Sensory neuron population expansion enhances odour tracking through relaxed projection neuron adaptation

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Abstract

From the star-nosed mole's eponymous mechanosensory organ to the platypus' electroreceptive bill, the expansion of sensory neuron populations detecting important environmental cues is a widespread evolutionary phenomenon in animals[1-6]. How such neuron increases contribute to improved sensory detection and behaviour remain largely unexplained. Here we address this question through comparative analysis of olfactory pathways in *Drosophila melanogaster* and its close relative *Drosophila sechellia*, which feeds and breeds exclusively on *Morinda citrifolia* noni fruit[7-9]. We show that *D. sechellia* displays selective, large expansions of noni-detecting olfactory sensory neuron (OSN) populations, and that this trait has a multigenic basis. These expansions are accompanied by an increase in synaptic connections between OSNs and their projection neuron (PN) partners that transmit information to higher brain centres. Quantification of odour-evoked responses of partner OSNs and PNs reveals that OSN population expansions do not lead to heightened PN sensitivity, beyond that due to sensory receptor tuning differences. Rather, these pathways – but not those with conserved OSN numbers – exhibit non-adapting PN activity upon odour stimulation. In noni odour plume-tracking assays, *D. sechellia* exhibits enhanced performance compared to *D. melanogaster*. Through activation and inhibition of defined proportions of a noni-sensing OSN population, we establish that increased neuron numbers contribute to this behavioural persistence. Our work reveals an unexpected functional impact of sensory neuron expansions that can synergise with peripheral receptor tuning changes to explain ecologically-relevant, species-specific behaviour.

Introduction

Brains display incredible diversity in neuron number between animal species[10-12]. Evolutionary increases in the number of neurons occur not only through the emergence of new cell types but also through expansion of pre-existing neuronal populations[13,14]. Of the latter phenomenon, some of the most spectacular examples are in sensory systems: the snout of the star-nosed mole (*Condylura cristata*) has ~25,000 mechanosensory organs, several fold more than other mole species[1]. Male (but not female) moths can have tens of thousands of neurons detecting female pheromones, representing the large majority of sensory neurons in their antennae[15]. A higher number of sensory neurons is generally assumed to underlie sensitisation to the perceived cues[3-6]. Surprisingly, however, it remains largely untested if and how such neuronal expansions impact sensory processing and behaviour.

The drosophilid olfactory system is an excellent model to address these questions[16,17]. The antenna, the main olfactory organ, houses ~1000 olfactory sensory neurons (OSNs) that, in *Drosophila melanogaster*, have been classified into ~50 types based on their expression of one (or occasionally more) Odorant receptors (Ors) or Ionotropic receptors (Irs)[17-19]. The size of individual OSN populations (ranging from ~10-65 neurons) is stereotyped across individuals, reflecting their genetically hard-wired, developmental programmes[20,21]. By contrast, comparisons of homologous OSN types in ecologically-distinct drosophilid species have identified several examples of expansions in OSN populations. Notably, *Drosophila sechellia*, an endemic of the Seychelles that specialises on *Morinda citrifolia* "noni" fruit[7-9], has an approximately three-fold

increase in the neuron populations expressing Or22a, Or85b and Ir75b compared to both *D. melanogaster* and a closer relative, *Drosophila simulans*[22-25] (**Fig. 1a**). All three of these neuron classes are required for long- and/or short-range odour-guided behaviours[23,26] and two of these (Or22a and Ir75b) also display increased sensitivity to noni odours through mutations in the corresponding *D. sechellia* receptor genes[22-24]. Together, these observations have led to a long-held assumption that these OSN population expansions are important for *D. sechellia*, but this has never been tested.

Results

Selective large increase in Or22a and Or85b populations in *D. sechellia*

The increase in Or22a and Or85b OSN numbers in *D. sechellia* reflects the housing of these cells in a common sensory hair, the antennal basiconic 3 (ab3) sensillum (**Fig. 1b, Extended Data Fig. 1a,b**). To determine how unique this increase is within the antenna, we quantified the number of the other ~20 morphologically-diverse, olfactory sensillar classes – which each house distinct, stereotyped combinations of 1-4 OSN types – in *D. sechellia*, *D. melanogaster* and *D. simulans* through RNA FISH of a diagnostic *Or* per sensillum (combined with published data on *Ir* neurons[22]) (**Fig. 1c**). We observed several differences in sensillar number between these species, including reductions in ab5, ab8 and ai1 in *D. sechellia*, but only ab3, as well as ac3I that house Ir75b neurons, showed a more than two-fold increase (~50 more ab3, 2.6-fold increase;~15 more ac3I, 3.7-fold increase) in *D. sechellia* compared to the other species.

OSN population expansion is a complex genetic trait

We next investigated the mechanism underlying the ab3 OSN population expansion in *D. sechellia*. The number of ab3 sensilla was not different when these flies were grown in the presence or absence of noni substrate (**Extended Data Fig. 1c**), arguing against an environmental influence. As the total number of antennal sensilla is similar across species (**Fig. 1c**), we asked whether the ab3 increase could be explained by simple transformation of sensillar fate. Previous electrophysiological analyses reported at least a partial loss of ab2 sensilla in *D. sechellia*, which was interpreted as a potential trade-off for the ab3 expansion[24,27]. However, we readily detected ab2 sensilla histologically in this species (**Fig. 1c, Extended Data Fig. 1d**), countering this possibility. Moreover, from an antennal developmental fate map in *D. melanogaster*[28], we did not observe any obvious spatial relationship between the sensory organ precursors for sensillar classes that display increases or decreases in *D. sechellia* to support a hypothesis of a simple fate switch, although both expanded populations (ab3 and ac3I) originate from peripheral regions of the map (**Extended Data Fig. 1e**).

We therefore reasoned that genetic changes specifically affecting the development of the ab3 lineage might be involved. We first tested for the existence of species-specific divergence in *cis*-regulation at the receptor loci. Using mutants for both *Or22a/(b)* and *Or85b* in *D. simulans* and *D. sechellia*[23], we analysed receptor expression in interspecific hybrids and reciprocal hemizygotes (lacking transcripts from one or the other receptor allele) (**Fig. 1d, Extended Data Fig. 1f**). In all hybrid allelic combinations (except those lacking both alleles) we observed a

similar number of Or22a and Or85b OSNs, arguing against a substantial contribution of *cis*-regulatory evolution at these loci to the expansion of receptor neuronal expression.

As little is known about the developmental programme of ab3 specification, we used an unbiased, whole-genome, quantitative trait locus (QTL) mapping strategy to characterise the genetic basis of the expansion in *D. sechellia*. For high-throughput quantification of ab3 numbers, we generated fluorescent reporters of Or85b neurons in *D. sechellia* and *D. simulans* (**Extended Data Fig. 2a,b**). Interspecific F1 hybrids displayed an intermediate number of Or85b neurons to the parental strains (**Fig. 1e**). We phenotyped >600 F2 individuals (backcrossed to either *D. sechellia* or *D. simulans*) (**Fig. 1e**), which were then genotyped using multiplexed shotgun sequencing[29]. The resulting QTL map (**Fig. 1f**) identified two genomic regions linked to variation in Or85b neuron number located on chromosomes 3 and X; these explain a cell number difference of about ~12 and ~7 neurons, respectively, between *D. sechellia* and *D. simulans* (**Fig. 1g**). No significant epistasis was detected between these genomic regions (**Methods**) and the relatively low effect size (21.0% and 12.3%, respectively) is consistent with a model in which more than two loci contribute to the species difference in Or85b neuron number. Consistent with the QTL map, introgression of fragments of the *D. sechellia* genomic region spanning the chromosome 3 peak into a *D. simulans* background led to increased numbers of Or85b neurons (**Extended Data Fig. 2c,d**). However, the phenotypic effect was lost with smaller introgressed regions, indicating that multiple loci influencing Or85b neuron number are located within this QTL region (**Extended Data Fig. 2d**).

In a separate QTL mapping investigating the genetic basis for the increase in ac3I (Ir75b) neurons in *D. sechellia*[22] (**Fig. 1c**), we also observed a complex genetic architecture of this interspecific difference, with no evidence for shared loci with the increase in ab3 sensilla (**Extended Data Fig. 2j,k)**. Thus, in contrast to the evolution of sensory specificity of olfactory pathways – where only one or a few amino acid substitutions in a single receptor can have a phenotypic impact[22,23,26], with some evidence for "hotspot" sites in different receptors[30] – species differences in the number of OSN types have arisen from distinct evolutionary trajectories involving changes in multiple loci.

OSN population expansions lead to increased pooling on cognate projection neurons

The axons of OSNs expressing the same receptor converge onto a common glomerulus within the antennal lobe in the brain[31] (**Fig. 2a**). Here, they form cholinergic synapses on mostly uniglomerular projection neurons (PNs) – which transmit sensory signals to higher olfactory centres – as well as on broadly-innervating local interneurons and a small proportion on other OSNs[31,32]. To investigate the structural and functional consequences of OSN number increases in *D. sechellia*, we generated PN-specific driver transgenes in this species using constructs previously-characterised in *D. melanogaster*[33,34]: *VT033006-Gal4*, which drives expression in many uniglomerular PN types and *VT033008-Gal4* which has sparser PN expression (**Fig. 2b**). Using these drivers to express photoactivable-GFP in PNs, we performed spatially-limited photoactivation of the DM2 and VM5d glomeruli – which receive input from Or22a and Or85b OSNs, respectively (**Fig. 2a**) – to visualise the partner PNs. We confirmed that DM2 is

innervated by 2 PNs in both *D. melanogaster* and *D. sechellia*[23] and, further found that VM5d also has a conserved number of PNs (on average 4) in these species (**Fig. 2c**). Together with data that the Ir75b glomerulus, DL2d, has the same number of PNs in *D. melanogaster*, *D. simulans* and *D. sechellia*[22,35], these observations indicate that *D. sechellia*'s OSN population expansions are not accompanied by increases in PN number.

To quantify the number of excitatory OSN-PN connections, we expressed a GFP-tagged Dα7 acetylcholine receptor subunit in PNs[32,36,37] in *D. melanogaster* and *D. sechellia* (**Fig. 2d**) and measured glomerular volumes and the number of postsynaptic puncta in DM2, VM5d and a control glomerulus (DM6). We first confirmed the larger glomerular volume of DM2 and VM5d in *D. sechellia*[22-25,35] (**Fig. 2e**). Consistent with an increased number of OSN inputs in these glomeruli, both displayed more postsynaptic GFP puncta in *D. sechellia* than in *D. melanogaster* (**Fig. 2e**). Although quantifications of fluorescent puncta are likely to substantially underestimate the number of synapses detectable by electron microscopy[31,32], these data suggest that individual PNs in *D. sechellia* form more synaptic connections with their pre-synaptic partner OSNs than in *D. melanogaster*.

OSN number increases do not lead to sensitisation or heightened reliability of PN responses

To investigate the physiological significance of OSN number increase, we expressed GCaMP6f in OSNs (using drivers recapitulating expression of the Or co-receptor Orco[23,38]) or PNs (using the drivers described above) in *D. melanogaster* and *D. sechellia*, and performed two-photon calcium imaging of odour-evoked responses. We first hypothesised that the larger number of OSNs in *D. sechellia* would be reflected in higher sensitivity of the corresponding PNs. To test this, we began by examining the Or85b pathway, as peripheral electrophysiological recordings of these OSNs' responses in ab3 sensilla to its best-known agonist, *2*-heptanone, demonstrated no difference in sensitivity between both species[23]. This conservation allowed us to assess specifically the impact of OSN population expansion. Consistent with the electrophysiological results, when measuring calcium responses to a short pulse of *2*-heptanone in OSN axon termini in the VM5d glomerulus, we observed no sensitivity differences (**Fig. 3a, Extended Data Fig. 3a**). This finding also indicates that any differences in OSN:OSN synapse number[31] in VM5d in *D. sechellia* does not impact these neurons' response sensitivity within the axon termini. Importantly, VM5d PNs also displayed no obvious increase in odour sensitivity in *D. sechellia* (**Fig. 3a, Extended Data Fig. 3b**).

We further tested our hypothesis by calcium imaging of Or22a OSNs and DM2 PNs after stimulation with the noni odour methyl hexanoate[24]. In this olfactory pathway, *D. sechellia* OSNs displayed responses at odour concentrations approximately two orders of magnitude lower than in *D. melanogaster* (**Fig. 3b, Extended Data Fig. 3c**), concordant with the known higher sensitivity of these neurons measured by electrophysiological recordings in ab3[23,24,27]. *D. sechellia* DM2 PNs displayed a similar degree of heightened sensitivity compared to those in *D. melanogaster*, suggesting that increased Or22a OSN number does not lead to further sensitisation of these PNs (**Fig. 3b, Extended Data Fig. 3d**). To test the sufficiency of differences in receptor properties[23] to explain the activity of *D. sechellia* DM2 PNs at lower stimulus concentrations, we expressed *D.*

melanogaster or *D. sechellia* Or22a in *D. melanogaster* Or22a neurons lacking the endogenous receptors, which is sufficient to confer a species-specific odour response profile to these OSNs[23]. Measurement of responses to methyl hexanoate in DM2 PNs revealed higher sensitivity in animals expressing *D. sechellia* Or22a compared to those expressing *D. melanogaster* Or22a (**Extended Data Fig. 3e**); notably, this difference was similar in magnitude to the endogenous sensitivity differences of *D. sechellia* and *D. melanogaster* DM2 PNs. Together, the analyses of Or85b and Or22a pathways argue that a larger OSN population does not contribute to enhanced PN sensitisation.

Pooling has also been suggested to reduce the noise in sensory representation by averaging the activity across many sensory neurons[39,40]. We therefore examined whether increased OSN number plays a role in reducing the signal-to-noise ratio in PN responses by comparing odour responses in VM5d PNs to multiple trials of *2*-heptanone stimulation. However, these experiments did not reveal any differences in PN response reliability between *D. melanogaster* and *D. sechellia* (**Fig. 3c-e**).

Pathways with OSN number increases display non-adapting PN responses to dynamic and prolonged stimulation

Most natural odours exist as turbulent plumes, which stimulate OSNs with complex, pulsatile temporal dynamics[41]. To test if odour temporal dynamics in these olfactory pathways are influenced by OSN number, we repeated the calcium imaging experiments using ten consecutive, short pulses of odour. Or85b OSNs displayed a plateaued response to pulses of *2*-heptanone in both *D. melanogaster* and *D. sechellia*, albeit with a slight decay over time in the latter species (**Fig. 3f**). *D. melanogaster* VM5d PNs showed decreasing responses following repeated exposure to short pulses, presumably reflecting adaptation, as observed in multiple PN types[42]. By contrast, VM5d PNs in *D. sechellia* displayed non-adapting responses throughout the series of odour pulses (**Fig. 3g**). This species difference in PN responses was also seen with long-lasting odour stimulation (**Extended Data Fig. 4**). Imaging the responses of Or22a OSN partner PNs in DM2 to pulsed odour stimuli (using concentrations of methyl hexanoate that evoked similar activity levels between the species (**Fig. 3b**)) revealed a similar result: *D. melanogaster* DM2 PN responses decreased over time while *D. sechellia* DM2 PNs responses were unchanged in magnitude (**Fig. 3h**). However, for two olfactory pathways where the number of cognate OSNs is not increased in *D. sechellia* (Or59b (DM4) and Or92a (VA2) (**Fig. 1c**)), the PNs in both species displayed decreasing responses over the course of stimulations (**Fig. 3i,j, Extended Data Fig. 5**). Together, our data indicate that OSN number increases in *D. sechellia*'s noni-sensing pathways might promote non-adapting PN responses to dynamic or long-lasting odour stimuli.

