides uroguanylin and guanylin are transduced through a final common pathway, perhaps both employing GC-D (Leinders-Zufall et al. 2007, Hu et al. 2007). Recent findings that bicarbonate, a product of CO₂ metabolism by carbonic anhydrase, can stimulate GC-D cyclase activity are consistent with this model (Sun *et al.* 2009). Together, these studies indicate that GC-D acts both as a chemosensory receptor and an effector of sensory transduction. Furthermore, the CAII enzyme could also be considered a specialized olfactory receptor.

***Drosophila* olfactory receptors: the ORs**

Drosophila and other insects possess multiple olfactory sensory structures that could help define olfactory subsystems in these species, as well. Chemosensory sensilla containing OSNs are found on both the distal segment of the antenna and on the maxillary palp (Laissue & Vosshall 2008). Each sensillar type (basiconic, trichoid or coeloconic on the antenna; basiconic only on the maxillary palp) contains unique complements of OSNs that differ in the receptors they express, the stimuli to which they respond, and their axonal targets in the antennal lobe. For example, OSNs in basiconic sensilla are largely responsive to food odors, while OSNs in trichoid sensilla appear to be pheromone-responsive (Laissue & Vosshall 2008). However, while the concept of olfactory subsystems may be reminiscent of the mammalian olfactory system, insects exhibit one key difference: the receptors used to recognize olfactory stimuli appear to be ion channels, not (or not only) GPCRs.

After numerous attempts to identify insect olfactory receptors based on homology to mammalian ORs or nematode olfactory receptors (both of which are GPCRs), several groups took advantage of the publication of the *Drosophila* genome to identify a family of 62 putative olfactory receptors in this species with a combination of *in silico* analysis (Vosshall *et al.* 1999, Clyne *et al.* 1999, Gao & Chess 1999) and differential screening (Vosshall *et al.* 1999). Thirteen of these ORs are specifically expressed in larval OSNs (Fishilevich *et al.* 2005, Kreher *et al.* 2005, Stocker 2008). Orthologous receptors were subsequently identified in numerous other insect species (Sato & Touhara 2008, Bohbot *et al.* 2007, Engsontia *et al.* 2008, Hill *et al.* 2002, Krieger *et al.* 2002, Nakagawa *et al.* 2005, Robertson & Wanner 2006, Wanner *et al.* 2007). Even though the *Drosophila* ORs showed no obvious homology to GPCRs other than a predicted seven-transmembrane structure, the precedent for GPCR-type olfactory receptors in both vertebrate and invertebrate species was strong (Mombaerts 2004a).

Indeed, there are obvious similarities between *Drosophila* and mammalian ORs. The expression of most *Drosophila* ORs is reminiscent of the punctate arrangement seen in canonical OSNs and VSNs of the mouse: of those ORs expressed in adult OSNs, each is expressed in a subset in either the antenna or maxillary palp, with all but OR35a expressed in basiconic and/or trichoid OSNs (Couto *et al.* 2005, Fishilevich & Vosshall 2005, Sato & Touhara 2008, Spletter & Luo 2009). However, unlike most mammalian OSNs, some *Drosophila* OSNs simultaneously express up to four distinct OR genes (Couto *et al.* 2005, Fishilevich & Vosshall 2005, Goldman *et al.* 2005). Therefore, the control of OR expression is unlikely to be conserved between insects and mammals.

One *Drosophila* OR family member, OR83b, is expressed in all OSNs that express at least one other OR (Vosshall *et al.* 1999, Larsson *et al.* 2004). OR83b orthologues are found in other insect species as well (Sato & Touhara 2008). OR83b, which heterodimerizes with other ORs (Neuhaus *et al.* 2005, Benton *et al.* 2006), is required for normal functioning of ORs and OR-expressing OSNs (Larsson *et al.* 2004, Laissue & Vosshall 2008, Sato & Touhara 2008, Benton *et al.* 2006). Two subpopulations of *Drosophila* OSNs do not express OR83b: the majority of coeloconic OSNs (see next section), and a small group of CO₂-sensitive basiconic OSNs. Surprisingly, the CO₂-sensitive receptors expressed in this latter

subpopulation, GR21a and GR63a, are members of the gustatory receptor family (Jones *et al.* 2007, Kwon *et al.* 2007).

