1
Genomic plasticity drives olfactory adaptation in a pest fly
18
19
Qi Xue[1], Hany K. M. Dweck[1, *]
20

21
[1]Department of Entomology, The Connecticut Agricultural Experiment Station, New
22
Haven, CT 06511, USA
23
24
*Corresponding author: hany.dweck@ct.gov

SUMMARY

Preference shifts in insects are often driven by changes in the olfactory system, yet the underlying mechanisms remain unclear. The worldwide pest *Drosophila suzukii*, which oviposits in ripe rather than overripe fruits, provides a powerful model to study these mechanisms and their behavioral consequences. Here, we show that this shift is linked to functional remodeling in four olfactory receptor neurons (ORNs): ab2B, ab3A, ab4B, and ab10A. While ab3A and ab10A exhibit tuning changes shared with the non-pest relative *D. biarmipes*, ab2B and ab4B display species-specific adaptations in *D. suzukii*. These changes result not only from receptor sequence divergence but also from novel innovations: receptor co-expression in ab3A and partitioned expression of Or67a paralogs in ab2B and ab10A. Together, these findings show how genomic plasticity in chemosensory gene families enables rapid sensory adaptation and niche transition.

INTRODUCTION

The olfactory system mediates the interactions between insects and their environment. It guides critical behaviors such as foraging, mate choice, and oviposition [1-4]. These behaviors are tightly linked to survival and reproductive success. This makes the olfactory system a key target of natural selection. The olfactory system, as a result, evolves rapidly in response to ecological shifts, particularly those involving changes in habitat, food resources, or reproductive sites [5-7]. However, the molecular mechanisms underlying olfactory adaptations remain poorly understood. While numerous studies have documented the remarkable variation in the copy number of chemosensory receptor genes, driven by gene gains and losses, across insect taxa[8-12], fewer have connected this genomic diversity to functional differences at the receptor and neuronal levels, or to shifts in behavior [6].

The worldwide fruit pest *D. suzukii* presents a powerful model to explore these evolutionary links. Unlike most *Drosophila* species, which are adapted to oviposit in fermenting fruit of no value, *D. suzukii* has evolved a distinct ecological niche [13,14]. It targets intact, ripening fruit for oviposition, causing significant agricultural losses[15]. This shift allows the species to exploit a previously underutilized resource, but it also poses new sensory and behavioral challenges. Navigating this niche requires the ability to detect and respond to a different set of volatile cues than those used by species that specialize on rotting substrates. Consequently, *D. suzukii*'s unique host preference is likely underpinned by extensive modifications to its olfactory system. Several molecular mechanisms are known to drive such adaptations, including amino acid substitutions that alter receptor tuning properties, changes in gene expression levels that modify receptor neuron sensitivity, and structural changes in the genome that increase or decrease receptor copy number through duplication, neofunctionalization, or pseudogenization [5,6,16-20].

Comparative genomic and transcriptomic analyses have revealed that *D. suzukii*'s odorant receptor (Or) repertoire exhibits distinctive evolutionary signatures [21-24]. Two gene expansions, *Or23a* and *Or67a*, set this species apart from its close relatives *D. biarmipes* and *D. melanogaster*. In *D. suzukii*, *Or23a* is present in four intact copies (*Or23a1*, *Or23a2*, *Or23a3*, and *Or23a4*), while *Or67a* is represented by four functional paralogs (*Or67a1*, *Or67a2*, *Or67a3*, and *Or67a4*) and one pseudogene (*Or67a5*). Interestingly, only the *Or67a* expansion is retained in *D. biarmipes* [22], suggesting that the expansion of *Or23a* occurred more recently in the *D. suzukii* lineage. In *D. melanogaster*, *Or23a* is expressed in the B neuron of antennal intermediate 2 (ai2) sensilla, but extensive functional screening has not identified strong ligands, leaving its role unresolved [25].

Or67a, by contrast, is better functionally characterized. In *D. melanogaster*, *Or67a* is expressed in the A neuron of ab10 sensilla, where it mediates strong responses to aromatic esters such as benzyl butyrate, benzyl acetate, and phenethyl propionate [25-27]. In *D. suzukii*, two copies of *Or67a* (*Or67a3* and *Or67a4*) exhibit signatures of positive selection [22], suggesting adaptive evolution potentially linked to the detection of odorants associated with ripening fruit.