Non-adapting responses of PNs are likely due to increased OSN numbers

Sustained PN responses in *D. sechellia* could be due to several, non-mutually exclusive mechanisms in the antennal lobe, such as the intrinsic physiological properties of PNs, OSN-PN synapses and/or the contribution of local interneurons. To investigate these possibilities, we performed PN calcium imaging with pharmacological blockage of synaptic components. Inhibition of GABAergic neurotransmission (which blocks inhibitory inputs from local interneurons[43]) did not

lead to significant adaptation in *D. sechellia* VM5d PNs (**Fig. 4a**). Such disinhibition caused a relative decrease in odour response as the baseline activity is increased in *D. sechellia* PNs, suggesting that VM5d PN activity becomes nearly saturated by this pharmacological treatment (**Extended Data Fig. 6a**).

We next pharmacologically impaired cholinergic neurotransmission, which diminishes excitatory inputs to PNs, notably OSN-PN synapses[44]. As expected, strong blockage essentially abolished odour responses (**Extended Data Fig. 6b**). More informatively, weak blockage led to adaptation in the responses of *D. sechellia* VM5d PNs (**Fig. 4b**), as seen in untreated *D. melanogaster*. These observations suggest that synaptic mechanisms, such as in cholinergic OSN-PN synapses, play a role in persistent PN responses. Consistent with this possibility, halving the number of OSN inputs through removal of one antenna (OSN axons project to antennal lobes in both brain hemispheres[31]) also rendered the *D. sechellia* VM5d PN responses adapting (**Fig. 4c**).

Through the course of our calcium imaging experiments, we noted that the dynamic range of VM5d and DM2 PNs, but not control DM4 and VA2 PNs, was smaller in *D. sechellia* than *D. melanogaster* (**Fig. 4d,e**), presumably due to the smaller window between the baseline and maximum activity of PNs when there is a larger number of cognate OSNs. These properties suggest that OSN number increases compress the PN dynamic range, potentially impacting PN adaptation properties (see **Discussion**).

Or22a is required for *D. sechellia* to track host odour stimuli

We next investigated if and how increased OSN population size impacts odour-tracking behaviour. Previously, we showed that both Or22a and Or85b pathways are essential for long-range attraction to noni in a wind tunnel[23]. To analyse the behavioural responses to pulsed odour stimuli, similar to that used in the calcium imaging experiments, we developed a tethered fly assay with a timed odour-delivery system (**Fig. 5a**). By measuring the beating amplitude of both wings while presenting a lateralised odour stimulus, we could quantify attractive responses to individual odours, as reflected in an animal's attempt to turn toward the stimulus source, leading to a positive delta wing beat amplitude (*ΔWBA*) (see **Methods**). We first tested responses of wild-type flies to consecutive short pulses of noni odours: as expected, multiple strains of *D. sechellia* displayed attractive responses that persisted through most or all of a series of odour pulses, while *D. melanogaster* strains displayed much more variable degrees of attraction (**Fig. 5b, Extended Data Fig. 7a**). The persistent attraction in *D. sechellia* was specific to noni odour and could not be observed using apple cider vinegar (**Extended Data Fig. 7b**), emphasising the ecological relevance of this behaviour.

To assess the contribution of distinct olfactory pathways to persistent noni attraction, we tested *D. sechellia* mutants for *Or22a*, *Or85c/b*, *Ir75b* and, as a control, *Or35a*, whose OSN population is also enlarged (as it is paired with Ir75b neurons in ac3I) but is dispensable for noni attraction[23]. Loss of *Or22a* abolished attraction of flies towards noni, while *Or85c/b* and *Ir75b* mutants retained some, albeit transient, turning towards this stimulus. Flies lacking *Or35a* behaved comparably to wild-type strains (**Fig. 5c**). These results point to Or22a as an important (albeit not the sole) olfactory receptor required for *D. sechellia* to respond behaviourally to noni odour.

To better understand the nature of *D. sechellia* plume-tracking, we used a wind-tunnel assay combined with 3D animal tracking[45] to record trajectories of freely-flying wild-type *D. melanogaster* and *D. sechellia*, as they navigated to the source of a noni juice odour plume (**Fig. 5d, Extended Data Fig. 8a,b**). Wild-type *D. sechellia* exhibited similar cast and surge dynamics as *D. melanogaster*[41] (**Fig. 5d**). However, we observed that *D. sechellia* maintained flight paths closer to the plume centreline (**Fig. 5d-f**), a difference that was particularly evident close (<20 cm) to the plume source (**Fig. 5d-f**). Consistent with the phenotype observed in the tethered-fly assay, *D. sechellia Or22a* mutants lacked strong plume-tracking responses (**Fig. 5d-f**), while not exhibiting obvious impairment in flight performance (**Extended Data Fig. 8c**). To extend analysis of these observations we quantified the distribution of flies within a 3 cm radius of the estimated odour plume centreline in the downwind and upwind halves of the wind tunnel (**Fig. 5e,g**). In the downwind half, wild-type *D. sechellia* and *D. melanogaster* had comparable course direction distributions (**Fig. 5g**). By contrast, in the upwind half, *D. sechellia* maintained a tighter upwind course distribution suggesting they were more likely to be in an upwind surging state compared to *D. melanogaster* as they approach the odorant source (**Fig. 5g**). *D. sechellia Or22a* mutants did not appear to be strongly oriented into the wind, notably in the downwind half, further indicating the importance of this receptor in stereotypical plume-tracking behaviours (**Fig. 5g**).

***D. sechellia*'s increase in OSN number is important for persistent odour-tracking behaviour**

To investigate the importance of Or22a neuron number for odour-tracking behaviour we expressed CsChrimson in Or22a neurons in *D. melanogaster* and *D. sechellia* to enable stimulation of this pathway with red light. This optogenetic approach had two advantages: first, it allowed us to calibrate light intensity to ensure equivalent Or22a OSN activation between species; second, because only Or22a neurons are activated by light, we could eliminate sensory contributions from other olfactory pathways that have overlapping odour tuning profiles to Or22a.

We first confirmed light-evoked spiking in Or22a neurons in *D. melanogaster* and *D. sechellia*, and determined the light intensity evoking equivalent spike rates (**Fig. 6a**). We then performed lateralised optogenetic activation of Or22a OSNs in the tethered fly assay, mimicking lateralised odour input by focussing the light beam on one antenna (**Fig. 6a, Extended Data Fig. 9a**). Pulsed optogenetic activation of *D. sechellia* Or22a OSNs induced attractive behaviour with a similar magnitude and dynamics as pulsed odour stimuli (**Fig. 6b**), demonstrating the sufficiency of this single olfactory pathway for evoking behaviour. Notably, the attractive behaviour was more persistent over the series of light pulses in *D. sechellia* than in *D. melanogaster* (**Fig. 6a, Extended Data Fig. 9b-d**), consistent with a hypothesis that a higher number of Or22a OSNs supports enduring behavioural attraction to a repeated stimulus.

To explicitly test this possibility, we generated genetic tools to reproducibly manipulate the number of active Or22a OSNs in *D. sechellia*, using the SPARC technology developed in *D. melanogaster*[46] (**Extended Data Fig. 10a**). Combining a *SPARC2-D-CsChrimson* transgene with *Or22a-Gal4* allowed us to optogenetically stimulate ~50% of these neurons (**Fig. 6c, Extended Data Fig. 10b**). Although we confirmed light-evoked Or22a neuron spiking in these animals, they did not display attractive behaviour towards the light stimulus, in contrast to

similar stimulation of all Or22a OSNs (**Fig. 6c, Extended Data Fig. 10c**). This result implies that the number of active OSNs is critical to induce attraction in *D. sechellia*.

In a complementary approach, we generated a *SPARC2-D-Tetanus Toxin* (*TNT*) transgene in *D. sechellia*, with which we could silence on average ~50% of Or22a OSNs (**Fig. 6d**), without affecting other peripheral or central neurons (**Extended Data Fig. 10d**). This transgene selectively reduced OSN input to DM2 PNs in an otherwise unaffected olfactory system. Importantly, when tested in our tethered flight assay, these flies showed only transient attraction towards noni odour, contrasting with the persistent noni attraction of control animals (**Fig. 6d**). Together these results support the hypothesis that the increased Or22a OSN number observed in *D. sechellia* is essential for sustained attractive olfactory behaviour.

Discussion

Amongst the many ways in which animal brains have diverged during evolution, species-specific increases in the number of a particular neuron type appears to be one of the most common. Surprisingly, the physiological and behavioural consequences of such apparently simple changes have remained largely untested. Here we have exploited an ecologically and phylogenetically well-defined model clade of drosophilids to study this phenomenon. We provide evidence for a function of sensory neuron expansion in underlying sustained PN responses in *D. sechellia* in response to repetitive or persistent stimulation with noni host odours. While we have shown that OSN number alone can determine persistence of odour-tracking behaviour, this neuron number-dependent modulation of central adaptation is likely to synergise with increases in peripheral sensory sensitivity conferred by changes in olfactory receptor tuning properties[22-24] to enable long-distance localisation of the unique host fruit of this species (**Fig. 6e**).

One important open question is the mechanism by which OSN population increase leads to reduced adaptation of PNs. While multiple (non-exclusive) explanations are possible, our favoured model is based both upon our analyses in *D. sechellia* and knowledge of antennal lobe sensory processing in *D. melanogaster*[44]. In brief, we suggest that a higher number of OSNs increases both baseline PN activity (due to OSN spontaneous activity) and odour-evoked activity. However, the upper limit in PN activity (due to short-term depression and a refractory period[42]) dampens the effect of increased OSN inputs during odour stimulation at high activity. This results in a reduced difference in activity between the beginning and end of an odour stimulus (or train of odour pulses), which sustains the PN responses to dynamic odour. Future electrophysiological analysis of *D. sechellia* PNs, requiring selective genetic markers for labelling specific PN types, will be critical to test these ideas. Regardless of the precise mechanism, could sustained PN responses convert to behavioural persistence? The main downstream partners of PNs are Kenyon cells, which have high input threshold[47] for sparse coding. Assuming the same input threshold of Kenyon cells in *D. sechellia* as in *D. melanogaster*, the sustainment of PN activity might elongate Kenyon cell responses to persistent odours, which could be relayed to downstream neurons that drive valence-specific behaviours[48].

Sensory habituation is advantageous for the brain to avoid information overload by attenuating constant or repetitive inputs and is a general feature across

sensory modalities[49]. However, this phenomenon might be disadvantageous when navigating through sensory cues for a long period of time, for example, during olfactory plume-tracking. The unanticipated role of OSN population increases in reducing adaptation selectively in their partner PNs provides an elegant resolution to this conflict in sensory processing, enabling central response adaptation in a specific sensory channel, while leaving conserved molecular effectors mediating synaptic neurotransmission and adaptation in other olfactory pathways intact.

Beyond *D. sechellia*, selective increases in ab3 neuron numbers have been reported in at least two other drosophilid species, which are likely to represent independent evolutionary events[4,50] (**Extended Data Fig. 11**). Furthermore, Or22a neurons display diversity in their odour specificity across drosophilids[50,51]. These observations suggest that this sensory pathway is an evolutionary "hotspot" where changes in receptor tuning and OSN population size collectively impact sensory processing, perhaps reflecting the potent behavioural influence of this pathway, as we have found in *D. sechellia*. More generally, given our demonstration of the important effect of OSN population size on host odour processing in *D. sechellia*, examination of how cell number increases modify circuit properties in other sensory systems, brain regions and species seems warranted.

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Author Contributions

S.T., T.O.A. and R.B. conceived the project. All authors contributed to experimental design, analysis and interpretation of results. Specific experimental contributions were as follows: S.T. performed all calcium imaging, photoactivation, tethered fly behavioural experiments and cloning of the *VT033006-LexA* construct. T.O.A. performed molecular biology experiments, generated transgenic lines, performed

histology, Or85b QTL analysis, cell number quantifications and electrophysiology. L.A. performed molecular biology experiments, histology and quantifications of post-synaptic puncta. S.D.S. performed the wind tunnel behavioural experiments, with guidance from F.v.B. J.R.A. co-led the Ir75b QTL analysis and contributed to the Or85b QTL analysis. L.P.-G. co-led the Ir75b QTL analysis. D.L.S. contributed to the QTL analyses and generated *UAS-CsChrimson* constructs. S.C. contributed to the Ir75b QTL analysis. R.A.O. performed histology in the *D. melanogaster* subgroup. C.F.R.W. generated the parent *SPARC2-TNT* construct. S.T., T.O.A. and R.B. wrote the paper with input from all other authors. All authors approved the final version of the manuscript.

Competing interests

The authors declare no competing interests.

Methods

Data reporting

Preliminary experiments were used to assess variance and determine adequate sample sizes in advance of acquisition of the reported data. For electrophysiological recordings, data were collected from multiple flies on several days in randomised order. Within datasets, the same odour dilutions were used for acquisition of the data. The experimenter was blinded to the genotype for quantification of OSN numbers, and SPARC2-CsChrimson and SPARC2-TNT tethered fly assays, but not for other behavioural or physiological experiments.

Drosophila strains

Drosophila stocks were maintained on standard wheat flour/yeast/fruit juice medium under a 12 h light:12 h dark cycle at 25°C. For all *D. sechellia* strains, a few g of Formula 4-24® Instant *Drosophila* Medium, Blue (Carolina Biological Supply Company) soaked in noni juice (Raab Vitalfood) were added on top of the standard food. Wild-type, mutant and transgenic *Drosophila* lines used in this study are listed in **Extended Data Table 2.**

To generate *lozenge* (*lz*) *trans*-heterozygous *D. sechellia/D. simulans* hybrid flies, we group-aged 25-35 virgin males of *D. simulans* (*Dsim03 Or85b*^{GFP}) for 6-7 days before combining them with 20-30 virgin females of *D. sechellia* (*Dsec07 Or85b*^{GFP}). We lowered the fly food cap to restrict space and force interactions between the animals (which otherwise had a very low tendency to mate). Tubes were maintained at 22°C with strong light exposure and flipped every 3-4 days into a new tube. Progeny were collected and phenotyped 7-10 days post-eclosion.

CRISPR/Cas9-mediated genome engineering

sgRNA expression vectors: for expression of single sgRNAs (targeting the *D. simulans Or85b* locus), oligonucleotide pairs (**Extended Data Table 3**) were annealed and cloned into *BbsI*-digested *pCFD3-dU6-3gRNA* (Addgene #49410) as described[52]. To express multiple sgRNAs from the same vector backbone (targeting the *D. sechellia* and *D. simulans lz* loci), oligonucleotide pairs (**Extended Data Table 4**) were used for PCR and inserted into *pCFD5* (Addgene #73914) via Gibson Assembly, as described[53].

Donor vectors for homologous recombination: homology arms (1-1.6 kb) for individual target loci (*Or85b*, *lz*) were amplified from *D. sechellia* (*Drosophila* Species Stock Center [DSSC] 14021-0248.07) or *D. simulans* (DSSC 14021-0251.195) genomic DNA and inserted into *pHD-DsRed-attP*[54] or *pHD-Stinger-attP*[23] via restriction cloning or Gibson Assembly.

D. sechellia UAS-SPARC2-D-CsChrimson: we digested a *SPARC2-backbone* vector (Addgene #133562) with *SalI* and inserted a *CsChrimson-Venus* cassette after PCR amplification from *pBac(UAS-ChR2 CsChrimson,3xP3::dsRed)* via Gibson Assembly. The resulting *SPARC2-D-CsChrimson* cassette was amplified via PCR and inserted after *NdeI* and *BsiWI* restriction digest into *pHD-3xP3-DsRed DattP-D. sechellia attP40* (this targeting vector for homologous recombination at the *D. sechellia attP40* equivalent site will be described in more detail elsewhere).