It was noted that insect OSNs do not contain typical GPCR motifs. Epitope mapping of OR83b indicated that this protein (and likely other insect ORs) had a flipped topology in comparison with GPCRs, with an intracellular N-terminus and extracellular C-terminus (Benton *et al.* 2006). This intriguing observation suggested that insect ORs might not be GPCRs at all. Two studies, which were published side-by-side, recently provided strong support for this hypothesis. The first (Sato *et al.* 2008) concluded that insect ORs are heteromeric ligand-gated ion channels in which the unique subunit (i.e., that which is not OR83b) provides for ligand selectivity of the complex. Several lines of evidence using ORs from *Drosophila* and other insect species support this model. First, stimulation of heteromeric ORs (e.g., *Drosophila* OR47a/OR83b) expressed in heterologous cells resulted in Ca²⁺ influx via a non-selective cation conductance dependent on OR83b. Pharmacological treatments showed that odor responses were independent of G protein signaling, cyclic nucleotide or phosphoinositide signaling cascades, and both ATP and GTP. Analyses of single channel currents in excised patches confirmed that heteromeric insect ORs act as ligand-gated ion channels.

However, a contemporaneous study (Wicher *et al.* 2008) came to a somewhat different conclusion. Patch clamp recordings in whole cell and excised patch configurations from heterologous cells expressing OR22a and OR83b revealed a fast odor-dependent response independent of ATP and GTP (a likely ionotropic response) as well as a slower ATP- and GTP-dependent component. In contrast to the study by Sato and colleagues (Sato *et al.* 2008), pharmacological analyses performed by Wicher and colleagues (Wicher *et al.* 2008) indicate that the later component of the odor response is mediated by a G protein-dependent signaling cascade that includes G α_s , adenylyl cyclase and cAMP. For example, odor stimulation activated co-expressed, cAMP-sensitive ion channels. Furthermore, the G protein inhibitor GDP- β -S increased the EC₅₀ for odor stimulation. Interestingly, odor induced cAMP signaling required OR22a (or OR47a, which was also tested) but was independent of OR83b. In contrast, cAMP (but not odors) induced a current in cells expressing only OR83b. Mutation of predicted channel pore residues in OR83b reduced the cAMP-dependent current. Together, the results of this study suggest a model in which the unique OR subunit contributes ligand selectivity and G protein coupling, and can mediate fast activation of the OR83b-dependent conductance; OR83b is also stimulated by cAMP, but on a slower time course.

How do we reconcile these two studies? It has been noted that the two studies focused on different parts of the odor response, and could thus each be seeing only part of the picture (Chesler & Firestein 2008). Indeed, Sato and colleagues (Sato *et al.* 2008) do report a small, ligand-independent sensitivity of some receptor complexes to cyclic nucleotides. Clearly, resolution of this potential conflict requires further investigation.

***Drosophila* olfactory receptors: the IRs**

Though the mechanisms of odorant detection by insect ORs had become slightly clearer, a major gap remained: olfactory receptors utilized by most coeloconic OSNs remained

unidentified (the exception being the coeloconic OSN population expressing OR35a/OR83b). Thus, the recent report of a third major class of insect chemosensory receptors (Benton *et al.* 2009) expressed in coeloconic, but not trichoid or basiconic OSNs, was not surprising. However, the protein family to which these receptors belong most certainly was. Building on results from an earlier bioinformatic screen for genes expressed in the olfactory system (Benton *et al.* 2007), Benton, Vosshall and colleagues identified a group of six genes encoding proteins related to ionotropic glutamate receptors (iGluRs) such as AMPA and NMDA receptors (Benton *et al.* 2009). Further bioinformatic analyses revealed these genes to be part of a large family (61 predicted intact genes and two pseudogenes) dubbed the IRs (ionotropic receptors) (Benton *et al.* 2009).