139
140   Concurrently, *D. suzukii* has lost several ancestral Or genes, including *Or74a*,
141   *Or85a*, and *Or98b* [22,23]. These losses could represent either relaxed selection for
142   receptors tuned to volatiles no longer relevant in the new ecological context, or
143   functional trade-offs associated with receptor repertoire remodeling.
144
145   Despite these striking genomic changes, the extent to which receptor gains and
146   losses have reshaped the peripheral olfactory architecture, altering neuron identities,
147   response properties, and overall coding capacity, remains largely unexplored.
148
Here, through a combination of electrophysiological recordings and comparative
analyses, we identified olfactory receptor neurons whose response profiles differ
markedly between *Drosophila suzukii* and its close relatives, *D. melanogaster* and *D.*
biarmipes. Using molecular genetics, CRISPR/Cas9 gene editing, AlphaFold, and
molecular docking, we elucidated the molecular mechanisms underlying these neuronal
differences. Moreover, our work revealed that both gene losses and gains have shaped
the olfactory repertoire of *D. suzukii*, driving its sensory adaptation and facilitating its
ecological niche transition from fermenting to ripening fruits. These findings highlight
how molecular changes at the receptor level translate into behavioral shifts that
underpin the evolutionary success and pest status of *D. suzukii*.
159
RESULTS
Neurons whose responses differ between *D. suzukii* and *D. melanogaster*
To identify neurons that differ in their responses between *D. suzukii* and *D.*
melanogaster, we compared odorant-evoked responses of olfactory receptor neurons
(ORNs) in the antennal basiconic, intermediate, and trichoid sensilla of both species
using single sensillum recordings (SSR). Modifications in the tuning of these neurons
could result from gene births and deaths accompanying *D. suzukii*'s transition to ripe
fruit and may underlie its novel specialization.
168
169   This analysis complements our prior work on maxillary palp basiconic and
170   antennal coeloconic sensilla in *D. suzukii* [28,29] and together provides a comprehensive
171   functional atlas of ORN responses across all sensillum types.
172
For this analysis, we used a panel of 113 ecologically relevant odorants, each
tested at a 10^{-2} dilution, including acids, esters, alcohols, aldehydes, ketones, lactones,
and terpenes. This analysis generated a dataset of 3,503 odorant–ORN combinations
(Figure 1A) in each species (n = 3–6 per combination in *D. suzukii* and n = 3 per
combination in *D. melanogaster*) and revealed that the odorant response profiles of
most ORNs are qualitatively similar between the two species (Figure S1; Extended Data
File S1 and S2). However, a subset of four ORNs displayed notable shifts in odorant
tuning (Figure 1A). These ORNs are ab2B, ab3A, ab4B, and ab10A.
181
182   To validate and further dissect these interspecific differences, we performed a
183   second round of SSR using an odorant panel that included the most potent ligands
184   identified in our initial screen, together with ligands previously reported for the

185 corresponding ORNs. All odorants were tested at a 10^{-4} dilution to approximate
186 naturalistic concentrations encountered by flies in the wild[30].
187
188   To differentiate between *D. suzukii*-specific changes and more broadly shared
189 evolutionary trends, we included *D. biarmipes* in our analysis. This species is the
190 closest extant relative of *D. suzukii* [31,32] and has no distinct preference for either
191 overripe or ripe fruit [13,14,21].
192
193   To assess the robustness of these shifts within *D. suzukii*, we included two
194 geographically distinct populations: the WT3 strain from California (*Dsuz-WT3*), which
195 served as the reference genome strain [31], and an independent strain collected in North
196 Carolina (*Dsuz*-NC).
197
Shared and species-specific shifts in *D. suzukii*
In ab3A neurons, we observed two kinds of changes, one of which is shared by *D.*
suzukii and *D. biarmipes*. These included markedly reduced responses to volatiles that
strongly activate this neuron in *D. melanogaster* (Figure 1B, D, E), including ethyl
hexanoate, which is a fermentation product[33], and increased responses to an alternative
set of esters, including isoamyl acetate and butyl acetate (Figure 1D), which are
produced during fruit ripening[33].
205
The second kind of change is unique to *D. suzukii*. These included significantly
stronger responses to isobutyl acetate, ethyl butyrate, and ethyl isovalerate compared
to *D. biarmipes* and *D. melanogaster* (Figure 1D, F), as well as robust, dose-dependent
responses to β-cyclocitral (Figure 1C, D, G), a volatile isoprenoid emitted by green
foliage, including strawberry leaves[33]. By contrast, over a range of dilutions, this
compound elicited little or no activity in the ab3A neurons of *D. biarmipes* and *D.*
melanogaster (Figure 1C, D, G).
213
214   We also found intraspecific variation in responses to β-cyclocitral across *D.*
215 *suzukii* strains. All ab3A neurons in the WT3 strain (California origin) responded robustly
216 to β-cyclocitral, whereas responses in the North Carolina strain were more
217 heterogeneous: some ab3A neurons responded strongly while others showed little or no
218 response (Figure 1D).
219
220   In ab10A neurons, both *D. suzukii* and *D. biarmipes* exhibited reduced sensitivity
221 to benzyl butyrate and benzyl acetate compared to *D. melanogaster* (Figure 1H,I) and
222 enhanced responses to geranyl acetate, β-citronellol, isoamyl butyrate, 1-octen-3-ol,
223 ethyl-3-hydroxyhexanoate, and diethyl succinate (Figure 1H,J,K).
224
225   In ab2B neurons, both *D. melanogaster* and *D. biarmipes* exhibited strong to
226 ethyl 3-hydroxybutyrate, a compound closely associated with fermentation[34,35], whereas
227 all three *D. suzukii* strains displayed strongly reduced sensitivity (Figure 2A, C, D). By
228 contrast, ab2B neurons in *D. suzukii* responded robustly to a distinct set of esters,
229 including isoamyl acetate, butyl acetate, pentyl acetate, benzyl acetate, and isoamyl

butyrate (Figure 2B,C,E,F). These esters are formed as part of the fruit ripening process[33-35].

In ab4B neurons, all three species responded to veratrole, whereas all three *D. suzukii* strains additionally responded to ethyl salicylate, methyl salicylate, methyl benzoate, acetophenone, and 4-ethylguaiacol (Figure 2G–J).

Together, these findings reveal a mosaic of shared and species-specific olfactory changes in *D. suzukii*. The shifts in ab3A and ab10A, shared with *D. biarmipes*, likely reflect phylogenetic divergence, whereas the unique sensitivity of ab3A neurons to β-cyclocitral and species-specific tuning in ab2B and ab4B neurons point to derived adaptations supporting *D. suzukii*'s specialization on ripe fruit.