D. sechellia UAS-SPARC2-D-TNT-HA-GeCO: we first generated a *pHD-3xP3-DsRed_DattP-UAS-TNT-GeCO* vector by amplifying a *TNT-GeCO* cassette from *pHD-37.1_AttP5_LexAop_90_10_TNT-HA_p2A_jRGeCO1a* together with a

UAS cassette and insertion into *pHD-3xP3-DsRed DattP* via Gibson Assembly. Subsequently, we transferred the *UAS-TNT-HA-GeCO* cassette into *pHD-3xP3-DsRed DattP-D. sechellia attP40* before assembling *pHD-3xP3-DsRed DattP-D. sechellia attP40 SPARC2-D-TNT-HA-GeCO* via Gibson Assembly (the GeCO calcium indicator was not used in the current study). Both *SPARC-D* transgenic lines in *D. sechellia* were generated via CRISPR/Cas9-mediated homologous recombination at the *attP40* equivalent location in *D. sechellia*. To test the functionality of the *UAS-TNT-HA-GeCO* cassette, we also generated *UAS-TNT-HA-GeCO* transgenic lines via homologous recombination at the *attP40* locus in *D. melanogaster* and *D. sechellia*. However, in both species successful transformants did not survive pupariation, which was potentially due to low-level, Gal4-independent expression of the TNT effector.

All plasmids were verified via Sanger sequencing before transgenesis. Full details and oligonucleotide sequences are available from the corresponding authors upon request.

Transgenesis

D. melanogaster VT033006-LexA: to generate a *VT033006-LexA* construct, *pLexA-SV40-attB* was digested with *NotI*. A *VT033006* enhancer fragment was PCR-amplified from *pVT033006-Gal4-attB*[33]. The insert and the linearised vector were joined by Gibson assembly. The vector was integrated into *D. melanogaster attP2* by BestGene Inc.

D. sechellia VT033006-Gal4 and *VT033008-Gal4*: constructs carrying the *D. melanogaster* enhancer sequences[33] were integrated into *Dsecwhite* (attP landing site on the X chromosome[23]). The *DsecnSyb-ΦC31* line was generated by integration of *nSyb-ΦC31* (Addgene #133868) into *DsecattP*[26] (see below).

*D. sechellia UAS-Dα7:*GFP: flies were generated by P element-mediated transgenesis of *p(UAS-Dα7:GFP)*[37] by WellGenetics.

DsecpBac(UAS-CsChrimson-Venus): we first amplified a *UAS-CsChrimson-Venus* cassette from *pUAS-ChR2 CsChrimson*[55] and a *pBac* backbone[56] and combined both via Gibson assembly resulting in *pBac(UAS-CsChrimson)*. Subsequently, we digested *pBac(UAS-CsChrimson)* with *AscI*, amplified a *3xP3-DsRed*, a *3xP3-opt-mTurquoise* (both derived from gene synthesis, Genetivision) or a *3xP3-eYFP cassette*[56] via PCR and combined the vector backbone with either amplicon via Gibson Assembly resulting in *pBac(UAS-CsChrimson,3xP3-DsRed)* (available at Addgene #tbd), *pBac(UAS-CsChrimson,3xP3-opt-mTurquoise)* (Addgene #tbd) and *pBac(UAS-CsChrimson,3xP3-eYFP)* (Addgene #tbd). Primer sequences for intermediate cloning steps are listed in **Extended Data Table 2**. For this study, flies were generated by piggyBac-mediated transgenesis of *pBac(UAS-CsChrimson-Venus,3xP3-DsRed)* and the insertion site mapped to the third chromosome using TagMap[57]. Beyond its use for optogenetic experiments, we took advantage of the visible 3xP3-DsRed marker to use the same line for introgression mapping (**Extended Data Figure 2c,d**).

***Drosophila* microinjections**

Transgenesis of *D. sechellia*, *D. simulans* and *D. melanogaster* was performed in-house following standard protocols[23] (except for two transgenes described above). For *piggyBac* and P-element transgenesis, we co-injected a *piggyBac* or *P-element* vector (300 ng μl^{-1}) and *piggyBac*[58] or *P-element* helper plasmid[59] (300 ng μl^{-1}). For

CRISPR/Cas9-mediated homologous recombination, we injected a mix of an sgRNA-encoding construct (150 ng μl^{-1}) and donor vector (500 ng μl^{-1}) into *D. sechellia nos-Cas9*[23]. Site-directed integration into *attP* sites was achieved by co-injection of an *attB*-containing vector (400 ng μl^{-1}) and *pBS130* (encoding *Φ*C31 integrase under control of a heat shock promoter (Addgene #26290)[60]). The *DsecattP*[26] site (on chromosome 4) was generated via *piggyBac*-mediated random integration and will be described in more detail elsewhere. All concentrations are given as final values in the injection mix.

Histology

Fluorescent RNA *in situ* hybridisation (using digoxigenin- or fluorescein-labelled RNA probes) and immunofluorescence on whole-mount antennae were performed essentially as described[61,62]. Probes were generated using *D. sechellia* genomic DNA (*Or47a*, *Or88a*) and primers listed in **Extended Data Table 3**. Other published probes were either targeting *D. sechellia* (*Or42b*, *Or22a*, *Or85b*, *Or13a*, *Or98a*, *Or35a*[23]), *D. simulans* (*Or67a*[63]) or *D. melanogaster* transcripts (*Or56a*, *Or59b, Or9a*, *Or69aA*[64]; *Or19a*[19]; *Or83c*, *Or67d*[28]); all probes were used at a concentration of 1:50. Immunofluorescence on adult brains was performed as described[65].

The following antibodies were used: guinea pig α-Ir75b 1:500 (RRID:AB_2631093[22]), mouse monoclonal antibody nc82 1:10 (Developmental Studies Hybridoma Bank), rabbit α-GFP 1:500 (Invitrogen), and rat α-HA 1:500 (Roche). Alexa488-, Cy3- and Cy5-conjugated goat α-guinea pig, goat α-mouse, goat α-rabbit and goat α-rat IgG secondary antibodies (Molecular Probes; Jackson Immunoresearch) were used at 1:500.

Image acquisition and processing

Confocal images of antennae and brains were acquired on an inverted confocal microscope (Zeiss LSM 710) with an oil immersion 40× objective (Plan Neofluar 40× Oil immersion DIC objective; 1.3 NA). For quantification of synapse numbers, images were taken using a 63× objective (Plan-Apochromat 63× Oil immersion DIC M27; 1.4 NA) with a zoom of 3×, centring the image on the glomerulus of interest. Images were processed in Fiji[66]. *D. sechellia* brains were imaged and registered to a *D. sechellia* reference brain[23] using the Fiji CMTK plugin (https://github.com/jefferis/fiji-cmtk-gui).

Cell number quantification: the number of OSNs expressing a specific *Or* was quantified using Imaris (Bitplane) or the Fiji Cell Counter tool. For GFP-expressing Or85b OSNs for the QTL analysis, we imaged GFP and, in the 568 nm channel, cuticular autofluorescence. After subtraction of the cuticular fluorescence signal from the GFP signal using the Subtraction tool in Fiji, we quantified the number of GFP-positive nuclei using the Surface Detection tool in Imaris. For Ir75b neurons, we found that α-Ir75b immunofluorescence resulted in labelled cells having a range of intensities. To ensure that the cell quantifications were reproducible, counting was performed manually by three experimenters. Images resulting in disagreements were re-checked and either resolved or removed from analyses.

Glomerular and synapse quantification: glomerular volumes were calculated following segmentation with the Segmentation Editor plugin of Fiji using the 3D Manager plugin. The number of post-synaptic sites per glomerulus was quantified in Imaris as described[32], setting punctum size to 0.45 μm^3 for all images.

Quantitative trait locus mapping

Or85b phenotyping: flies expressing nuclear-localised GFP in Or85b neurons were placed individually into 96-well plates whose bottom was replaced by a metal mesh. Antennae were removed via shock-freezing in liquid nitrogen and collected in 4% paraformaldehyde-3% Triton-PBS as described[61]. After 3 h of fixation, antennae were washed twice in 3% Triton-PBS and twice in 0.1% Triton-PBS and mounted in Vectashield (Vectorlabs) on 30-well PTFE printed slides (Electron Microscopy Sciences) before imaging on a Zeiss LSM710 confocal microscope. The fly bodies were transferred (by inversion) into separate 96-well plates and frozen at -20°C. Genomic DNA of individual flies was extracted using the ZR-96 Quick-gDNA MiniPrep kit (Zymo Research).

Ir75b phenotyping: flies were processed as described above. For antennae, after washing in 0.1% Triton-PBS, immunofluorescence was performed using an α-Ir75b antibody as described in the histology section. Antennae were mounted in Vectashield (Vectorlabs) on 30-well PTFE printed slides (Electron Microscopy Sciences) before imaging on a Zeiss LSM710 confocal microscope.

Sequencing and genotyping: genomic DNA of individual flies was tagmented with in-house Tn5 as described[67]. In brief, Tn5 was charged with adaptors and mixed at a concentration of 5 ng/μl with 1 μl of genomic DNA. After tagmentation, Tn5 was de-activated by addition of 0.2% sodium dodecyl-sulphate and sample specific sequencing adaptors were added by PCR amplification. The resulting PCR amplicons were cleaned-up with AMPure XP bead-based reagents (Beckman Coulter Life Science), DNA concentration and fragment distribution quantified on a fragment analyser (Agilent) and single-end sequenced on an Illumina HiSeq sequencer.

Data analysis: to align sequencing reads, the parental genomes dsim r2.02 and dsec r1.3 were used as reference. Introgressed genomic regions were inferred using MSG software (http://www.github.com/JaneliaSciComp/msg). Output of MSG was thinned using the "pull_thin" utility (http://www.github.com/dstern/pull_thin) and read into R (v4.4.1) using the "read_cross_msg" utility (http://www.github.com/dstern/read_cross_msg). QTL mapping was carried out with the qtl package (v1.5) using the Haley-Knott method and significance was determined using 1000 permutation tests (n.perm = 1000). Tests for interactions between the QTL on chromosomes 3 and X for the Or85b mapping experiment were performed using the "fitqtl" function.

Two-photon calcium imaging

Animal preparation: flies of the appropriate genotype (described in the respective figure legends) were collected (females and males co-housed) and reared in standard culture medium (see above). Female flies aged 5-8 days after eclosion were used for the experiments.

Sample preparation: flies were anesthetised by placing them into an empty vial that was cooled on ice for no longer than ~10 min. Further steps were performed under a dissection microscope, adapting a previous protocol[68]. A small drop of blue light-curing glue (595987WW, Ivoclar Vivadent) was placed on top of the copper grid (G220-5, Agar Scientific). Single flies were introduced into the mounting block (as described, fixing the back of the fly head to the copper grid with the curing glue. The fly head was slightly bowed down with forceps (to achieve antennal lobe imaging from the dorsal side) while the blue curing light (bluephase

C8, Ivovlar Vivadent; placed at least 1 cm from the fly to avoid tissue damage) was focused. We avoided using the wire that was previously used to pull down the antennal plate[23,68], as we found this very frequently damaged the antennal nerves and therefore disrupted central olfactory responses (particularly in *D. sechellia*); the cactus spine and screw previously used to immobilise the fly head were also no longer necessary. An antennal shield[68] was placed over the top of the fly head with the hole positioned centrally, fixed with beeswax to the top of the mounting block. Two-component silicon (Kwik-Sil, World Precision Instruments) was mixed with a toothpick and poured into the hole of the antennal shield to seal the gap between the plate and the fly head, avoiding any leakage onto the antennae. As the silicon was left to harden (during 10-15 min), we used blunt forceps to gently remove silicone on the cuticle on top of the head capsule. A drop of adult haemolymph (AHL) saline (108 mM NaCl, 5 mM KCl, 2 mM $CaCl_2$, 8.2 mM $MgCl_2$, 4 mM $NaHCO_3$, 1 mM NaH_2PO_4, 5 mM trehalose, 10 mM sucrose, 5 mM HEPES, pH 7.5) was added into the hole of the antennal shield. Using a blade-splitter, a small rectangular hole was cut in the head cuticle between the eyes and above the antennal plate. Tracheae and glands above the brain were removed with fine forceps. Finally, the brain was rinsed with AHL saline at least 3 times until the antennal lobe appeared clear under the dissection microscope.

Odorant preparation: serial dilutions of odours were prepared in a fume hood. The solvents used for odour dilutions were different between glomeruli, as some glomeruli were extremely responsive to particular solvents: Or85b/VM5d (*2*-heptanone (CAS 110-43-0) in dichloromethane (DCM)), Or22a/DM2 (methyl hexanoate (CAS 106-70-7) in paraffin oil), Or59b/DM4 (methyl butyrate (CAS 623-42-7) in DMSO (for dose-responses) or paraffin oil (for pulsed stimuli)), Or92a/VA2 (*2*,*3*-butanedione (CAS: 431-03-8) in paraffin oil). Or85b/VM5d neurons were especially sensitive to odorant contamination, so we prepared a new set of *2*-heptanone dilutions when solvent responses started to become evident (approximately every two weeks). Furthermore, before preparing *2*-heptanone and methyl butyrate, we washed the odour-containing vial, lid and pipetting tips with DCM and DMSO, respectively. As DCM is highly volatile at room temperature, *2*-heptanone/DCM odour dilutions were stored at 4°C.

Image acquisition: images were acquired using a commercial upright two-photon microscope (Zeiss LSM 710 NLO). An upright Zeiss AxioExaminer Z1 was fitted with a Ti:Sapphire Chameleon Ultra II infrared laser (Coherent) as excitation source. Images were acquired with a 20× water dipping objective (Plan-Apochromat 20× W; NA 1.0), with a resolution of 128×128 pixels (0.8926 pixels μm^{-1}) and a scan speed of 6.30 µs $pixel^{-2}$ (for one-time odour stimulation) or 3.15 s $pixel^{-2}$ (for pulse train odour stimulation). The excitation wavelength was set to 930 nm. The output power was modified according to the baseline fluorescence of GCaMP6f, which varied substantially between animals (except for pharmacology experiments, where laser output was consistent to enable comparison of raw fluorescence across animals). The power was set such that the baseline fluorescence was above the detection limit, and that the maximum fluorescence was below saturation, and thereafter unchanged for a given animal. Emitted light was filtered with a 500-550 nm band-pass filter, and photons were collected by an internal detector. Each measurement consisted of 50 images acquired at 4.17 Hz (for one-time odour stimulation) or 8.34 Hz (for pulse train odour stimulation), with stimulation starting ~5 s after the beginning of the acquisition and lasting for 1 s (for

one-time odour stimulation) or 200 ms followed by a 200 ms interval repeated ten times (for pulse train odour stimulation).

Olfactory stimulation: antennae were stimulated using a custom-made olfactometer[23,68]. In brief, antennae were permanently exposed to air flowing at a rate of 1.5 l min^{-1} by combining a main airstream of humidified room air (0.5 l min^{-1}) and a secondary stream (1 l min^{-1}) of normal room air. Both air streams were generated by vacuum pumps (KNF Neuberger AG) and the flow rate was controlled by two independent rotameters (Analyt). The secondary airstream was guided either through an empty 2 ml syringe or through a 2 ml syringe containing 20 µl of odour or solvent on a small cellulose pad (Kettenbach GmbH) to generate odour pulses. To switch between control air and odour stimulus application, a three-way magnetic valve (The Lee Company, Westbrook, CT) was controlled using Matlab via a VC6 valve controller unit (Harvard Apparatus). The order of the odour stimuli was always from lower to higher concentrations, preceded by the solvent control. Successive odour stimulations were separated by 1 min interval.