Several factors establish the IRs as a novel class of odorant receptors (Benton *et al.* 2009, Spletter & Luo 2009). Most obviously, they are not members of the GPCR superfamily. But furthermore, unlike the insect ORs and most mammalian olfactory receptors (ORs, TAARs, V1Rs and V2Rs), the IRs are not members of the even larger class of seven transmembrane domain proteins. Instead, they appear to have three membrane-spanning segments and a pore-forming domain; this topology is an obvious similarity to iGluRs. An apparent structural similarity between IRs and iGluRs is also suggested in the bipartite ligand-binding domain (Benton *et al.* 2009). However, it appears that glutamate is not the cognate ligand for most or any *Drosophila* IRs. The putative ligand-binding domains of individual IRs are highly variable, with little evidence for conservation of key residues important for glutamate binding in iGluRs (Benton *et al.* 2009). This hypervariability in areas likely to interact with olfactory stimuli is reminiscent of the hypervariable regions seen in putative ligand-binding pockets of the mammalian ORs (Buck & Axel 1991, Mombaerts 2004a), and suggests that the IR family responds to a number of distinct stimuli.

Coeloconic odorant receptors should meet several criteria, including: expression in the dendrites of coeloconic OSNs; an expression pattern consistent with coeloconic OSN functional subtypes (Yao *et al.* 2005); and the ability to confer odor sensitivity in a predictable way upon ectopic expression in novel coeloconic OSNs. Indeed, the IRs meet these criteria. *In situ* hybridization experiments in *Drosophila* antenna using probes to any of several IR genes as well as OR83b revealed that IRs are expressed in coeloconic OSNs or in neurons of the arista and sacculus (two specialized antennal structures); they are not expressed in basiconic or trichoid OSNs (Benton *et al.* 2009). IRs are not coexpressed with ORs, with the exception of one single coeloconic OSN that expresses IR76b, OR83b and OR35a. Antibodies recognizing IR25a, which is broadly expressed in several coeloconic OSNs as well as in the arista and sacculus, revealed immunoreactivity enriched in the outer dendrites, the site of olfactory transduction (Benton *et al.* 2009).

Interestingly, systematic double-label *in situ* hybridizations revealed stereotypical patterns of IR expression. Certain IRs are always expressed in adjacent coeloconic OSNs, establishing four distinct clusters of IR-expressing OSNs (Benton *et al.* 2009). This expression pattern was reminiscent of four coeloconic OSN subtypes previously defined by their distinct, though overlapping, stimulus tuning profiles (Yao *et al.* 2005). Indeed, the maps of OSN clusters, defined by unique IR expression profiles, and functional maps, established by recording electrophysiological responses to odors diagnostic of OSN

functional subtypes, were highly correlated (Benton *et al.* 2009). To what extent individual IRs contribute to odor recognition remains unclear. Coeloconic OSNs express up to three IR genes, suggesting that IRs, like iGluRs, could function as heteromeric receptors. Individual IRs may also serve distinct functions, including ligand recognition, stimulus transduction or receptor trafficking. For example, experiments in which three IRs normally expressed in phenylacetaldehyde-sensitive OSNs, IR75d, IR76a and IR84a, were ectopically expressed in phenylacetaldehyde-insensitive OSNs showed that only IR84a expression conferred phenylacetaldehyde sensitivity on the targeted OSNs (Benton *et al.* 2009). However, the specific chemosensory functions of most IRs remain to be determined.