D. suzukii ab3A neurons co-express two odorant receptors, one of which is specifically tuned to β-cyclocitral
We next focused on ab3A neurons, which display a robust response to the strawberry leaf volatile β-cyclocitral. We hypothesized that this neuronal type in *D. suzukii* co-expresses two receptors, one of which is specifically tuned to β-cyclocitral. This hypothesis was based on three observations: (1) only *D. suzukii* ab3A neurons respond robustly to β-cyclocitral, despite both *D. suzukii* and *D. biarmipes* having a single functional gene (referred to as the *Or22a*-like receptor) at the locus that determines ab3A responses in drosophilids, with 91% sequence identity between the two species; (2) the North Carolina strain of *D. suzukii* harbors two ab3A populations, one responsive to β-cyclocitral and one not; and (3) the chemical structure of β-cyclocitral, a cyclic isoprenoid aldehyde, differs markedly from the long- and short-chain esters that typically activate ab3A neurons in *D. suzukii* and other *Drosophila* species.

To test this hypothesis, we first expressed the *D. suzukii Or22a* (*DsuzOr22a*) in the *D. melanogaster* ab3A "empty neuron" system [36], where the endogenous *Or22a/Or22b* locus is deleted and replaced by *Gal4* (Figure 3A). Ectopic expression of *DsuzOr22a* restored responses to a suite of esters that matched the tuning profile of native *D. suzukii* ab3A neurons (Figure 3B, D). However, these neurons did not confer responses to β-cyclocitral (Figure 3C, D), indicating that *DsuzOr22a* is not sufficient for β-cyclocitral detection and that a second co-expressed receptor is required.

We next used CRISPR/Cas9-mediated mutagenesis to generate loss-of-function alleles of *DsuzOr22a*. Two independent alleles were recovered: *DsuzOr22a¹*, carrying a 25-nt deletion, and *DsuzOr22a²*, carrying a 4-nt deletion. Both mutations are predicted to produce truncated, non-functional proteins of 106 amino acids (Figure 3E). To control for potential background effects, we also generated heteroallelic *DsuzOr22a* mutant combinations using these homozygous lines.

Compared to Wild-type, *DsuzOr22a¹/⁺*, and *DsuzOr22a²/⁺* flies, ab3A neurons in *DsuzOr22a¹, DsuzOr22a², and DsuzOr22a¹/Or22a²* mutant flies exhibited drastically reduced responses to all tested esters (Figure 4F, H), demonstrating that *DsuzOr22a* is required for ester sensitivity. However, responses to β-cyclocitral were intact in all

276 mutants, confirming that a second receptor mediates detection of this compound (Figure
277 4G, H).
278
279   To determine whether the β-cyclocitral receptor belongs to the odorant receptor
280 (OR) or ionotropic receptor (IR) family, we measured responses from large basiconic
281 sensilla in *D. suzukii Orco* mutant flies. Because *Orco* is an obligate co-receptor for all
282 functional ORs but not IRs, the presence or absence of β-cyclocitral responses in this
283 background would distinguish the receptor class.
284
285   We found that β-cyclocitral did not elicit any response in any of the 117 basiconic
286 sensilla examined in *DsuzOrco* mutant flies, indicating that β-cyclocitral detection
287 depends on *Orco* and thus is mediated by an OR rather than an IR (Figure S2).
288
289   Together, these results demonstrate that *D. suzukii* ab3A neurons co-express two
290 odorant receptors: *Or22a*, which has shifted its tuning toward several ripening fruit esters
291 such as isobutyl acetate, butyl acetate, and isoamyl acetate, and a second, as-yet-
292 unidentified receptor that is specifically tuned to β-cyclocitral.
293
A Single Amino Acid Substitution Alters Ligand Specificity of *Or22a* in *D. suzukii*
We next investigated the molecular basis of the tuning shift of *DsuzOr22a*. We aligned
the *Or22a* amino acid sequences from *D. melanogaster*, *D. suzukii*, and *D. biarmipes*
using Clustal Omega and visualized the alignment with MView (Figure S3A). This analysis
revealed 97 amino acid substitutions shared between *D. suzukii* and *D. biarmipes* relative
to *D. melanogaster*, including a substitution at position 201 (aspartic acid [D] to alanine
[A]). In *D. melanogaster* strains, the residue at this position is predicted to lie within the
odorant-binding pocket[37], which is proposed to form within the extracellular leaflet of the
plasma membrane between helices TM1–TM6[38]. Previous work showed variation at this
site, together with changes at residue 92, alters ligand-binding specificity and contributes
to phenotypic variation in ab3A responses among natural populations of *D.
melanogaster*[38]. Since residue 92 is conserved across all three species, the substitution
at position 201 likely plays a major role in the tuning shift of *DsuzOr22a*.
307
To determine the functional impact of this substitution, we used AlphaFold2 to
model the wild-type *DsuzOr22a* (D201A) and an *in silico* variant with the A201D
substitution. We then performed molecular docking with isobutyl acetate, a key ligand for
DsuzOr22a. The predicted models revealed that the A201D substitution induces a
pronounced reorganization of the binding pocket architecture, producing a conformation
distinct from that of the wild-type receptor (Figure S3B). This suggests that D201A
significantly alters receptor–ligand interactions and contribute to the tuning shift of
DsuzOr22a.
316
317   We then tested this prediction by generating a site-directed mutant of *DsuzOr22a*
318 (A201D) and expressing it in the *D. melanogaster* ab3A "empty neuron" system. This
319 substitution did not increase the response of *DsuzOr22a* to any of the compounds that
320 strongly activate *D. melanogaster* ab3A (Figure 3I,J). By contrast, it reduced responses
321 to all tested odorants (Figure 3I,J). Interestingly, responses of the A201D variant to

isobutyl acetate across a range of dilutions more closely resembled that of *D. melanogaster* ab3A than of *D. suzukii* ab3A or wild-type *DsuzOr22a* (Figure 3J), indicating a partial reversion toward the ancestral tuning state. These results support a critical role for residue 201 in reshaping *Or22a* ligand specificity in *D. suzukii*, particularly for fruit-ripening esters.