Pharmacology: for pharmacological experiments, drugs were diluted in AHL saline to the following final concentrations: 100 µM Picrotoxin (P1675-1G, Sigma-Aldrich, CAS 124-87-8), 50 µM CGP54626 Hydrochloride (1088/10, TOCRIS, CAS 149184-21-4), 200 µM (low dose) or 2 mM (high dose), mecamylamine hydrochloride (M9020-5MG, Sigma-Aldrich, CAS 826-39-1). Drugs were applied to the fly after normal recording ("naïve") by exchanging the AHL saline with drug-diluted saline five times and incubating the preparation for a further 15-40 min before performing further recordings. For mecamylamine application experiments, samples were subsequently washed with AHL saline five times and incubated for 15-40 min, followed by another recording session ("Washed-out"). The lens was meticulously washed with ultrapure water between each session.

Data analyses: data were processed using Fiji and custom written scripts in R. First, the image stacks were passed through the StackReg plugin[69] (transformation: Rigid Body) to correct for movement artefacts. Using Fiji, a circular region of interest (ROI) was set within the glomerulus of interest on the left half of the brain image (except when the signal was weak, in which case the right half of the image was used). The signal intensity averaged across the ROI for each timeframe (hereafter F) was used to calculate the normalised signal $\Delta F/F_0 = \frac{F-F_0}{F_0}$. Here, F_0 (baseline fluorescence) was calculated as the average F during frames 16-19 (1 s before olfactory stimulus onset). The peak $\Delta F/F_0$ value (which represents the odour response intensity) was calculated as the maximum $\Delta F/F_0$ value during frames 20-23 (1 s during olfactory stimulation). We noticed that the maximum $\Delta F/F_0$ value itself was often very different between species/genotypes, presumably due to different expression levels of GcaMP6f. This should, in theory, not affect the normalised $\Delta F/F_0$ value, but we did observe a saturation of neuronal responses above a certain odour concentration, even if the peak $\Delta F/F_0$ value was lower than in other species/genotypes. To compare the dose-response effect between species and genotypes, we further introduced a normalisation step. Normalised peak response for each odour dilution ($\tilde{p}$) was calculated as follows: $\tilde{p} = \frac{p-p_0}{p_{max}-p_0}$. Here, p denotes peak $\Delta F/F_0$ value of a given dilution (median value across animals), p_{max} denotes maximum p among all the dilutions, and p_0 denotes p from the minimum response. Thus, the normalised peak response $\tilde{p}$ takes a value between 0 and 1, where 0 means absence of odour responses and 1 means saturation. This step allowed us to compare the dose-response curve based on the

relative response within species and genotypes, regardless of the absolute $\Delta F/F_0$ value. Dynamic ranges were quantified as $p_{max} - p_0$ in each animal rather than taking the median values across animals.

Photoactivation

Animal preparation: flies of the appropriate genotype (see figure legends) were collected and reared in standard culturing medium (with an addition of blue food with noni juice for *D. sechellia*). Female flies aged 6-9 days after eclosion were used for the experiments. Flies were prepared in the same way as for the two-photon calcium imaging.

Photoconversion and image acquisition: the hardware setup was the same as in two-photon calcium imaging. Glomerular location was identified by a brief 930 nm scanning of the entire antennal lobe. An oval ROI was placed inside the glomerulus of interest, where the ROI was made small enough so that the movement during photoconversion did not result in non-specific labelling. Where non-specific labelling was observed after imaging, data were excluded from further analyses. During photoconversion, the resolution was set to 512×512 pixels (3.5704 pixels μm^{-1}) and the scan speed to 0.79 µs $pixel^{-2}$. Excitation wavelength was shifted to 760-780 nm with a power output of 5-15%. Photoconversion was performed by scanning inside the ROI repeatedly (in a single z-plane) for ~15 min. Around 5 min after the beginning of the session, a brief 930 nm scan was performed to check the conversion efficacy and specificity. If photoconversion was weak at this point, we increased the power output. After photoconversion, the sample was placed in a humidified chamber for 30-60 min to allow the diffusion of C3PA-GFP. Finally, the fly's body was removed to reduce motion artefacts and the sample placed again under the two-photon microscope. For imaging, the resolution was set to 1024×1024 pixels (2.3803 pixels μm^{-1}) and the scan speed to 1.58-3.15 µs $pixel^{-2}$. The excitation wavelength was shifted back to 930 nm with the power output adjusted to enable visualisation of neurite processes. Z-stack images were obtained with a spacing of 1 µm.

Electrophysiology

Single sensillum electrophysiological recordings were performed essentially as previously described[23], using 5-7 day-old female flies, which were grown on standard medium mixed with 0.2 mM all-*trans* retinal[55], with an addition of 10% noni juice for *D. sechellia*. Optogenetic stimulation was performed by exposing one antenna with increasing light intensities via an optic fibre as described in the **Tethered fly assay** section (see below). In SPARC2 experiments, ab3 sensilla were identified by location and the use of diagnostic odours. For the data shown in **Fig. 6c**, light-sensitive (experimental group) and non-responding neurons (control) were analysed. Corrected responses were calculated as the number of spikes in a 0.5 s window from the beginning of illumination, subtracting the number of spontaneous spikes in a 0.5 s window 2 s prior to illumination, and multiplying by 2 to obtain spikes s^{-1}. Recordings were performed on a maximum of three sensilla per fly. Exact *n* values and mean spike counts for all experiments are provided in **Extended Data Table 1**.

Tethered fly assay

Assay: The assay was built on a solid breadboard (Thorlabs). The fly tether was made by inserting and gluing an insect pin (Austerlitz, φ = 0.20 mm) to a 200 µl

pipette tip, which was mounted on a magnetic articulated stand (NOGA). Two microphones (lavalier microphone, RODE) were placed ~1 mm from the tip of the wings of the fly, connected to a USB audio interface (Rubix 22, Roland) via TRS-XLR adaptors (VXLR, RODE). The audio interface was connected to Raspberry Pi computer (Raspberry Pi 4 1.5 GHz Quad-Core, 8GB RAM), which ran the real-time feedback programme (described below) based on the acoustic inputs. The output of the feedback system was SPI-connected to a DotStar LED strip (1528-2488-ND, Adafruit; cut to 30 LEDs), which was bent to make a U-shape that covers >180° of the fly's horizontal view. The spatial frequency of the visual guide was set to ~0.036 mm^{-1} (one illumination in every 4 LEDs). The PTFE odour port was placed at ~30° from the right side, facing the fly ~1 cm apart to provide unilateral olfactory stimulation. The suction port was placed at the opposite end of the odour port, ~2 cm from the fly, to stabilise the odour plume. For optogenetic experiments, single antennae were illuminated using a custom-made optic fibre (G050UGA, Tubing: FT030, End 1: SMA, End 2: Flat Cleave, Thorlabs), of which the cleaved end was placed ~0.1 mm next to the antenna. The position of the optic fibre was adjusted using a 3D microcontroller (UM-3C, Narishige), and was monitored by a Pi NoIR camera prior to each session. The fibre was connected to 660 nm fibre-coupled LED (M660FP1, Thorlabs) via a compact LED driver (LEDD1B, Thorlabs).

Real-time feedback system: the feedback system was run by a custom Python script. The recording was performed binocularly from each wing at the rate of 44,100 Hz. Each session (20 s) was divided into 0.1 s intervals. The raw wing beat amplitude ($r_{[L]}$, $r_{[R]}$) was defined by the difference between the maximum and minimum sound amplitude within each interval. The raw wing beat was filtered by calculating the median across the three most recent intervals ($r_{f[L]}$, $r_{f[R]}$). Prior to the experimental session, each fly was calibrated by a "mock" session, where the visual guide was fixed and the flies beat their wings to obtain the mean ($\mu_{mock[L]}$, $\mu_{mock[R]}$) and SD ($\sigma_{mock[L]}$, $\sigma_{mock[R]}$) of the filtered wing beat amplitude as well as the SD of the difference between the left and right wing beat amplitudes ($\sigma_{mock[L-R]}$). In the experimental sessions, the filtered raw wing beat amplitudes were standardized using the mean and SD obtained in the mock session ($z_{[L]}=\frac{r_{f[L]}-\mu_{mock[L]}}{\sigma_{mock[L]}}$, $z_{[R]}=\frac{r_{f[R]}-\mu_{mock[R]}}{\sigma_{mock[R]}}$). The ΔWBA was defined by $z_{[L]}$-$z_{[R]}$ as a readout of turning behaviour. In each interval, the visual guide was rotated counter-clockwise (by shifting by one adjacent LEDs) if $\Delta WBA > 3\sigma_{mock[L-R]}$ and clockwise if clockwise if $\Delta WBA < 3\sigma_{mock[L-R]}$. The $z_{[L]}$, $z_{[R]}$ values were saved after each session for downstream analyses.

Animal preparation: flies of the appropriate genotype were collected (females and males co-housed). For odour response experiments, females 5-9 days after eclosion were used. For experiments with apple cider vinegar (Migros, M-Classic), flies were starved for 5-7 h. Fly rearing for optogenetic experiments is as described in **Electrophysiology** section above. Flies were reared in retinal-containing food for 6-7 days, and females 6-8 days after eclosion were used.

Sample preparation: flies were anesthetised on ice and attached to the fly tether using blue-curing glue. For optogenetic experiments, fly forelegs were cut to prevent the flies from perturbing the optic fibre. The fly tether was mounted on a magnetic stand, and the fly positioned centrally and equidistantly between the microphones. For optogenetic experiments, videos were taken during positioning

of optic fibres to confirm that the illumination (at intensity 3, as described below) was confined to one antenna. For SPARC2-D-TNT-HA experiments, as transgene expression was not detected in a fraction of flies for unknown reasons, post-hoc staining was performed with HA tag (in the antennae and/or the brain) and selected the animals with positive labelling in OSN cell bodies and/or axon termini for downstream analysis.

Olfactory stimulation: odorants (5 ml) were contained in 15 ml Falcon tubes with two syringe needles pierced at the lid. Tubes were connected to the syringe needle outlets to provide odour stimulation from the headspace. The flies were permanently exposed to water vapour at a rate of 0.5 l min^{-1}. A three-way magnetic valve (The Lee Company, Westbrook, CT) was controlled using MATLAB via a VC6 valve controller unit (Harvard Apparatus) to switch the airflow from water to odorants. Either 10 consecutive pulses of 500 ms with 500 ms intervals or a single 10 s pulse were used as olfactory stimuli. Noni juice was diluted in water while benzaldehyde was diluted in paraffin oil.

Optogenetic stimulation: LED illumination was controlled by sending TTL signals to the LED driver. 10 consecutive pulses of 500 ms with 500 ms intervals were used. The intensity of the illumination was modified by the dial on the LED driver, which could be modulated from intensity 0 (mock-stimulation) to 6 (maximum). Intensity 4 was used for stimulation in most experiments, except for low-intensity stimulation (intensity 2) to match the OSN spike rate with SPARC2-D-CsChrimson experiments. For SPARC2-D-CsChrimson experiments, we noticed that the animals either displayed expression of CsChrimson in a small proportion of Or22a OSNs or had no expression at all. The reason for this heterogeneity is unknown but we performed post-hoc imaging of the antenna to analyse data from animals displaying CsChrimson expression.

Data analyses: data were analysed with custom programmes in R. The quantification was performed in 1 s time windows corresponding to pre-stimulus baseline (4-5 s) and individual odour-pulse responses (1st peak: 5-6 s, 2nd peak: 6-7 s, …, 10th peak: 14-15 s). For quantification of *ΔWBA* in each time window, the *ΔWBA* values above the 50% quantile were used, to avoid picking outliers and non-attractive epochs.

Wind tunnel assay

Free flight tracking was performed in a 1 m × 0.5 m × 0.5 m wind tunnel housed in a temperature- and humidity-controlled room (22°C, 60% RH). The wind tunnel floor was illuminated by blue LEDs underneath a light-diffusive film that lined the tunnel floor, overlaid with a grid of infrared transmissible film; this grid formed a checkerboard-like lattice on the floor to provide flies with ventral optic flow information. The walls of the wind tunnel tapered from blue on the floor to black along the ceiling. Along the top of the wind tunnel were two white LED strips, to provide sufficient orange light for *Drosophila* photoreceptor re-isomerisation[70]. Total illumination in the wind tunnel was 452 Lux as measured from the wind tunnel centre (LX1330B light sensor, Dr. Meter).

Fly tracking was performed with 12 synchronised Basler acA720 cameras (Basler AG, Ahrensburg) recording at 100 Hz (**Extended Data Fig. 8a**). The walls and floor of the wind tunnel were homogenously illuminated with arrays of infrared LEDs, and cameras were outfitted with IR pass filters to track flies using only infrared wavelengths. Tracking was performed using Braid software[45]. Odour plumes were introduced in the wind tunnel through an odour port constructed from

a 20 cm tall rigid acrylic tube that had a 90° bend towards the top so that its outward facing opening was parallel to the wind (**Extended Data Fig. 8b**). The odour port was installed on the far upwind end of the tunnel and its open face was covered by an aluminium mesh to prevent flies from entering the odour plumbing. Plumes were generated by fluxing air through a mass flow controller (Alicat Scientific, Tuscon) at 200 cm^3 min^{-1}. The air was then bubbled into 150 ml noni juice at the bottom of a jar and subsequently through tubing leading to the odour port in the wind tunnel.

For wind tunnel experiments we used 3-7 day old female flies. 15 animals were collected in the morning and starved by placing them into a tube containing a moist Kimwipe for 8 h. The flies were placed in the wind tunnel with a 40 cm s^{-1} air flow and tracking initiated. Flies were allowed to fly about the wind tunnel volume for 16-20 h before the recording was terminated the following day.

Data analyses: data were analysed using Python (v3.11). We first filtered out all trajectories from flies that were walking on the tunnel floor or ceiling to focus analyses on flying animals. Our trajectory inclusion criteria were: (i) >500 ms long; (ii) >10 cm in the horizontal plane; (iii) a median position of >5 cm away from any of the tunnel walls; (iv) passed within a 10 cm radius of where the odour plume was aligned in the y-z plane (this excluded flies that simply transited the wind tunnel along the ceiling, far away from the plume).

To analyse the radial distance from the plume, we binned the point cloud generated by all trajectories into 5 cm thick cross-sections, beginning 5 cm downwind of the plume source. We then pared the point cloud further to 10 cm above and below the plume ($0.1<z<0.3$) to isolate trajectory portions that were most likely interacting with the plume (**Extended Data Fig. 8e**), for analyses with or without this restriction. Based on the occupancy maps of trajectories in space from both wild-type *D. sechellia* and *D. melanogaster*, we assumed that the plume sank by 5 cm from the odour nozzle to the end of the wind tunnel and calculated the plume centreline using this mode (for comparisons of straight versus sloped plume models see **Extended Data Fig. 8e-f**). From each of the segmented point clouds we report the mean as the mean of all points, independent of trajectories that contributed to them. Results were robust to whether or not we instead analysed each trajectory as an independent sample. For course direction distributions, we included only the point cloud within a 3 cm radius of our estimated plume volume, and calculated the kernel densities of the course direction of all points within the estimated plume volume. We further divided the data to the point cloud in the downwind half of the wind tunnel, where trajectories typically began, and the upwind half of the wind tunnel, terminating 5 cm downwind of the plume's origin.

Statistics and reproducibility

Data were analysed and plotted using Excel, R (v3.2.3; R Foundation for Statistical Computing, Vienna, Austria, 2005; R-project-org) and Python (v3.11).

Data, code and biological material availability

All relevant data supporting the findings of this study are included as source data or available from the corresponding authors upon request. Code used for analyses and all unique biological materials generated in this study are available from the corresponding authors upon request.