Conclusions

The structural and functional diversity of olfactory receptors is far greater than what was anticipated even a decade ago. Do any other olfactory receptor families remain unidentified? In mammals, at least, this seems likely. The rodent olfactory system contains several subsystems for which chemosensory receptors have not been established. Some of these subsystems may utilize recognized olfactory receptor families. For example, ORs (Fleischer *et al.* 2006), TAARs (Fleischer *et al.* 2007) and GC-G (a paralogue of GC-D) (Fleischer *et al.* 2009) are expressed in neurons of the Grueneberg ganglia, which mediates the response to alarm pheromone (Brechtbuhl *et al.* 2008) and is responsive to cool temperatures (Mamasuew *et al.* 2008). However, distinct sensory neuron subpopulations in the MOE that appear to use cyclic nucleotide-independent transduction mechanisms could employ novel olfactory receptors. These putative OSNs for which no olfactory receptor has been identified include one population expressing the ion channel TRPM5 and effector enzyme phospholipase C β 2 (Lin *et al.* 2007), and expressing olfactory marker protein but not the cAMP-specific phosphodiesterase 4A that innervates necklace glomeruli (the MOB target of GC-D-expressing OSNs) (Cockerham *et al.* 2009, Juilfs *et al.* 1997). The possibility that the VNO epithelium displays an unrecognized cellular (and receptor) diversity on par with that of the MOE remains to be seen.

Why do animals require so many different olfactory receptor families? A remote possibility is that the diversity of receptor families is simply a byproduct of evolutionary chance. This seems unlikely, as there is strong evidence for adaptive evolution of vertebrate ORs, TAARs, V1Rs and V2Rs (Kambere & Lane 2007) as well as for insect ORs [e.g., (McBride *et al.* 2007, Nozawa & Nei 2007)]. Instead, multiple olfactory receptor families may help animals derive critical information from a complex chemosensory world. Most odors are complex mixtures of chemicals. In biologically important sources of chemosensory cues such as urine, feces and glandular secretions, the classes of compounds that can serve as olfactory stimuli can be quite diverse (e.g., gases, volatile compounds, peptides and proteins). As different types of receptors seem to be preferentially tuned to certain types of stimuli (e.g., TAARs respond to trace amines, GC-D is stimulated by peptides), a large repertoire of diverse olfactory receptor families can increase the range of chemical sensitivity in the olfactory system. However, this is not to say that stimulus selectivity is not tightly controlled. The restricted expression of specific olfactory receptor families to one or a few olfactory subsystems (Munger *et al.* 2009; Spletter and Luo, 2009) affords the opportunity to extract different kinds of information from the same olfactory stimulus. For

example, mice in which the dorsal aspects of the main olfactory system have been genetically-disrupted fail to avoid, but can still detect, odorants associated with predators or with spoiled food (Kobayakawa *et al.* 2007). Results such as these indicate the kind of information derived from the detection of a particular chemostimulus depends on the olfactory subsystem detecting it. Therefore, the use of diverse olfactory receptor families can increase both stimulus sensitivity and selectivity of the olfactory system.

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Abbreviations used

GPCR	G protein-coupled receptor
OR	odorant receptor
OSN	olfactory sensory neuron
MOE	main olfactory epithelium
VNO	vomeronasal organ
VSN	vomeronasal sensory neuron
TAAR	trace amine-associated receptor
V1R	vomeronasal type 1 receptor
V2R	vomeronasal type 2 receptor
MHC	major histocompatibility complex
MUP	major urinary protein
ESP	exocrine gland-secreting peptide
GC	guanylyl cyclase
GC-D	receptor guanylyl cyclase type D
CAII	carbonic anhydrase type II
IR	ionotropic receptor