Functional Analysis of *Or23a* and *Or67a* Paralogs in *D. suzukii*
Having demonstrated that the response to β-cyclocitral in *D. suzukii* ab3A depends on an odorant receptor other than Or22a and deciphered the molecular basis of the *DszuOr22a* tuning shift, we next investigated the contributions of the expanded Or23a (four paralogs) and Or67a (five paralogs) receptor subfamilies to β-cyclocitral sensitivity in ab3A neurons, as well as to tuning shifts in ab10A and ab2B neurons. To do this, we expressed each paralog individually in the *D. melanogaster* ab3A "empty neuron" system and measured odor-evoked responses across a broad panel of compounds.

We found that all *Or23a* paralogs showed little (<30 spikes/s) or no responses to any of the tested odorants (Extended Data File S3), indicating that their key ligands remain unidentified. Similarly, *Or67a5* did not respond to any odorant, consistent with its annotation as a pseudogene due to a premature stop codon (TAA) at nucleotide position 174 (Extended Data File S4).

By contrast, *Or67a1*, *Or67a2*, *Or67a3*, and *Or67a4* each exhibited robust and specific responses to multiple odorants (Figures 4). However, none of these receptors responded to β-cyclocitral with the same magnitude or sensitivity as the native ab3A neuron, indicating that the receptor mediating this response remains unidentified.

Co-expression of *Or67a1* and *Or67a2* Produces a Response Profile Closely Matching the Native ab10A Odor Response in *D. suzukii*
Or67a1 and *Or67a2* responded to an overlapping set of odorants, but differed in response magnitude for several compounds, including geranyl acetate, α-phellandrene, and β-citronellol (Figure 4A). The odorant response profile of *Or67a2* more closely resembled that of the native *D. suzukii* ab10A neurons than did *Or67a1* (Figure 4A), with a mean Euclidean distance of 116 ± 0.8 (SE) compared to 122 ± 1 for *Or67a1*.

To determine whether co-expression of both receptors is required to fully replicate the ab10A response profile, we expressed *Or67a1* and *Or67a2* together in the *D. melanogaster* ab3A "empty neuron" system. This co-expression produced responses that closely matched the ab10A response profile (Figure 4A), with a smaller Euclidean distance (107 ± 2.5) than either receptor alone. The simple interpretation of these results is that *Or67a1* and *Or67a2* are likely co-expressed in the *D. suzukii* ab10A neurons and that their combined activity produces the characteristic tuning of this neuronal type.

***Or67a4* is expressed in the ab2B neurons of *D. suzukii* and mediates their responses to odorants**
Or67a3 and *Or67a4*, on the other hand, displayed odorant response profiles that diverged markedly from that of ab10A neurons (Figure 4B). Surprisingly, the response profile of

each of *Or67a3* and *Or67a4* closely resembled that of the native *D. suzukii* ab2B neurons
(Figure 4B), with Or67a4 showing a smaller mean Euclidean distance (180 ± 2.5)
compared to Or67a3 (319 ± 2.7). However, co-expression of *Or67a3* and *Or67a4* in the
D. melanogaster ab3A "empty neuron" system produced a response profile more similar
to *Or67a3* (192 ± 1.4 SE, mean Euclidean distance) but distinct from that of each of the
native *D. suzukii* ab2B (229 ± 2.5) and *Or67a4* alone (218 ± 1.1) (Figure 4B). Taken
together, these results suggest that Or67a4 is the primary receptor expressed in ab2B
neurons and largely determines the response profile of this neuronal type.
376
377   To test this, we used CRISPR/Cas9 to generate an independent loss-of-function
378   allele of *DsuzOr67a*, carrying a 22-bp deletion (*DsuzOr67a4[1]*) (Figure 5A). We also
379   established a heterozygous line from the homozygous mutant.
380
381   While wild-type and the heterozygous line responded indistinguishably, the ab2B
382   neurons in the *DsuzOr67a4[1]* mutant allele exhibited extremely reduced responses to all
383   tested odorants (Figure 5B,C). These results suggest that *Or67a4* is expressed in *D.*
384   *suzukii* ab2B neurons and underlies their novel odorant response, which differs from that
385   of ab2B neurons in *D. melanogaster* and *D. biarmipes*.
386
Together, these findings reveal a clear functional and spatial partitioning among
the *Or67a* paralogs in *D. suzukii*. *Or67a1* and *Or67a2* are likely co-expressed in ab10A
neurons, while *Or67a4* is expressed in a separate neuronal type, ab2B. This partitioning
of expression suggests that gene duplication in the *Or67a* lineage has facilitated
subfunctionalization across distinct olfactory neuron types, enabling *D. suzukii* to broaden
its olfactory repertoire and fine-tune its detection of ecologically relevant odorants.
393
DISCUSSION
Our results reveal that the evolutionary shift in preference from overripe to ripe fruit in
Drosophila suzukii, a worldwide berry fly pest*,* is mirrored by functional changes in a
limited subset of ORNs. Specifically, four ORNs (ab2B, ab3A, ab4B, and ab10A) exhibit
altered odorant tuning in *D. suzukii* relative to *D. melanogaster*. Of these, ab3A and
ab10A exhibit shared tuning shifts in *D. suzukii* and its non-pest sibling species *D.*
biarmipes. These shared shifts likely reflect ancestral adaptations predating the
transition to ripe fruit use. By contrast, ab2B and ab4B show unique tuning profiles in *D.*
suzukii.
403
Importantly, these modifications are not solely the result of receptor sequence
evolution but are also mediated by innovative mechanisms, including the co-expression
of two distinct odorant receptors in a single ORN (as observed in ab3A) and the
partitioned expression of gene duplicates across different ORNs (as seen with the
Or67a paralogs in ab2B and ab10A). These strategies provide a flexible framework for
expanding olfactory function without requiring the evolution of entirely new neuronal
types, facilitating rapid and efficient sensory adaptation during ecological transitions.
411
Receptor Co-expression Enables Novel Odor Tuning in ab3A of *D. suzukii*