Figure Legends

Figure 1: Selective expansion of noni-sensing olfactory sensory neuron populations is a complex developmental trait.

a, *D. sechellia* specialises on noni fruit compared to the generalists *D. simulans* and *D. melanogaster*. Ma, million years ago.

b, Left top, schematic of the drosophilid third antennal segment covered by sensilla of diverse morphological classes and housing the sacculus. Left bottom, antennal basiconic 3 (ab3) sensilla house two neurons expressing the odorant receptor Or22a (and Or22b in *D. melanogaster* and *D. simulans*; this paralog is lost in *D. sechellia*) in the A neuron (hereafter, "Or22a neuron") and Or85c/b in the B neuron (both paralogs are co-expressed; hereafter, "Or85b neuron"). Right, antennal *Or22a/(b)* and *Or85b* expression in *D. sechellia* (*Drosophila* Species Stock Center (DSSC) 14021-0248.07, females) and *D. simulans* (DSSC 14021-0251.004, females). Scale bar, 25 µm. In addition to ab3 sensilla (dashed line), Or85b is expressed in ~10 spatially-segregated OSNs in ab6 sensilla in all three species (**Extended Data Fig. 1b**).

c, Comparison of olfactory sensilla numbers in *D. melanogaster* (*Canton-S*), *D. simulans* (DSSC 14021-0251.004) and *D. sechellia* (DSSC 14021-0248.07) (all females) as assessed by RNA FISH using a diagnostic *Or* probe (grey background) for each sensillum class. Data for Ir-expressing coeloconic sensilla and sacculus chamber 3 (sac3) neurons are from[22]; Ir75d neurons common to ac1, ac2 and ac4 sensilla are not shown. Box plots in this and all following panels show the median and first and third quartiles of the data, overlaid with individual data points. Wilcoxon signed-rank test with comparison to *D. melanogaster*. NS, not significant ($P > 0.05$); *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$.

d, Reciprocal hemizygosity test of the *Or22a/(b)* and *Or85c/b* loci for contributions to species-specific OSN numbers in *D. simulans*/*D. sechellia* hybrids. Using RNA FISH to quantify numbers of *Or22a/(b)* and *Or85b* expressing OSNs in the indicated genotypes (*Dsec* - = *DsecOr22a*^{RFP} or *DsecOr85b*^{GFP}, *Dsec* + = *D. sechellia.07* wild-type, *Dsim* - = *DsimOr22a/b*^{RFP} or *DsimOr85b*^{GFP}, *Dsim* + = *D. simulans.04* wild-type), no allele-specific expression differences were observed at either loci. Wilcoxon signed-rank test with comparison to wild-type hybrids. NS, not significant ($P > 0.05$).

e, Number of GFP-expressing neurons in antennae of *DsecOr85b*^{GFP}, *DsimOr85b*^{GFP} and F1 hybrid males and females, and in the F2 progeny of the backcrosses of F1 hybrid females to either parental strain. The black line indicates the mean cell number.

f, Logarithm of odds (LOD) score across all four chromosomes for loci impacting Or85b neuron numbers based on the phenotypic data in **e**. Dashed horizontal lines mark $P = 0.05$; non-dashed horizontal lines mark $P = 0.01$.

g, Effect sizes for the significant QTL intervals on chromosome 3 and X in the *D. simulans* backcross. A, *D. simulans* allele; B, *D. sechellia* allele. A candidate gene, *lozenge* – encoding an AML-1/Runt family transcription factor involved in sensilla specification development[71] – that is located directly below the highest score of our trait map on the X chromosome, did not affect OSN numbers (**Extended Data Fig. 2e-i**).

Figure 2: Increased sensory and synaptic pooling in noni-sensing glomeruli.
a, Schematic of OSN-PN connectivity in the antennal lobe. Or22a OSNs (orange) and Or85b OSNs (blue) have cell bodies in the antenna and axons projecting to the DM2 and VM5d glomerulus, respectively. The soma of second-order PNs (green) are located in three distinct clusters around the antennal lobe (ad, anterodorsal; l, lateral; v, ventral); these neurons synapse with OSNs (the majority constrained to a single glomerulus) and send axonal projections to higher olfactory centres.
b, Transgenic labelling of PNs in the *D. sechellia* antennal lobe using the *VT033006-Gal4* or *VT033008-Gal4* drivers to express *UAS-GcaMP6f* (here used simply as a fluorescent reporter). Immunofluorescence on whole-mount brains was performed with antibodies against GFP (detecting GcaMP6f) and nc82 (labelling the synaptic protein Bruchpilot[72]). The VM5d glomerulus is demarcated by a white line in the *VT033008-Gal4* line. Scale bar, 25 µm.
c, Left, representative image of VM5d PNs labelled by photo-activatable GFP (PA-GFP) in *D. melanogaster* and *D. sechellia*. Genotypes: *D. melanogaster UAS-C3PA-GFP/+;UAS-C3PA-GFP/VT033008-Gal4* (for VM5d PNs) or *UAS-C3PA-GFP/+;UAS-C3PA-GFP/VT033006-Gal4* (for DM2 PNs); *D. sechellia UAS-C3PA-GFP/VT033008-Gal4* (for VM5d PNs) or *UAS-C3PA-GFP/VT033006-Gal4* (for DM2 PNs). Arrows indicate the PN cell bodies; faint background GFP signal in other soma are irrelevant neuron types. The antennal lobe (AL) is demarcated by a dashed line. Scale bar, 25 µm. Right, quantification of Or22a and Or85c/b PN number innervating the DM2 and VM5d glomeruli, respectively, by labelling with PA-GFP (using two different transgenic driver lines for VM5d PNs) in *D. sechellia* and *D. melanogaster*. Mann-Whitney *U*-test, NS, not significant ($P > 0.05$).
d, Visualisation of post-synaptic puncta in VM5d, DM2 and DM6 (innervated by Or67a OSNs) PNs. Top left, post-synaptic sites are labelled by Dα7-GFP expression. Upper panels, labelling of post-synaptic puncta in *D. melanogaster* DM2 and VM5d glomeruli. Lower panels, labelling of post-synaptic puncta in *D. sechellia* DM2 and VM5d glomeruli. Scale bar, 20 µm (whole antennal lobe), 5 µm individual glomeruli.
e, Left, quantification of the volumes of three glomeruli in *D. sechellia* and *D. melanogaster* (females). Wilcoxon signed-rank test. $^{**}P < 0.005$; $^{***}P < 0.001$. Right, quantification of the number of post-synaptic puncta in the same three glomeruli in both species. Wilcoxon signed-rank test. $^{**}P < 0.005$; $^{***}P < 0.001$.

Figure 3: Sustained representation of noni odour stimuli in PNs of *D. sechellia*.
a-b, Dose-dependent, odour-evoked calcium responses in Or85b/VM5d (**a**) and Or22a/DM2 (**b**) OSN axon termini and PN dendrites in the antennal lobe of *D. melanogaster* and *D. sechellia* (schematised on the left), reported as normalised GCaMP6f fluorescence changes. Plots are based on the data in **Extended Data Fig. 3**. EC_{50} values [Log] are as follows: Or85b OSNs: -6.50 (*Dmel*), -6.51 (*Dsec*); VM5d PNs: -7.82 (*Dmel*), -7.87 (*Dsec*); Or22a OSNs: -7.42 (*Dmel*), -8.23 (*Dsec*); DM2 PNs: -7.97 (*Dmel*), -9.61 (*Dsec*). Genotypes are as follows. OSN calcium imaging: *D. melanogaster UAS-GCaMP6f/Orco-Gal4*,*UAS-GCaMP6f*, *D. sechellia UAS-GCaMP6f/UAS-GCaMP6f;;+/DsecOrco^{Gal4}*. PN calcium imaging: *D. melanogaster UAS-GCaMP6f/+;+/VT033008-Gal4* (for VM5d PNs), *D. melanogaster UAS-GCaMP6f/+;+/VT033006-Gal4* (for DM2 PNs), *D. sechellia*

UAS-GCaMP6f/VT033008-Gal4 (for VM5d PNs), *UAS-GCaMP6f/VT033006-Gal4* (for DM2 PNs).

c-e, Odour response reliability of VM5d PNs. Calcium responses of VM5d PNs in response to repeated stimulation with *2*-heptanone (concentration (Log) indicated on the figure) in *D. melanogaster* (**c**) and *D. sechellia* (**d**). Left, quantification of peak $\Delta F/F_0$ from eight trials of stimulation. Dunnett's test, compared to control (Trial 1). NS ($P > 0.05$). $n = 8$ animals each. Right, time courses of responses in trial 1 and 8 shown as mean ± SEM $\Delta F/F_0$ The odour stimulus (1 s) is shown with a black bar. **e**, Quantification of mean, standard deviation and coefficient of variation of peak $\Delta F/F_0$ across the eight stimulation trials. Welch's *t*-test. NS ($P > 0.05$).

f, Responses of Or85b OSNs to pulsed odour stimuli (ten 200 ms pulses, each separated by 200 ms, as indicated by the black bars). For both species, left panels show the time course (mean ± SEM $\Delta F/F_0$)) and right panels show the quantification of $\Delta F/F_0$ peak to the 1st and 10th stimulation. Paired *t*-test. ** $P < 0.01$, * $P < 0.05$. $n = 8$ animals each.

g-h, Pulsed odour responses of VM5d PNs (**g**) and DM2 PNs (**h**). Paired *t*-test, ** $P < 0.01$. $n = 8$ animals each.

i-j, Pulsed odour responses of VA2 (Or92a) and DM4 (Or59b) PNs (two control pathways where the number of cognate OSNs is conserved between species (**Fig. 1c**)). Paired *t*-test, *** $P < 0.001$; ** $P < 0.01$. $n = 6$ animals each. Dose response data for these neurons are provided in **Extended Data Fig. 5**. Genotypes are as for DM2 imaging in **a**.

Figure 4: Mechanisms of sustained PN responses in *D. sechellia*.

a, Odour pulse responses of VM5d PNs following application of a GABA antagonist. PN responses in normal AHL saline (left) or containing 100 µM picrotoxin + 50 µM CGP54626 (right). Paired *t*-test, *** $P < 0.001$, NS $P > 0.05$. $n = 8$ animals each. Genotypes are indicated in **Fig. 3a** legend.

b, Odour pulse responses of VM5d PNs following application of low doses (200 µM) of mecamylamine (nAChR antagonist) to weakly block cholinergic inputs. *D. melanogaster* and *D. sechellia* PN responses in normal AHL saline, mecamylamine, and AHL saline wash-out. Paired *t*-test, *** $P < 0.001$, * $P < 0.05$, NS $P > 0.05$. $n = 7$ animals each.

c, Odour pulse responses of *D. sechellia* VM5d PNs in intact (top) and right antenna-ablated (bottom) animals, in which the OSN input is halved. Paired *t*-test, * $P < 0.05$, NS $P > 0.05$. $n = 7$ each.

d, Comparison of peak $\Delta F/F_0$ between OSN axon termini and PN dendrites in Or85b/VM5d and Or22a/DM2 pathways. The identity lines are overlaid. Plots are based on the data in **Extended Data Fig. 3**.

e, Comparison of dynamic ranges (obtained from dose-response experiments) of the indicated PN populations between *D. melanogaster* and *D. sechellia.* Welch's *t*-test, *** $P < 0.001$; ** $P < 0.05$, NS $P > 0.05$. Dose response data for these neurons are provided in **Extended Data Figs. 3** and **5**.

Figure 5: Persistent behavioural tracking of noni odours in *D. sechellia*.

a, Schematic of the tethered fly behavioural assay. *ΔWBA*: left-right difference of standardised wing beat amplitudes (see **Methods** for details), TTL: Transistor–transistor logic.

b, Odour-tracking behaviour towards noni juice and control stimuli (H_2O) in wild-type *D. sechellia* (DSSC 14021-0248.07) and *D. melanogaster* (CS) flies. Left

panels indicate the time course of *ΔWBA* (mean ± SEM) where black bars indicate the timing of odour stimulation (ten 500 ms pulses with 500 ms intervals). Right panels display the quantification in 1 s time windows immediately prior to stimulus onset ("pre") and thereafter corresponding to individual stimulus pulses ("1-10"). Paired *t*-test *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$, otherwise $P > 0.05$. $n = 30$ animals each.

c, Odour-tracking behaviour towards noni juice in *D. sechellia Or* and *Ir* mutants. Paired *t*-test, *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$, otherwise $P > 0.05$. $n = 30$ animals each.

d, Left, example trajectories (black lines) in the x-y plane of *D. sechellia* (DSSC 14021-0248.07), *D. melanogaster* (a hybrid *Heisenberg-Canton-S* (*HCS*); our *CS* strain exhibited poor flight performance in this assay) and *D. sechellia Or22a*^{RFP} mutants flying in the presence of a noni plume (origin at the orange dot). Right, occupancy heat maps of trajectories that came at least once within 10 cm of the plume centreline for *D. melanogaster* (n = 1346 trajectories, 4 recording replicates, 60 flies), *D. sechellia* wild-type (n = 835 trajectories, 7 recording replicates, 105 flies) and *D. sechellia Or22a*^{RFP} mutants (n = 509 trajectories, 6 recording replicates, 90 flies).

e, Annotated view of the *D. sechellia* trajectories (from **d**) illustrating the data analyses performed in **f,g**. Based upon the trajectory distribution, we inferred that the noni juice plume sank by ~5 cm from the odour nozzle to the end of the tracking zone in the wind tunnel; this is likely due to the odour-laden air's higher water content (and so higher density) than the surrounding air. We therefore estimated the plume centre as a line connecting the nozzle and a point 5 cm lower in the z-axis at the end of the wind tunnel. Our results are qualitatively robust whether or not we account for plume sinking (**Extended Data Fig. 8d-f**).

f, Mean radial distance of the point cloud from the plume centreline for the trajectories in **d**. Data were binned into 5 cm y-z plane cross-sections starting 5 cm downwind from the plume origin, and restricted to 10 cm altitude above or below the estimated plume model. Non-parametric bootstrapped comparison of medians $P < 0.001$.

g, Kernel density of the course direction distribution of points within a 3 cm radius of the plume centreline (orange circle on cross-section in **e**), further parsed into the point cloud in the downwind or upwind halves of the wind tunnel (see **e**). Downwind half kernels: *D. melanogaster* (20,912 points from 511 unique trajectories), *D. sechellia* wild-type (15,414 points from 367 trajectories), *D. sechellia Or22a*^{RFP} (3,244 points from 164 unique trajectories). Upwind half kernels: *D. melanogaster* (80,594 points from 615 unique trajectories), *D. sechellia* wild-type (136,827 points from 501 unique trajectories), *D. sechellia Or22a*^{RFP} (40,560 points from 286 unique trajectories).