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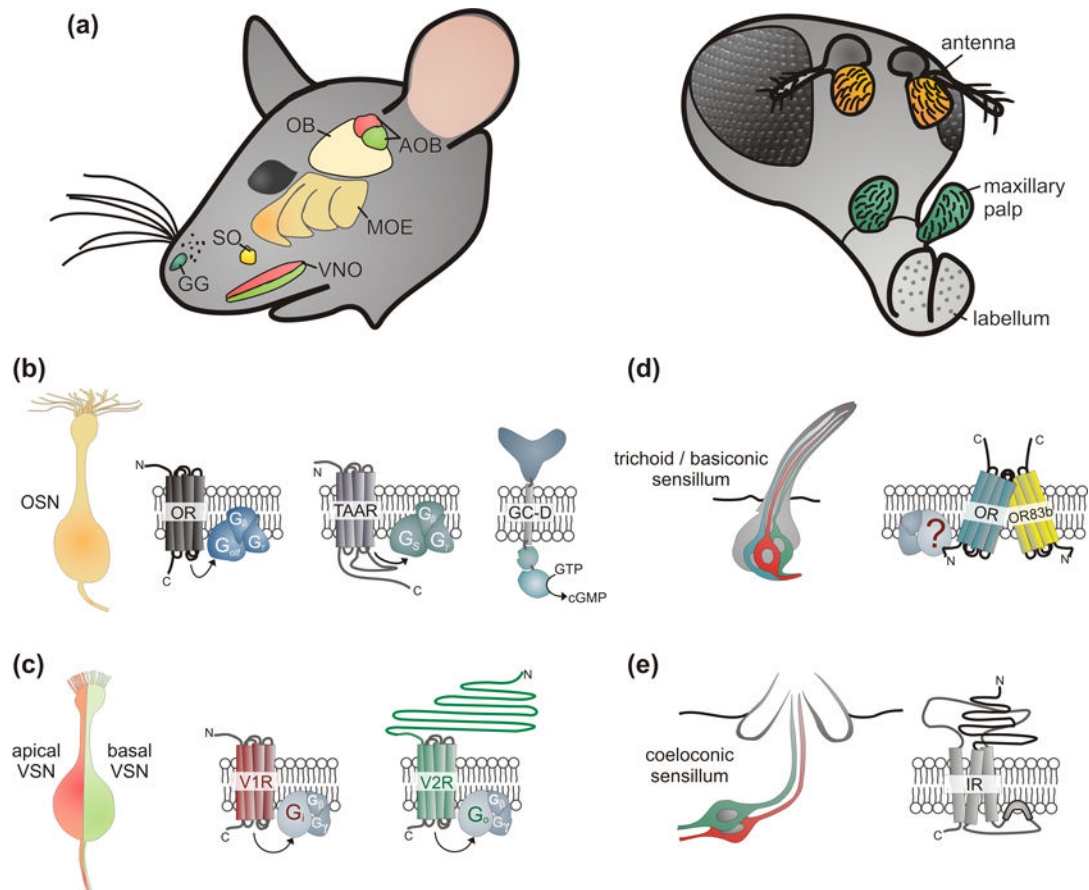


Figure 1.

Olfactory receptors of mouse and fruitfly. **(a) Left panel:** In the mouse nasal cavity, chemosensory neurons are found within several sensory organs, including the Grueneberg ganglion (GG), septal organ of Masera (SO), vomeronasal organ (VNO), and main olfactory epithelium (MOE). The VNO neuroepithelium is divided into apical (red, contains V1R-expressing VSNs) and basal (green, contains V2R-expressing VSNs); VSNs in these two regions innervate the rostral and caudal divisions of the accessory olfactory bulb (AOB), respectively. OR-, TAAR-, and GC-D-expressing OSNs are found in the MOE; their axons project to the main olfactory bulb (MOB). **Right panel,** The fruitfly *Drosophila melanogaster* has two olfactory organs: the distal segment of the antenna (orange) and the maxillary palp (green). The labellum contains gustatory receptors. **(b)** Receptors expressed in ciliary OSNs of the mouse MOE include two groups of GPCRs, the ORs and the TAARs, as well as the receptor guanylyl cyclase GC-D. Both ORs and TAARs appear to couple to the G protein $G_{\alpha_{olf}}$. **(c)** V1Rs are expressed in apical VSNs, while V2Rs are expressed in basal VSNs. Both may couple to layer-specific G proteins ($G_{\alpha_{12}}$ and G_{α_o} , respectively). **(d)** *Drosophila* ORs, almost exclusively expressed in basiconic and trichoid OSNs, are heteromeric receptors. The common subunit OR83b appears to be an ion channel, while the partner OR (isoforms vary between OSN subtypes) dictates ligand selectivity and may also couple to a G protein. **(e)** IRs are found in coeloconic OSNs and are ligand-gated ion channels. In some cases they may form homomeric or heteromeric complexes.