The ab3A neurons of *D. suzukii* illustrate two distinct molecular innovations that align with
its shift to ripe fruit. First, these neurons have lost responses to key fermentation volatiles
that strongly activate ab3A in *D. melanogaster*. Instead, they have gained increased
sensitivity to a new set of ripening-associated short-chain esters. Second, ab3A neurons
in *D. suzukii* have acquired strong sensitivity to β-cyclocitral, a volatile isoprenoid
commonly found in green plant tissues such as strawberry leaves[33]. This represents a
major functional innovation, as neither *D. melanogaster* nor *D. biarmipes* ab3A neurons
respond to this compound. Thus, detection of β-cyclocitral likely serves as a vegetative
cue that signals the presence of a host plant bearing fruit, providing *D. suzukii* with a
sensory advantage in locating oviposition sites while the fruit is still attached to the plant.
423
The capacity for functional plasticity in ab3A neurons is a recurring theme in
Drosophila evolution. This neuronal type has repeatedly shifted its odorant tuning across
species and even among populations, often in response to divergent ecological
pressures[37,39-43]. These shifts are frequently mediated by amino acid changes in the *Or22*
locus, which encodes the primary odorant receptor(s) in ab3A[20,41,43]. In the noni-specialist
D. sechellia, for example, *Or22a* has acquired substitutions that enhance its sensitivity to
methyl esters, which are abundant in noni fruit[41]. Genetic approaches have demonstrated
that these sequence changes are sufficient to alter the ab3A sensitivity and that this
receptor is important for mediating long-range attraction to noni[41].
433
Similarly, in *D. suzukii*, we identified multiple amino acid substitutions in *Or22a*,
including two at known functional hotspots, I45A and D201A, previously implicated in
tuning modulation in other *Drosophila* species[20,41]. Our structural modeling and molecular
docking analyses indicate that the D201A substitution plays a key role in the tuning shift
of *Or22a* in *D. suzukii*. This substitution reorganizes the architecture of the ligand-binding
pocket, likely altering the shape and electrostatic environment of the odorant interface.
Furthermore, functional assays using a site-directed A201D mutant revealed markedly
reduced responses to odorants, with its responses to isobutyl acetate across dilutions
more closely resembling those of *D. melanogaster* ab3A than *D. suzukii* ab3A or wild-
type *DsuzOr22a*, indicating partial reversion to the ancestral tuning state. However,
similar tuning shifts and a substitution at position 201 were also observed in *D. biarmipes*,
suggesting that *Or22a* diversification occurred prior to the shift to ripe fruit and may have
evolved under different selective pressures.
447
Despite the functional impact of *Or22a* sequence evolution, it alone cannot account
for the novel β-cyclocitral sensitivity. This response is absent in both *D. melanogaster*
and *D. biarmipes*, indicating that the gain of β-cyclocitral sensitivity is a derived feature
unique to *D. suzukii*. Our genetic and functional analyses revealed that β-cyclocitral
sensitivity is mediated by a second odorant receptor co-expressed with *Or22a* in ab3A
neurons. The response to β-cyclocitral was eliminated in *Orco* mutant flies confirming that
the receptor that mediates this response belongs to the OR family rather than the
ionotropic or gustatory receptor families. Recruitment of a second receptor likely reflects
the chemical dissimilarity of β-cyclocitral from typical *Or22a* ligands and represents a
strategic expansion of the odorant space encoded by a single ORN. This co-expression
may also enable more refined odorant coding: combined input from both receptors