Figure 6: Behavioural significance of OSN number increase.

a, Optogenetic stimulation of Or22a OSNs in *D. melanogaster* (top) and in *D. sechellia* (bottom). Left, expression of CsChrimson in the antenna detected by expression of the Venus tag. Scale bar, 20 µm. Middle, single-sensillum recordings of Or22a OSNs in response to optogenetic stimulation of CsChrimson-expressing and control sensilla. The red line links the mean neuronal response at each light intensity, overlaid with individual data points. The black frame indicates the light intensity used for behavioural experiments. n = 5-10 (exact numbers are listed in **Extended Data Table 1**), unpaired Student's *t*-test, *** $P < 0.001$; * $P < 0.05$,

otherwise $P > 0.05$. Right, behavioural responses of the same genotypes in response to red light stimulation (ten 500 ms pulses with 500 ms intervals, indicated by the red bars). Paired *t*-test, ** $P < 0.01$; * $P < 0.05$, otherwise $P > 0.05$. $n = 29$ (*D. melanogaster*) and 30 (*D. sechellia*) animals. Genotypes: *D. melanogaster w;UAS-CsChrimson-Venus/+* (control), *w;UAS-CsChrimson-Venus/Or22a-Gal4* (experimental), *D. sechellia w;;UAS-CsChrimson-Venus/+* (control), *w;Or22a^{Gal4}/+;UAS-CsChrimson-Venus/+* (experimental).

b, Behavioural responses of *D. sechellia* upon optogenetic stimulation of Or22a OSNs (top) and to noni odour stimulation (middle), in the same animals. Bottom, comparison of *ΔWBA* between light and odour responses. Paired *t*-test, *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$, otherwise $P > 0.05$. $n = 27$ animals each. Genotype as in **a**.

c, Sparse activation of *D. sechellia* Or22a OSNs. Left, expression of CsChrimson in an antenna of *D. sechellia* expressing *UAS-SPARC2-D-CsChrimson-Venus* in Or22a OSNs. Fluorescent labelling was sparser than in *UAS-CsChrimson-Venus* expressing animals (**Fig. 6a**) but the dense packing of membrane-labelled neurons prevented quantification. Experiments in *D. melanogaster* (**Extended Data Fig. 10b**) and with the *UAS-SPARC2-D-TNT-HA* transgene (below) support expression in 50% of Or22a OSNs with this SPARC version. Scale bar, 20 µm. Middle, single-sensillum recordings of Or22a OSNs in response to optogenetic stimulation of CsChrimson-expressing sensilla. Ab3 sensilla were identified by diagnostic odours. Light sensitive neurons (experimental group) and non-responding neurons (control) are shown. n = 8-9 (exact numbers are listed in **Extended Data Table 1**), unpaired *t*-test, *** $P < 0.001$; * $P < 0.05$, otherwise $P > 0.05$. Right, *D. sechellia* behaviour upon optogenetic activation of about half of their Or22a expressing neurons. Paired *t*-test, *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$. $n = 26$ animals. Genotypes: *D. sechellia w;Or22a^{Gal4}/UAS-SPARC2-D-CsChrimson-Venus;;nSyb-ΦC31/+*.

d, Sparse inhibition of *D. sechellia* Or22a OSNs. Left, α-HA staining in an antenna of *D. sechellia* (females) expressing *UAS-SPARC2-D-TNT-HA* in Or22a OSNs. Scale bar, 20 µm. Middle, *D. sechellia* odour-tracking behaviour towards noni juice of flies in effector control (top), driver control (middle), or in experimental animals with blocked synaptic transmission in approximately half of their Or22a neurons (bottom). Paired *t*-test, *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$. $n = 34$ animals each. Genotypes: *D. sechellia w; UAS-SPARC2-D-TNT-HA-GeCO/+;;+/+* (effector control), *D. sechellia w;Or22a^{Gal4}/+;;nSyb-ΦC31/+* (driver control), *D. sechellia w;Or22a^{Gal4}/UAS-SPARC2-D-TNT-HA-GeCO;;nSyb-ΦC31/+* (experimental group).

e, Summary of the current study. Top, schematic of the complementary effects of olfactory receptor sensitisation (e.g. Or22a and Ir75b pathways[22-24]) and OSN population increase (e.g. Or22a, Or85b (and putatively also Ir75b) pathways) on odour detection; one possible model for the latter is proposed (see **Discussion**) but several mechanisms might underlie the observed physiological properties. Bottom, these olfactory system adaptations are likely to synergise to promote sensitive and persistent long-range odour tracking toward the noni host fruit by *D. sechellia*, but not *D. melanogaster*.

Extended Data Figure Legends

Extended Data Figure 1: Investigation of potential mechanisms underlying ab3 sensilla expansion.

a, Number of *Or22a/(b)* RNA expressing OSNs in the antenna of six *D. sechellia*, *D. simulans* and *D. melanogaster* strains. For strain details see **Extended Data Table 2**. Wilcoxon signed-rank test, *P* values adjusted for multiple comparisons using the Benjamini and Hochberg method. Comparisons to *Dsec07* (genetic background of transgenic lines) are shown. NS, not significant ($P > 0.05$); $^{**}P < 0.01$; $^{***}P < 0.001$.

b, Top, immunofluorescence for GFP and RNA FISH for *Or85b* on whole-mount antennae from *D. melanogaster Or49b-GFP* animals. Arrowheads indicate paired neurons. Or85b neurons are housed in ab3 and ab6 sensilla (together with Or49b neurons), but only the ab3 population is expanded in *D. sechellia* (**Fig. 1c**). Scale bar, 25 µm.

c, Comparison of the number of *Or22a* RNA-expressing OSNs in the antenna of *D. sechellia* raised on (left) and without (right) noni supplement. Scale bar, 25 µm. Quantification to the right. Wilcoxon rank-sum test. NS, $P > 0.05$.

d, Top left, schematic of the ab2 sensillum housing Or59b and Or85a neurons. Top right, RNA FISH for *Or59b* on whole-mount antennae from *D. melanogaster, D. simulans and D. sechellia* wild-type animals (females). Scale bar, 25 µm.

e, Top, schematic of developmental transitions from larval antennal disc to adult antenna. Schematic of the larval antennal disc, within which concentric arcs of sensory organ progenitors (SOPs) are specified, each of which gives rise to a sensillum. Different SOP types have a stereotyped developmental origin in a given arc (adapted from[28]). Arrows indicate the change in relative population size in *D. sechellia* compared to *D. melanogaster*. No obvious relationship between ab3 number increase and compensatory reduction in sensilla derived from SOPs in the same or neighbouring arcs is evident.

f, Representative pictures of the reciprocal hemizygosity test at the *Or22a/b* (top) and *Or85c/b* (bottom) loci using RNA FISH results shown in **Fig. 1d**. Schematics on top indicate expression from the respective alleles.

Extended Data Figure 2: Genetic analysis of OSN cell number expansion.

a, Left, schematics depicting the introduction of a nuclear-localised GFP reporter (GFPnls) at the *Or85b* locus of *D. sechellia* and *D. simulans* via CRISPR/Cas9 genome engineering. Right, GFP signal in antennae of *DsecOr85b*^{GFP} and *DsimOr85b*^{GFP} animals. Scale bar, 25 µm.

b, Immunofluorescence for GFP and *Or22a* RNA FISH on whole-mount antennae from *DsecOr85b*^{GFP} animals. Arrowheads indicate neighbouring neurons. Scale bar, 25 µm.

c, Introgression of chromosomal fragments marked with a transgenic RFP marker (dashed line) from *D. sechellia* into *D. simulans* spanning varying extents of the QTL peak on chromosome 3.

d, Left, number of GFP-expressing neurons in F2 backcrosses of the *D. sechellia* RFP transgenic line comparing RFP positive and negative siblings (females only). Right, number of GFP-expressing neurons in the five *D. sechellia* introgression lines depicted in (**a**) comparing RFP positive and negative siblings. $n = 9–41$ female flies (exact numbers listed in the figure). Wilcoxon signed-rank test. NS, not significant ($P > 0.05$); $^{*}P < 0.05$; $^{***}P < 0.001$.

e, Left, location of the *lozenge* (*lz*) gene (dashed line) relative to the QTL peaks detected on the X chromosome. Right, schematics depicting the *lozenge* gene organisation and the structure of mutant alleles in both *D. sechellia* and *D. simulans*. The fluorescent marker was integrated into the first coding exon.
f, Comparison of antennal morphology in wild-type and *lz* mutant *D. sechellia* and *D. simulans*. In both species, loss of *lz* results in a lack of basiconic sensilla (white arrowheads) compared to wild-type, similar to *D. melanogaster lz* mutants[71]. Scale bar, 25 µm; inset scale bar, 5 µm.
g, Number of GFP-expressing neurons in $DsimlZ^{RFP}$ heterozygote mutant and wild-type siblings (females only). Wilcoxon signed-rank test. $^{**}P < 0.01$.
h, Number of GFP-expressing neurons in $DseclZ^{RFP}$ heterozygote mutant and wild-type siblings (females only). Wilcoxon signed-rank test. $^{***}P < 0.001$.
i, Number of GFP-expressing neurons in *trans*-heterozygote hybrid siblings (females only) carrying either a $DseclZ^{RFP}$ or $DsimlZ^{RFP}$ allele. Wilcoxon signed-rank test. NS, not significant ($P > 0.05$).
j, Number of Ir75b neurons in wild-type *D. sechellia* (DSSC 14021-0248.25) and *D. simulans* (DSSC 14021-0251.195) (mixed genders) and respective F2 progeny derived from backcrosses of F1 hybrid females to either parental strain (separated by gender). The black line indicates the average cell number count.
k, Logarithm of odds (LOD) score across all four chromosomes for loci impacting Ir75b neuron numbers based on phenotyping data shown in **j**. Dashed horizontal lines mark $P = 0.05$; non-dashed horizontal lines mark $P = 0.01$.

Extended Data Figure 3: Dose-response odour responses of OSNs and PNs in Or85b and Or22a pathways.
a-b, Representative odour-evoked calcium responses in the axon termini of Or85b OSNs (**a**) and dendrites of VM5d PNs (**b**) in *D. melanogaster* and *D. sechellia.* Far left, schematic of the OSN-PN populations under investigation; the population subject to imaging analysis in shown in a darker colour. Left, representative confocal images of the raw fluorescence of GaMP6f showing the plane used for imaging with glomerular labels; corresponding solvent and odour stimulus-induced fluorescent changes are also shown. Middle panels, time courses in response to solvents and two odour dilutions (mean ± SEM $\Delta F/F_0$, bars indicate the timing of stimulus). Right, quantifications of peak $\Delta F/F_0$ for a dilution series of each odour (Dunnett's test, control: solvent, *** $P < 0.001$; * $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$, n = 7 (*D. melanogaster* OSNs), 8 (*D. sechellia* OSNs), 7 (*D. melanogaster* PNs), 6 (*D. sechellia* PNs) animals. Genotypes are indicated in **Fig. 3a** legend.
c-d, Representative odour-evoked calcium responses in the axon termini of Or22a OSNs (**c**) and DM2 PNs (**d**) in *D. melanogaster* and *D. sechellia. n* = 10 animals each. Genotypes are indicated in **Fig. 3a** legend.
e, Calcium imaging DM2 PNs following reintroduction of *D. melanogasterOr22a* or *D. sechelliaOr22a* in Or22a OSNs in *D. melanogaster* lacking endogenous receptor expression. Time courses of odour responses are shown in the left. Quantifications of peak $\Delta F/F_0$ are shown in the middle (Dunnett's test, control: solvent, *** $P < 0.001$; * $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$,). $n = 7$ animals each. Normalised GCaMP6f fluorescence changes are shown in the right. Genotypes: *D. melanogaster w;Or22a/b^{Gal4}/Or22a/b^{Gal4};UAS-DmelOr22a,VT033006-LexA/VT033006-LexA,LexAop-GCaMP6m* (*DmelOr22a* allele rescue), *w;Or22a/b^{Gal4}/Or22a/b^{Gal4};UAS-DsecOr22a,VT033006-LexA/VT033006-LexA,LexAop-GCaMP6m* (*DsecOr22a* allele rescue).

Extended Data Figure 4: *D. sechellia* VM5d PNs show persistent response to long odour stimulation

Calcium responses of Or85b/VM5d neurons in response to long odour stimulation of *D. melanogaster* Or85b OSNs (**a**), *D. melanogaster* VM5d PNs (**b**), *D. sechellia* OSNs (**c**), and *D. sechellia* PNs (**d**). Left panels show the time courses of the odour response (mean ± SEM $\Delta F/F_0$). Bars indicate the timing of long odour stimulation (10 sec). Right panels, the maximum $\Delta F/F_0$ in the first and last 2.5 s time windows are compared. Paired *t*-test, ** $P < 0.01$; ** $P < 0.05$. $n = 7$ (*D. melanogaster* OSNs), 7 (*D. sechellia* OSNs), 8 (*D. melanogaster* PNs), 8 (*D. sechellia* PNs) animals. Genotypes are indicated in the **Fig. 3a** legend.

Extended Data Figure 5: Odour response sensitivity in control glomeruli.

Odour-evoked dose-dependent calcium responses in control glomeruli of *D. melanogaster* VA2 (Or92a) PNs (**a**), *D. sechellia* VA2 PNs (**b**), *D. melanogaster* DM4 (Or59b) PNs (**c**), and *D. sechellia* DM4 PNs (**d**). Left panels show the time courses in response to solvents and specific odour dilutions (mean ± SEM $\Delta F/F_0$, bars indicate the timing of stimulus). Right panels show the quantifications of peak $\Delta F/F_0$ (Dunnett's test, control: solvent, *** $P < 0.001$; * $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$,). $n = 7$ each. The genotype for the VA2 and DM4 PN calcium imaging is the same as for DM2 PN imaging shown in **Fig. 3a**.

Extended Data Figure 6: Pharmacological manipulations of lateral inhibition and OSN inputs.

a, Raw GCaMP fluorescence intensity in VM5d PNs in *D. melanogaster* (left) and *D. sechellia* (right) following GABA antagonist application. Mean fluorescence before (4-5 s; as "Baseline") and during (5-9 s; as "Odour") the odour stimulus was quantified. Paired *t*-test, ** $P < 0.01$, * $P < 0.05$, NS $P > 0.05$. $n = 8$ animals each. Genotype as in **Fig. 3a**.

b, Odour pulse responses of *D. sechellia* VM5d PNs following high dose (2 mM) of mecamylamine application (middle). Control PN responses in normal saline (left), and after saline wash out (right) are shown. Paired *t*-test, NS $P > 0.05$. $n = 7$ animals. Genotype as in **Fig. 3a**.

Extended Data Figure 7: Odour-tracking behaviour of various wild-type strains and towards apple cider vinegar.

a, Odour-tracking behaviour towards noni juice in other wild-type strains of *D. sechellia* and *D. melanogaster* (see **Extended Data Table 2**). The indications are the same as in **Fig. 3**. Paired *t*-test, *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$. $n = 30$ (*DmelBK, DmelrHR, Dsec19, Dsec31*) or 27 (*DmelOR, Dsec28*) animals.

b, Odour-tracking behaviour towards apple cider vinegar in wild-type *D. sechellia* strains. Paired *t*-test, *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$. $n = 30$ animals each.

Extended Data Figure 8: Odour tracking in a wind tunnel.

a, Array of 12 tracking cameras above the wind tunnel used for 3D tracking of flies in presence of a noni plume.

b, Side view of wind tunnel system along with the acrylic port used to flux noni odour into the tunnel volume.

c, Comparison of mean trajectory ground speeds for the three genotypes studied.
d, Schematic of two plume models used to analyse data compared to the point cloud distribution of *D. sechellia* trajectories in the wind tunnel volume. A "straight" model (solid orange line) which is aligned in space with the odour port, or a "sloped" model (dashed orange line) for which the plume sinks by 5 cm from the odour port to the tunnel end.
e, Radial distance calculations comparing mean radial distance of points from the plume centreline considering either the sloped or straight plume model (left two plots). Additionally, shows the same data without the restriction to limit this analysis to 10 cm above or below the plume's altitude (right two plots).
f, Left, course direction distributions within a 3 cm radius of the plume centreline for either the sloped plume model (as in **Fig. 5g**) for the downwind and upwind halves of the wind tunnel, up to 5 cm downwind from the plume origin. Right, the same analysis assuming a straight plume model.

Extended Data Figure 9: Additional conditions of optogenetic stimulation.
a, Optic fibre-mediated illumination of one antenna in the tethered fly. The photo was taken from below the apparatus.
b, Behavioural responses to optogenetic stimulation of Or22a/b OSNs in *D. melanogaster* using a *Gal4* knock-in line (see **Fig. 6a** for methodological details) Genotype: *D. melanogaster w;Or22a/b^{Gal4}/UAS-CsChrimson-Venus*. Left, time course of *ΔWBA*. Right, quantification within each phase. Paired *t*-test, $P > 0.05$.
c, Behavioural responses to optogenetic stimulation of effector control flies (*UAS-CsChrimson-Venus*) in *D. melanogaster* (left) and *D. sechellia* (right). Paired *t*-test, $P > 0.05$. Genotypes: *D. melanogaster w;+/UAS-CsChrimson-Venus, D. sechellia w;;;+/UAS-CsChrimson-Venus.*
d, Behavioural responses to optogenetic stimulation of Or22a OSNs in *D. sechellia* using CsChrimson by stimulating the left antenna induces leftward turning behaviour. Paired *t*-test, ** $P < 0.01$; * $P < 0.05$; otherwise $P > 0.05$. Genotype as in **Fig. 6a**.