indicates the presence of a high-quality oviposition site, while activation of *Or22a* alone
signals suboptimal substrates. Such combinatorial coding could sharpen host selection
and oviposition decisions.
462
***Or67a* Gene Family Expansion and Deployment Across Neurons**
The ab10A and ab2B neurons in *D. suzukii* have also undergone substantial functional
and molecular remodeling. In *D. melanogaster*, ab10A neurons express a single receptor,
Or67a, tuned to a broad range of compounds[25,26], whereas ab2B neurons express *Or85a*,
which responds to esters and alcohols typically associated with microbial fruit
degradation[25-27,34].
469
The response profiles of these two neuronal types have shifted markedly during
Drosophila evolution[44-46]. Changes in ab10A are likely driven by *Or67a* gene expansion;
for example, *D. simulans* carries three *Or67a* paralogs, all expressed in ab10A and
contributing to its novel response profile[16]. By contrast, the mechanisms underlying ab2B
tuning shifts remain less well understood. In several species, changes in ab2B odorant
response profiles are associated with the loss of *Or85a*[44,45], but the receptors that replace
it remain unidentified.
477
In *D. suzukii*, *Or85a* is not detected in the genome[22,23], while *Or67a* has
expanded into five paralogs: four intact paralogs (*Or67a1* through *Or67a4*) and one
pseudogene, *Or67a5*, which contains a premature stop codon[22,23]. Our functional
characterization of these paralogs revealed a clear partitioning of activity. *Or67a1* and
Or67a2 are likely co-expressed in ab10A neurons, and their co-expression produced a
response profile that is more similar to that of ab10A than either receptor alone. By
contrast, Or67a4 (and to a lesser extent Or67a3) exhibited responses that are similar to
those of ab2B neurons, and deletion of *Or67a4* severely reduced ab2B responses to
odorants, providing direct evidence that this receptor underlies the novel tuning of ab2B
neurons in *D. suzukii*.
488
489　　　　*D. biarmipes* has also expanded *Or67a* into four functional paralogs. However,
490 only ab10A neurons show a tuning shift resembling that of *D. suzukii*, while ab2B
491 neurons retain a *D. melanogaster*-like odorant response profile, consistent with the
492 detection of *Or85a* in its genome.
493
These differences suggest that the recruitment of *Or67a4* (and most likely
Or67a3) into the ab2B neurons is a unique feature to *D. suzukii*, likely emerging after
the genomic loss of *Or85a*. As such, *D. biarmipes* represents an intermediate
evolutionary state: while it shows early signs of olfactory adaptation in ab3A and ab10A
neurons, it does not exhibit β-cyclocitral sensitivity in ab3A neurons, which in *D. suzukii*
arises from the co-expression of a second receptor alongside *Or22a*, nor does it show
evidence for receptor reassignment in ab2B.
501
502　　　　In summary, by co-expressing a second OR with *Or22a* in ab3A and partitioning
503 *Or67a* paralogs between ab10A and ab2B, *D. suzukii* expands its odorant tuning
504 without creating new neuronal classes or rewiring central circuits. This illustrates how

gene loss, duplication, functional divergence, and receptor redeployment can reprogram olfactory function to meet the demands of novel ecological niches.

Limitations of the study

A key limitation of our study is that, although we discovered that *D. suzukii* ab3A neurons express an additional receptor enabling detection of β-cyclocitral, the identity of this receptor remains unknown. Additionally, while our data indicate that *Or67a1* and *Or67a2* are co-expressed in ab10A neurons and that *Or67a4* has replaced the ancestral *Or85a* in ab2B neurons, *Or67a3* is also a strong candidate for ab2B expression, as its ectopic expression produces responses resembling those of native ab2B neurons, and no other ORN responses resemble those of Or67a3. Notably, *Or67a3* lies immediately downstream of *Or67a4*, separated by fewer than 500 base pairs, raising the possibility that our CRISPR-mediated knockout of *Or67a4* may have inadvertently affected *Or67a3* expression. Finally, the regulatory mechanisms governing the partitioned expression of *Or67a* paralogs across these distinct neurons in *D. suzukii* remain unresolved.

Methods

***Drosophila* stocks**

Flies, 5-7 days old, were reared on corn syrup and soy four culture medium (Archon Scientifc) at 24°C and 50% relative humidity in a 12:12-h light–dark cycle. *D. melanogaster* Canton-S stock was CS-5. *D. suzukii* Connecticut (CT), North Carolina (NC), and California genome (WT3) strains were obtained from Dr. Richard S. Cowles, Dr. Maxwell J. Scott, and Dr. Joanna C. Chiu, respectively. *D. biarmipes* (14,023–0361.04) stock was obtained from the Drosophila Species Stock Center. *D. suzukii* $Orco^3$ mutant line was obtained from Dr. Benjamin Prud'homme. The *D. melanogaster* empty neuron system ($Or22ab^{Gal4}$) was obtained from Dr. John R. Carlson.

Odorants

Odorants of the highest available purity were obtained from Millipore Sigma, TCI America, or Thermo Scientific Chemicals and stored as recommended. A complete list of odorants is provided in Table S1. Odorants were dissolved in hexane (Millipore Sigma, Catalog #139386). Odor presentation was performed by inserting a Pasteur pipette tip into a hole in a 20 cm delivery tube, which directed a continuous airstream over the labium. The airflow through the pipette was controlled using a Stimulus Air Controller CS-55 V2 (Syntech), delivering a 0.5 s pulse. The wind speed at the position of the mounted animal, after adding the odorized stimulus to the continuous airflow, was approximately 50 cm s^{-1}. As an odor source, a cellulose filter disc (~1 cm diameter) soaked with 10 µl of diluted odorant was placed inside a disposable borosilicate glass Pasteur pipette (2 ml capacity, Fisher Scientific GSA). Odorants were presented sequentially, with at least 60 s between presentations. For dose–response analyses, odorants were delivered in increasing concentrations in logarithmic steps.

Electrophysiology

A single fly was placed in a 200-µL plastic pipette tip with its head directed towards the narrower end to allow only the antennae to protrude. The pipette tip was then securely attached to a glass microscope slide. The antenna was gently stabilized on a cover slip

using a glass capillary. The slide was then placed under a light microscope (BX51WI,
Olympus, Tokyo, Japan) equipped with a 50 × objective (LMPLFLN 50X, Olympus) and
10 × eyepieces. A reference tungsten electrode (catalog no. 716000, A-M Systems),
electrolytically sharpened to 1 μm tip diameter by dipping it repeatedly in a 10% KNO3
solution, was inserted into the eye. The recording tungsten electrode, identical to the
reference electrode, was inserted gently into the base of a coeloconic sensillum. Signals
were amplified (10 × ; Syntech Universal AC/DC Probe; http://www.syntech.nl), sampled
(10,667 samples s^{-1}), and filtered (100–3000 Hz with 50/60 Hz suppression) via a USB-
IDAC connection (Syntech) to a computer. Action potentials were extracted using
Syntech AutoSpike 32 software. Responses as the increase (or decrease) in the action
potential frequency (spikes/s) were calculated by subtracting the number of action
potentials during the 0.5 s preceding the odor stimulation from the number of action
potentials during the 0.5 s of odor stimulation. We then subtracted the response to
hexane from the response to the odorant, and the differences are what we reported.
The lifetime kurtosis (K) was calculated using the following formula described in [47].
566
Continuous airflow
A 20 cm glass tube with an inner diameter of approximately 4 mm supplied activated
charcoal-filtered humidified air to the labium. Air, continuous and pulsed, was generated
by a Stimulus Air Controller CS-55 V2 from Syntech (https://www.ockenfels-
syntech.com/products/stimulus-controllers/). The end of the tube was placed about 1 cm
from the preparation, and the continuous airflow near the mounted animal had a speed
of approximately 40 cm s−1.
574
***Generating UAS-DsuzOr* lines**
Five *D. suzukii* WT3 females were collected, and whole animals were immediately
homogenized for RNA extraction using TRIzol reagent (Invitrogen). The extracted RNA
was treated with TURBO DNase (Invitrogen) to remove residual genomic DNA. 1 μg of
purified RNA was used for cDNA synthesis with oligo(dT) primers using SuperScript IV
Reverse Transcriptase (Invitrogen) for the generation of PCR template for subsequent
amplifications of *DsuzOr* genes. PCR reactions were conducted using Phusion High-
Fidelity DNA Polymerase (Thermo Scientific) under standard thermal cycling conditions
in a Bio-Rad thermocycler. PCR products were separated on 1.0% agarose gel, and
DNA fragments of the expected sizes were excised and purified according to the
manufacturer's instructions (Wizard SV Gel and PCR Cleanup System, Promega).
586
DsuzOrs were cloned into the pJFRC81-10XUAS-IVS-Syn21-GFP-p10 vector
(pJFRC81, Addgene plasmid #36432). Forward and reverse PCR primers
of *DsuzOrs* were designed with 20 bp overhangs complementary to the regions flanking
the GFP coding sequence in pJFRC81. The pJFRC81 vector was linearized by PCR
using primers flanking the GFP sequence, with effective removal of the GFP coding
region. Gibson assembly (NEB) was then used to ligate the amplified *DsuzOr* fragments
into the linearized vector. The resulting constructs were transformed into bacteria and
sequence-verified. Verified plasmids were injected into embryos of BDSC Stock #8622
by BestGene Inc. for PhiC31-mediated site-specific integration. Primers are provided in
Table S2.

CRISPR–Cas9-mediated genome engineering

Single guide RNAs (sgRNAs) targeting *DsuzOrs* were designed using the online CHOPCHOP tool (https://chopchop.cbu.uib.no/). sgRNAs were synthesized through *in vitro* transcription using the GeneArt Precision gRNA Synthesis Kit (Thermo Fisher Scientific). The sgRNA was mixed with Cas9 protein (TrueCut, Invitrogen) at a final concentration of 200 ng/µl and 500ng/µl, respectively, in a 10 µl reaction with 1 µl of injection buffer (300 mM sodium phosphate and 1 mM potassium chloride) and an additional 1 µl of 2M potassium chloride. The sgRNA/Cas9 mixture was incubated at 37ºC for 10 min in a thermocycler to promote ribonucleoprotein (RNP) complex formation. The resulting RNP solution was passed through a Millipore Ultrafree-MC filter (0.45 µM pore size) and kept on ice until ready to use.

The microinjection of RNPs into *Drosophila* embryos was performed using a FemtoJet 4i microinjector (Eppendorf). Injection needles were prepared from capillary tubes (World Precision Instrument, 1B100F-4) using a micropipette puller (Model P-1000, Sutter Instrument). One day before microinjection, approximately 300 flies (3-5 days old) were transferred to an egg-laying chamber (Flystuff Cat #59-100) containing a Petri dish filled with 10 ml of egg-laying substrate composed of 25g agar and 200ml molasses dissolved in 500 ml of water. To diminish the older eggs retained in the females' ovaries, the egg-laying Petri dish was replaced every 20 min for at least 5 times before injection. Only embryos laid within 20 min were used for injection, and the entire injection process was completed within 1h.

G0 females that emerged from injected embryos (G0) were crossed to wild-type flies to generate G1 heterozygotes. G1 individuals with potential CRISPR-induced mutations were crossed again to wild-type flies to produce G2 heterozygotes. G1 flies were sacrificed for genotyping to confirm the mutation types. G2 heterozygotes were self-crossed to obtain homozygous mutants and establish stable mutant lines. Mutants were identified using a PCR-based screening strategy. Primers for sgRNA synthesis and mutant screening are listed in Table S3.

Structural prediction and molecular docking.

The 3D homotetrameric structures of *DsuzOr22a*$^{WT(D201A)}$ and *DsuzOr22a*^{A201D} were generated with AlphaFold2[48]. The highest-confidence predictions (*model_0*) were selected for docking. The ligand, isobutyl acetate (SDF file), was obtained from PubChem (https://pubchem.ncbi.nlm.nih.gov/) and converted to mol2 format with OpenBabel (v3.1.1)[49]. Structural preparation of both the ligand and receptor subunits was performed in PyMol (v3.1.4), and the resulting files were converted to PDBQT format with AutoDockTools (v1.5.7). Molecular docking was carried out using AutoDock Vina (v1.2.7) with a cubic grid box (20 Å x 20 Å x 20 Å) centered on the transmembrane domains. Receptor–ligand interactions were analyzed with the Protein-Ligand Interaction Profiler (v2.4.0) and visualized in PyMol (v3.1.4).