Extended Data Figure 10: SPARC2 allows genetic manipulation of a subset of Or22a OSNs.
a, Schematic illustrating the principle of SPARC2[46]. Top, *Φ*C31-mediated recombination leads to removal of a stop cassette flanked by attP-attP sites. Co-expression of Gal4 in the same cell leads to transcriptional activation of a reporter gene. Middle, recombination with an alternative attP site does not lead to a functional read-out. Depending on the attP version present in the cassette, recombination efficiencies vary (D, dense; I, intermediate; S, sparse). Bottom, after recombination, a proportion of Gal4-expressing cells – in this study Or22a OSNs – will express the respective SPARC2 transgene.
b, Left, immunofluorescence for GFP on whole-mount antennae from animals expressing different *SPARC2-X-GFP* versions in Or22a neurons. Right, quantification of the number of Or22a OSNs labelled by SPARC2 versions in *D. melanogaster*. Genotypes: *D. melanogaster nSyb-ΦC31/+;Or22a^{Gal4}/UAS-SPARC2-X-GFP*. The SPARC2-D transgene labelled roughly 50% of Or22a expressing OSNs (compare with **Fig. 1c**) and was therefore used to generate transgenic constructs in *D. sechellia*.
c, Optogenetic stimulation of Or22a OSNs in *D. sechellia* using a lower light intensity. Electrophysiological measurements confirm that this light intensity

evokes a similar degree of OSN firing as in the SPARC2-D-CsChrimson experiment. Paired *t*-test, * $P < 0.05$; otherwise $P > 0.05$. Data is re-plotted from **Fig. 6a**.

d, Immunohistochemical staining for HA and nc82 on a whole-mount brain of *D. sechellia Or22a*^{Gal4} transgenic flies expressing *UAS-SPARC2-D-TNT-HA-GeCO*, revealing selective strong expression in Or22a OSNs projecting to DM2. The white arrowheads point to a few cells (putative glia due to their apparent lack of processes) labelled in the central brain. Scale bar = 50 µm.

Extended Data Figure 11: Variation in basiconic sensilla neuron numbers in the *D. melanogaster* species subgroup.

Numbers of Or42b, Or59b and Or22a/(b) neurons (housed in ab1, ab2 and ab3 sensilla, respectively) based on RNA FISH on whole-mount antennae across the *D. melanogaster* species subgroup; Ma, million years ago (n = 7-14, females). For strain details see **Extended Data Table 2**.

Extended Data Table 1: Spike counts for electrophysiological experiments.

Extended Data Table 2: Wild-type and transgenic lines used and generated in this study.

Extended Data Table 3: Oligonucleotides used to generate single sgRNA expression vectors and *in situ* probe templates.

Extended Data Table 4: Oligonucleotides used to generate multi-sgRNA expression vectors.

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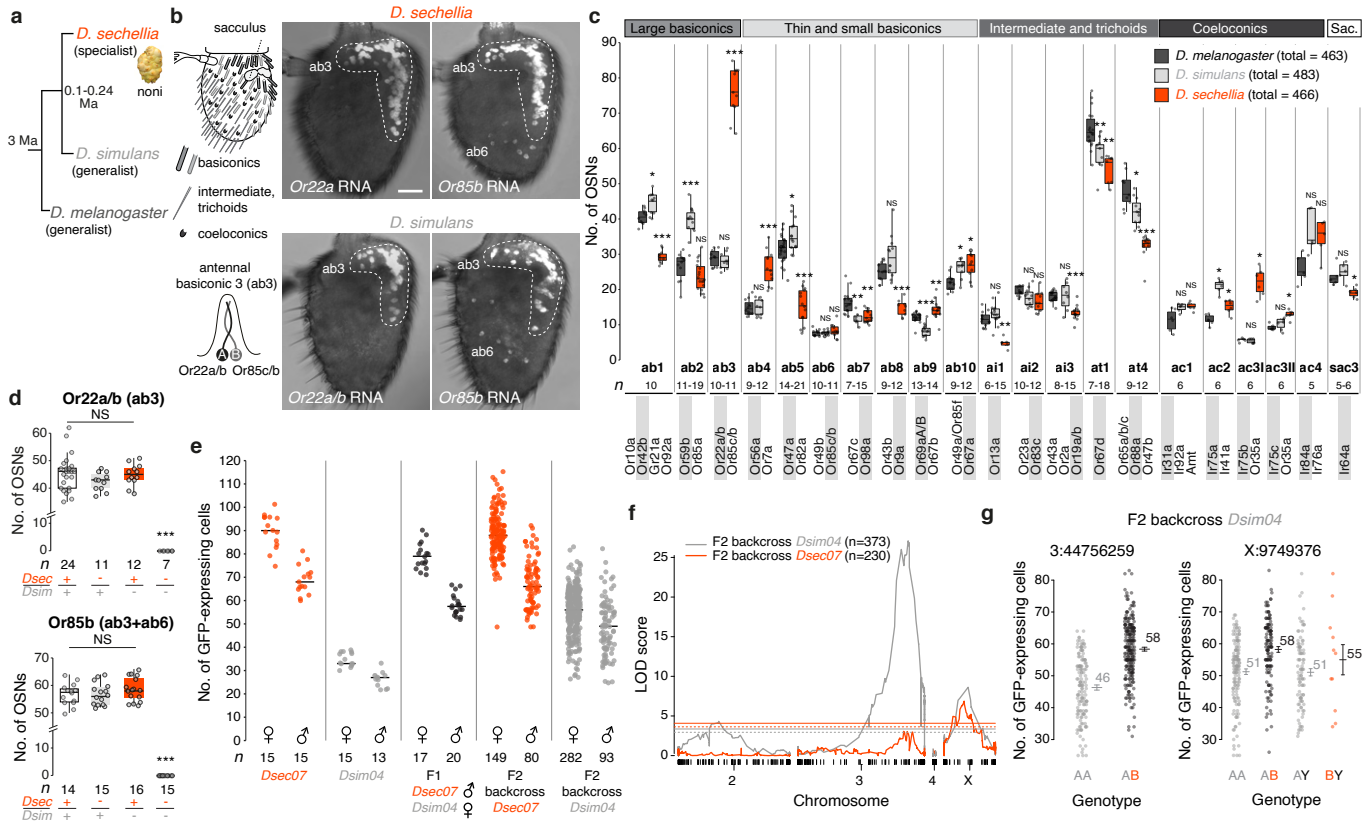
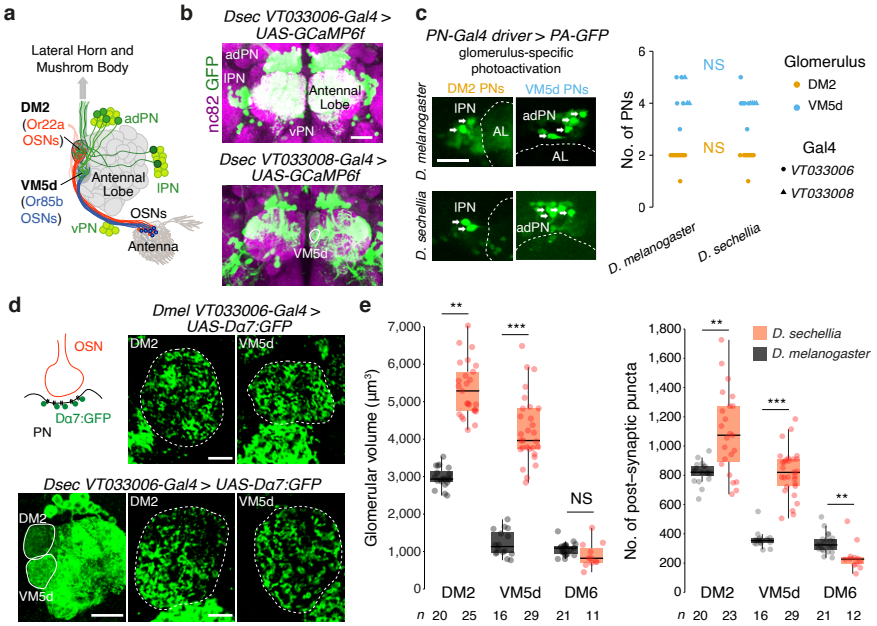

a
D. sechellia
(specialist)
noni
0.1-0.24 Ma
3 Ma
D. simulans
(generalist)
D. melanogaster
(generalist)
b
sacculus
basiconics
intermediate, trichoids
coeloconics
antennal basiconic 3 (ab3)
Or22a/b Or85c/b
D. sechellia
ab3
ab6
Or22a RNA
Or85b RNA
D. simulans
Or22a/b RNA
Or85b RNA
c
Large basiconics
Thin and small basiconics
Intermediate and trichoids
Coeloconics
Sac.
D. melanogaster (total = 463)
D. simulans (total = 483)
D. sechellia (total = 466)
No. of OSNs
ab1 ab2 ab3 ab4 ab5 ab6 ab7 ab8 ab9 ab10 ai1 ai2 ai3 at1 at4 ac1 ac2 ac3I ac3II ac4 sac3
n 10 11-19 10-11 9-12 14-21 10-11 7-15 9-12 13-14 9-12 6-15 10-12 8-15 7-18 9-12 6 6 6 6 5 5-6
Or10a Or42b Gr21a Or92a
Or59b Or85a
Or22a/b Or85c/b
Or56a Or7a
Or47a Or62a
Or49b Or85c/b
Or67c Or98a
Or43b Or9a
Or69aA/B Or67b
Or49a/Or85f Or67a
Or13a
Or23a Or83c
Or43a Or2a Or19a/b
Or67d
Or65a/b/c Or88a Or47b
Ir31a Ir92a Amt
Ir75a Ir41a
Ir75b Or35a
Ir75c Or35a
Ir84a Ir76a
Ir64a
d
Or22a/b (ab3)
NS
No. of OSNs
n 24 11 12 7
Dsec + - + -
Dsim + + - -
Or85b (ab3+ab6)
NS
No. of OSNs
n 14 15 16 15
Dsec + - + -
Dsim + + - -
e
No. of GFP-expressing cells
n 15 15 15 13 17 20 149 80 282 93
Dsec07
Dsim04
F1 Dsec07 ♂ Dsim04 ♀
F2 backcross Dsec07
F2 backcross Dsim04
f
F2 backcross Dsim04 (n=373)
F2 backcross Dsec07 (n=230)
LOD score
Chromosome
g
F2 backcross Dsim04
3:44756259
X:9749376
No. of GFP-expressing cells
Genotype
AA AB
AA AB AY BY


a
Lateral Horn and Mushrom Body
DM2
(Or22a OSNs)
adPN
VM5d
(Or85b OSNs)
Antennal Lobe
lPN
OSNs
vPN
Antenna
b
Dsec VT033006-Gal4 > UAS-GCaMP6f
nc82 GFP
adPN
lPN
Antennal Lobe
vPN
Dsec VT033008-Gal4 > UAS-GCaMP6f
VM5d
c
PN-Gal4 driver > PA-GFP
glomerulus-specific photoactivation
DM2 PNs
VM5d PNs
D. melanogaster
D. sechellia
lPN
AL
adPN
No. of PNs
NS
Glomerulus
DM2
VM5d
Gal4
VT033006
VT033008
d
OSN
Dα7:GFP
PN
Dmel VT033006-Gal4 > UAS-Dα7:GFP
DM2
VM5d
Dsec VT033006-Gal4 > UAS-Dα7:GFP
e
Glomerular volume (μm³)
No. of post-synaptic puncta
D. sechellia
D. melanogaster
DM2
VM5d
DM6
n 20 25 16 29 21 11
n 20 23 16 29 21 12

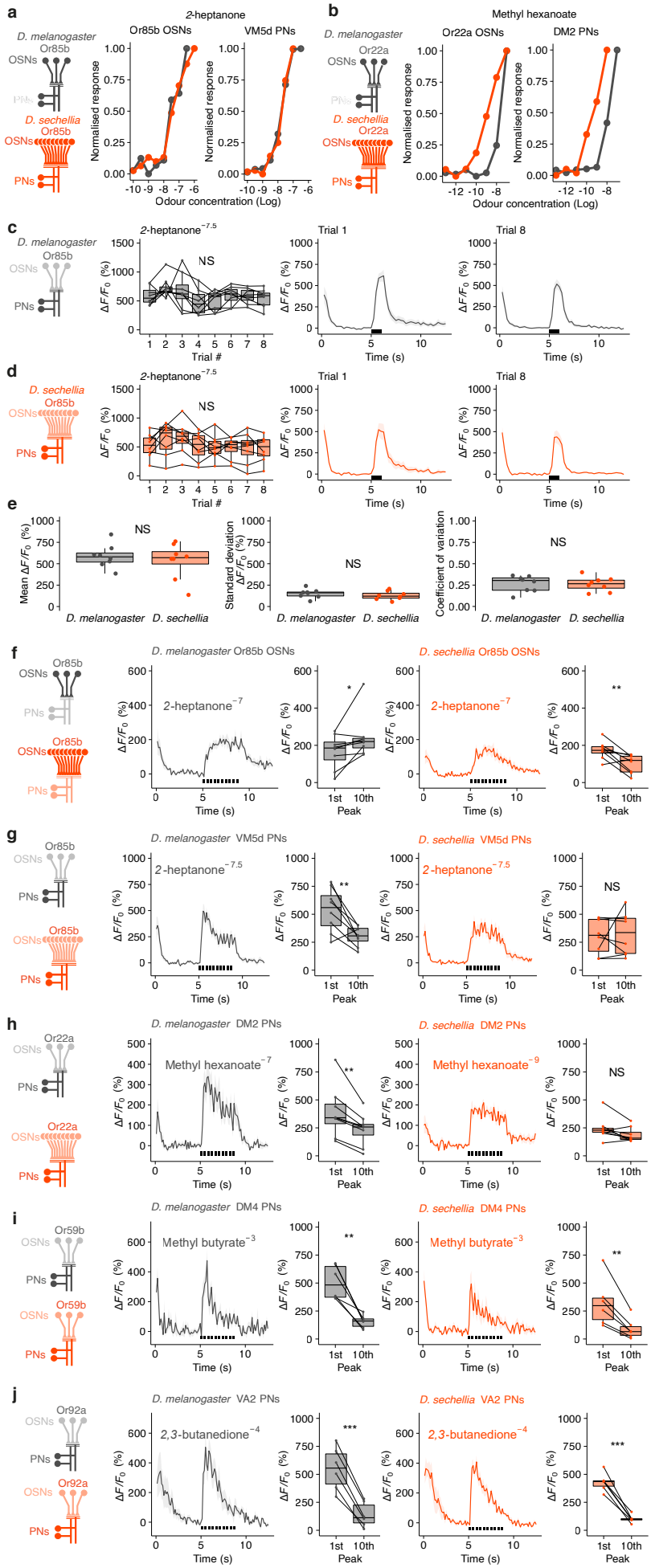
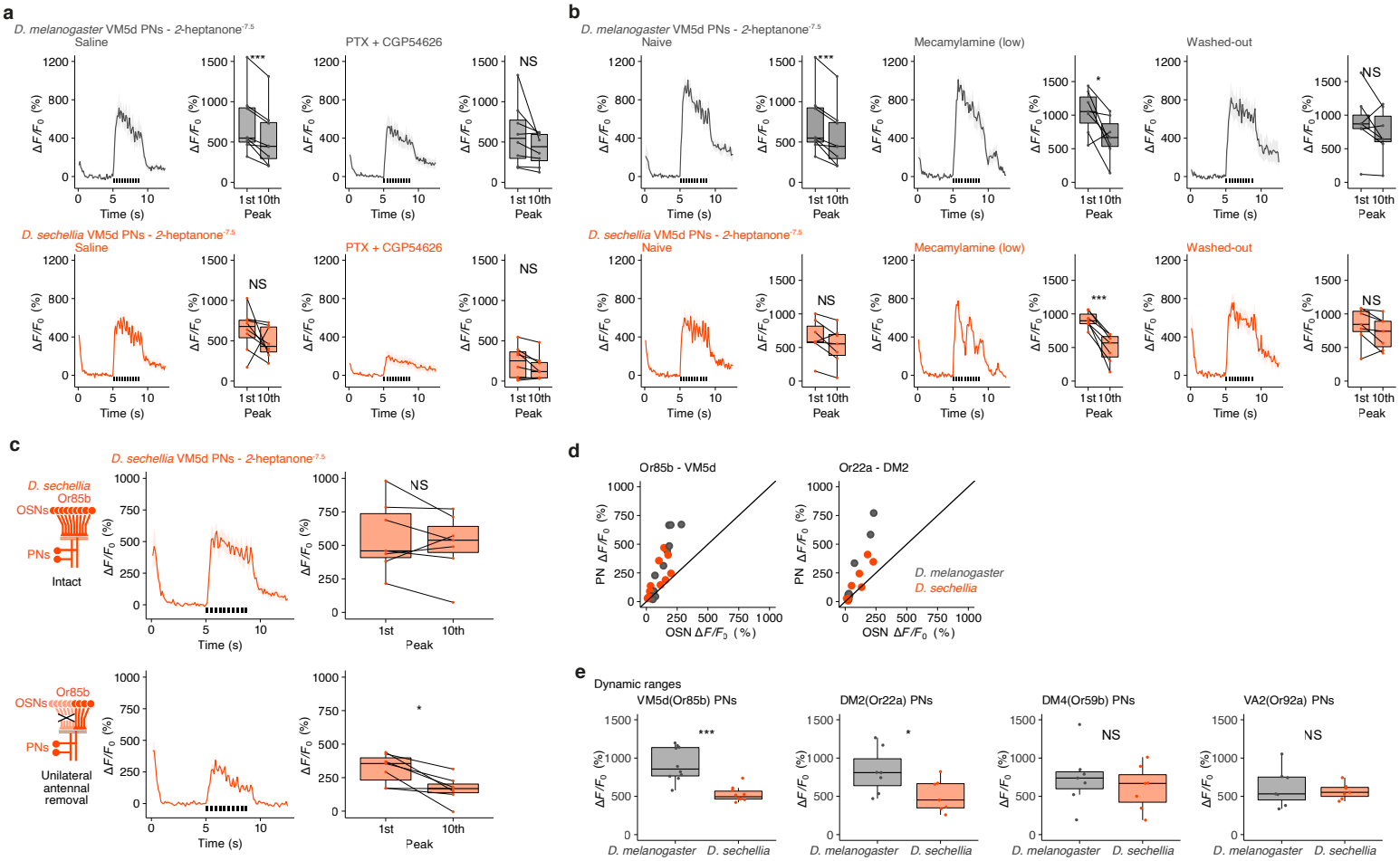

a
2-heptanone
Or85b OSNs
VM5d PNs
D. melanogaster
Or85b
OSNs
PNs
D. sechellia
Or85b
OSNs
PNs
Normalised response
Odour concentration (Log)
b
Methyl hexanoate
Or22a OSNs
DM2 PNs
D. melanogaster
Or22a
OSNs
PNs
D. sechellia
Or22a
OSNs
PNs
Normalised response
Odour concentration (Log)
c
D. melanogaster
Or85b
OSNs
PNs
2-heptanone$^{-7.5}$
NS
ΔF/F0 (%)
Trial #
Trial 1
Trial 8
Time (s)
d
D. sechellia
Or85b
OSNs
PNs
2-heptanone$^{-7.5}$
NS
ΔF/F0 (%)
Trial #
Trial 1
Trial 8
Time (s)
e
Mean ΔF/F0 (%)
NS
Standard deviation ΔF/F0 (%)
NS
Coefficient of variation
NS
D. melanogaster
D. sechellia
f
Or85b
OSNs
PNs
Or85b
OSNs
PNs
D. melanogaster Or85b OSNs
D. sechellia Or85b OSNs
2-heptanone^{-7}
ΔF/F0 (%)
Time (s)
Peak
1st
10th
g
Or85b
OSNs
PNs
Or85b
OSNs
PNs
D. melanogaster VM5d PNs
D. sechellia VM5d PNs
2-heptanone$^{-7.5}$
NS
h
Or22a
OSNs
PNs
Or22a
OSNs
PNs
D. melanogaster DM2 PNs
D. sechellia DM2 PNs
Methyl hexanoate^{-7}
Methyl hexanoate^{-9}
NS
i
Or59b
OSNs
PNs
Or59b
OSNs
PNs
D. melanogaster DM4 PNs
D. sechellia DM4 PNs
Methyl butyrate^{-3}
j
Or92a
OSNs
PNs
Or92a
OSNs
PNs
D. melanogaster VA2 PNs
D. sechellia VA2 PNs
2,3-butanedione^{-4}

Figure 4


a
D. melanogaster VM5d PNs - 2-heptanone-7.5
Saline
PTX + CGP54626
D. sechellia VM5d PNs - 2-heptanone-7.5
Saline
PTX + CGP54626
b
D. melanogaster VM5d PNs - 2-heptanone-7.5
Naive
Mecamylamine (low)
Washed-out
D. sechellia VM5d PNs - 2-heptanone-7.5
Naive
Mecamylamine (low)
Washed-out
ΔF/F0 (%)
Time (s)
Peak
1st
10th
NS
c
D. sechellia VM5d PNs - 2-heptanone-7.5
D. sechellia
Or85b
OSNs
PNs
Intact
Unilateral antennal removal
d
Or85b - VM5d
Or22a - DM2
PN ΔF/F0 (%)
OSN ΔF/F0 (%)
D. melanogaster
D. sechellia
e
Dynamic ranges
VM5d(Or85b) PNs
DM2(Or22a) PNs
DM4(Or59b) PNs
VA2(Or92a) PNs
D. melanogaster
D. sechellia

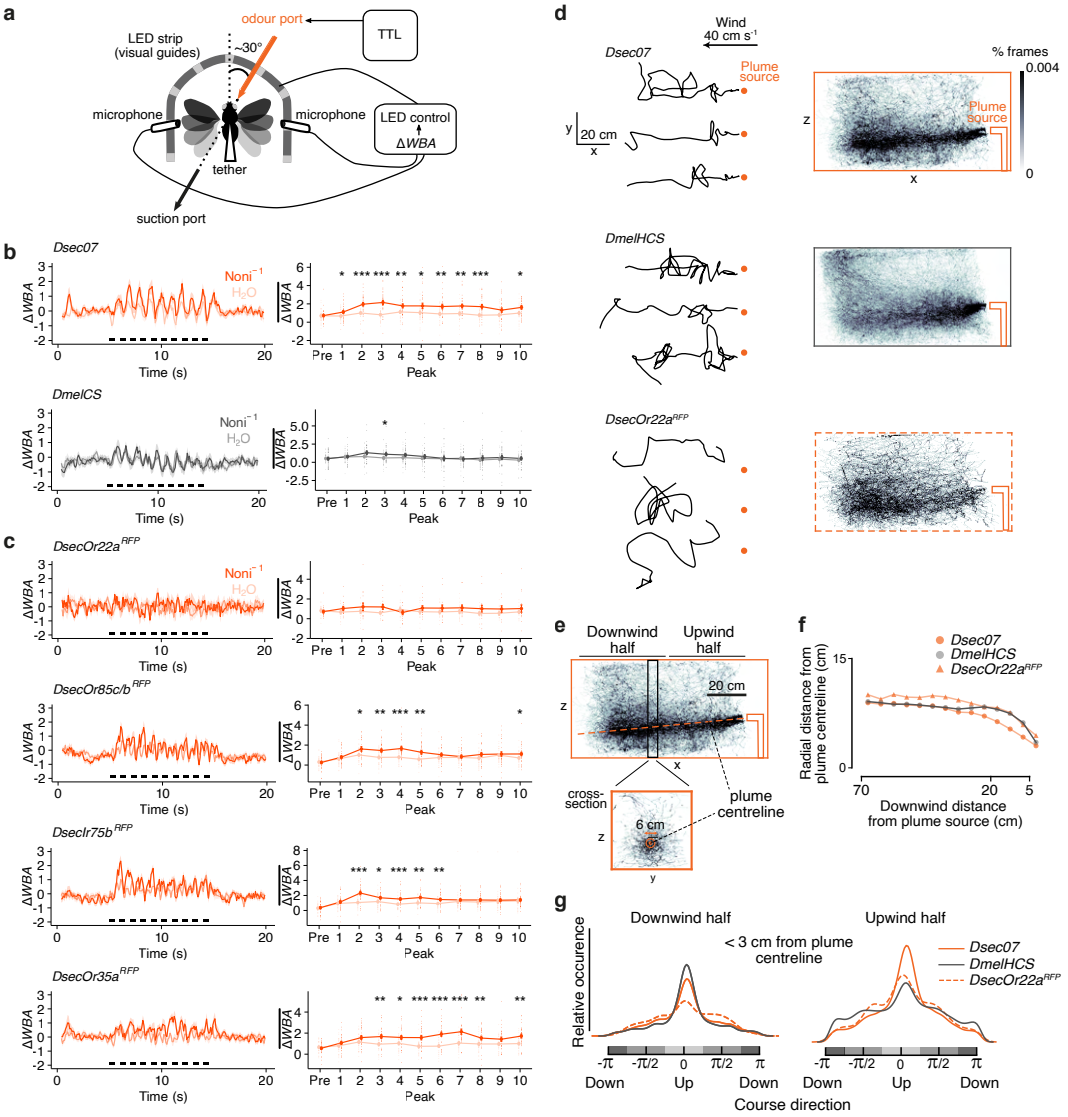
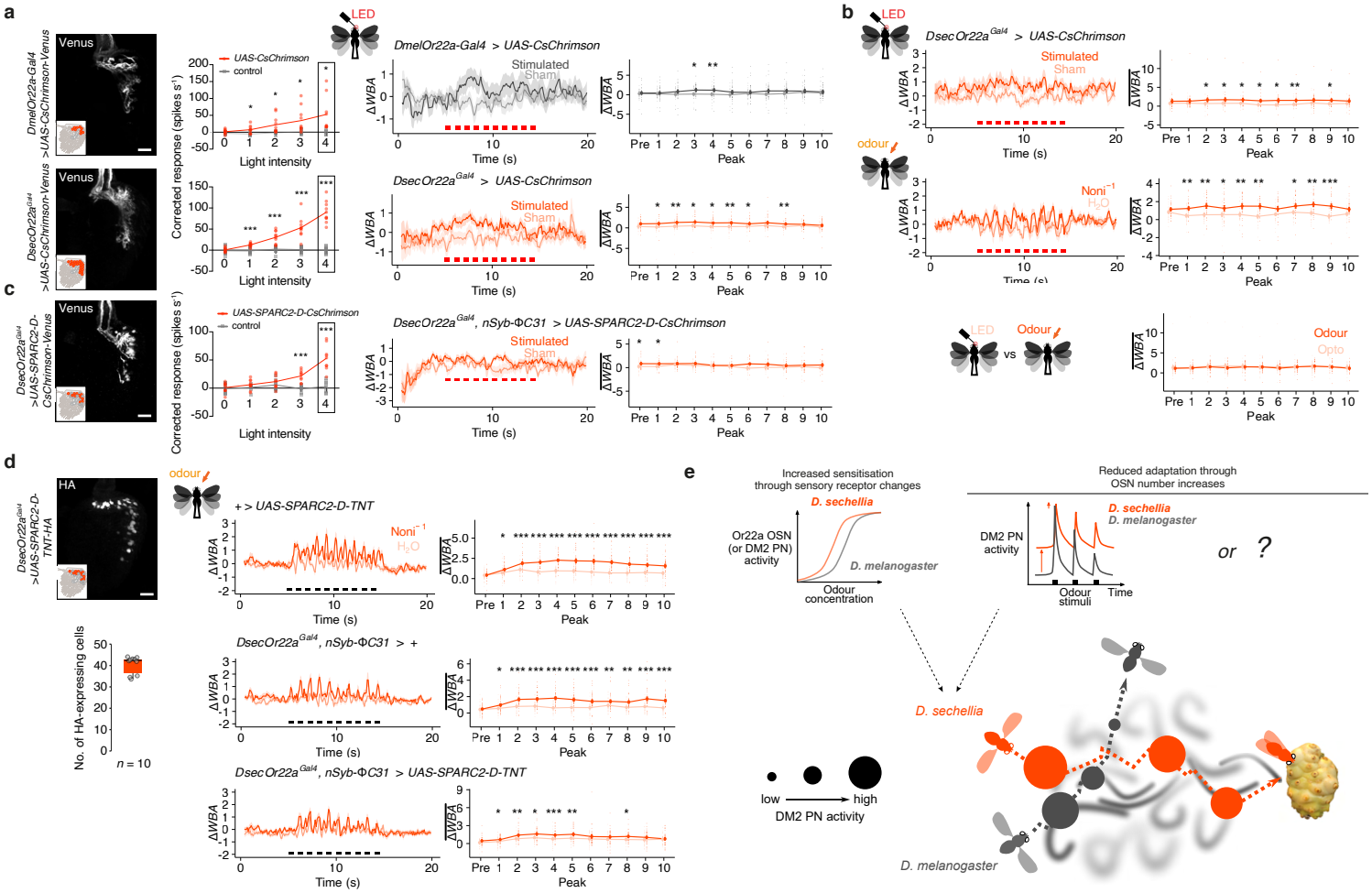

a
odour port
TTL
LED strip
(visual guides)
~30°
microphone
microphone
LED control
ΔWBA
tether
suction port
b
Dsec07
Noni⁻¹
H₂O
ΔWBA
Time (s)
Peak
DmelCS
c
DsecOr22a RFP
DsecOr85c/b RFP
DseIr75b RFP
DsecOr35a RFP
d
Wind
40 cm s⁻¹
Dsec07
Plume source
% frames
0.004
0
20 cm
DmelHCS
DsecOr22a RFP
e
Downwind half
Upwind half
20 cm
cross-section
plume centreline
6 cm
f
Dsec07
DmelHCS
DsecOr22a RFP
Radial distance from plume centreline (cm)
Downwind distance from plume source (cm)
g
Downwind half
Upwind half
< 3 cm from plume centreline
Relative occurence
Dsec07
DmelHCS
DsecOr22a RFP
Down
Up
Down
Course direction

Figure 6



a
b
c
d
e
Venus
LED
odour
HA
DmelOr22a-Gal4 > UAS-CsChrimson
DsecOr22a^Gal4 > UAS-CsChrimson
DsecOr22a^Gal4, nSyb-ΦC31 > UAS-SPARC2-D-CsChrimson
UAS-CsChrimson
control
UAS-SPARC2-D-CsChrimson
Corrected response (spikes s⁻¹)
Light intensity
Stimulated
Sham
Noni⁻¹
H₂O
Opto
ΔWBA
Time (s)
Peak
Pre
+ > UAS-SPARC2-D-TNT
DsecOr22a^Gal4, nSyb-ΦC31 > +
DsecOr22a^Gal4, nSyb-ΦC31 > UAS-SPARC2-D-TNT
No. of HA-expressing cells
n = 10
Increased sensitisation through sensory receptor changes
Reduced adaptation through OSN number increases
D. sechellia
D. melanogaster
Or22a OSN (or DM2 PN) activity
Odour concentration
DM2 PN activity
Odour stimuli
Time
or ?
low
high
DM2 PN activity