Quantification and statistical analysis
The heatmaps were generated in PAST. Euclidean distances were calculated in R
(version 4.2.3) using the 'moments' package, and other statistical tests were performed
in GraphPad Prism (version 10.0.1 [316]).

Acknowledgements
This work was supported by NIH grant K01 DC020145 to H.K.M.D.

Contributions

H.K.M.D. conceived the study. H.K.M.D. and Q.X. designed the experiments. H.K.M.D.
and Q.X. carried out the experiments. H.K.M.D. and Q.X. analysed the data. H.K.M.D.
and Q.X. prepared the original draft of the manuscript. H.K.M.D. and Q.X. read and
approved the final version of the manuscript.

Figure legends

Figure 1. Shared shifts in odor tuning of ab3A and ab10A in *D. suzukii* and *D. biarmipes*.

(A) Responses of ab2B, ab3A, ab4B, and ab10A neurons in *D. suzukii* (n = 3–6) and *D. melanogaster* (n = 3) to the indicated odorants. Each odorant was tested at a 10^{-2}
dilution. Error bars indicate SEM.

(B) Example traces of the response of the ab3 sensillum type to a 10^{-4} dilution of ethyl
hexanoate in *D. suzukii* (CT-strain), *D. biarmipes*, and *D. melanogaster*.

(C) Example traces of the response of the ab3 sensillum type to a 10^{-4} dilution of β-
cyclocitral in *D. suzukii* (CT-strain), *D. biarmipes*, and *D. melanogaster*.

(D) Responses of ab3A in three strains of *D. suzukii*, *D. biarmipes*, and *D. melanogaster*
to a 10^{-4} dilution of each of the indicated odorants. One-way ANOVA followed by
Tukey's multiple comparison test; n = 10. Values marked with different letters are
significantly different. Error bars represent SEM.

(E-G) Responses of ab3A to different dilutions of ethyl hexanoate (E), isobutyl acetate
(F), and β-cyclocitral (G) in *D. suzukii* (CT-strain), *D. biarmipes*, and *D. melanogaster*.
One-way ANOVA followed by Tukey's multiple comparison test; n = 5 for each dilution.
Values indicated with different letters are significantly different. Error bars represent
SEM.

(H) Responses of ab10A in three strains of *D. suzukii*, *D. biarmipes*, and *D. melanogaster* to a 10^{-4} dilution of each of the indicated odorants. One-way ANOVA
followed by Tukey's multiple comparison test; n = 10. Values indicated with different
letters are significantly different. Error bars represent SEM.

(I-K) Responses of ab3A to different dilutions of benzyl butyrate (I), β-citronellol (J), and
geranyl acetate (K) in *D. suzukii* (CT-strain), *D. biarmipes*, and *D. melanogaster*. One-
way ANOVA followed by Tukey's multiple comparison test; n = 5 for each dilution.
Values indicated with different letters are significantly different. Error bars represent
SEM.

Figure 2. Species-specific shifts in odor tuning of ab2B and ab4B in *D. suzukii*.

(A) Example traces of the response of the ab2 sensillum type to a 10^{-4} dilution of ethyl
3-hydroxybutyrate in *D. suzukii* (CT-strain), *D. biarmipes*, and *D. melanogaster*.

(B) Example traces of the response of the ab2 sensillum type to a 10^{-4} dilution of
isoamyl acetate in *D. suzukii* (CT-strain), *D. biarmipes*, and *D. melanogaster*.

(C) Responses of ab2B in three strains of *D. suzukii*, *D. biarmipes*, and *D. melanogaster*
to a 10^{-4} dilution of each of the indicated odorants. One-way ANOVA followed by
Tukey's multiple comparison test; n = 10. Values marked with different letters are
significantly different. Error bars represent SEM.

(D-F) Responses of ab2B to different dilutions of ethyl 3-hydroxybutyrate (D), isoamyl
acetate (E), and butyl acetate (F) in *D. suzukii* (CT-strain), *D. biarmipes*, and *D.*
melanogaster. One-way ANOVA followed by Tukey's multiple comparison test; n = 5 for
each dilution. Values indicated with different letters are significantly different. Error bars
represent SEM.

(G) Responses of ab4B in three strains of *D. suzukii*, *D. biarmipes*, and *D.*
melanogaster to 10^{-4} dilution of the indicated odorants. One-way ANOVA followed by
Tukey's multiple comparison test; n = 10. Values indicated with different letters are
significantly different. Error bars represent SEM.

(H-J) Responses of ab4B to different dilutions of ethyl salicylate (H), methyl salicylate
(I), and methyl benzoate (J) in *D. suzukii* (CT-strain), *D. biarmipes*, and *D.*
melanogaster. One-way ANOVA followed by Tukey's multiple comparison test; n = 5 for
each dilution. Values indicated with different letters are significantly different. Error bars
represent SEM.

Figure 3. ab3A neurons in *D. suzukii* express two odorant receptors, one of which
is tuned to β-cyclocitral.

(A) Illustration of the *D. melanogaster* empty neuron system.

(B) Example traces of the responses of *D. suzukii* ab3A neurons and *DsuzOr22a* to a
10^{-4} dilution of isobutyl acetate.
(C) Example traces of the responses of *D. suzukii* ab3A neurons and *DsuzOr22a* to a
10^{-4} dilution of β-cyclocitral.

(D) Responses of *D. suzukii* ab3A neurons and *DsuzOr22a* to eleven odorants, each tested at a 10^{-4} dilution. ns=not significant; ****p<0.0001; Mann-Whitney test; n = 10. Error bars represent SEM.

(E) Schematic illustrating the generation of DsuzOr22a mutants using CRISPR/Cas9-mediated gene disruption.

(F) Example traces of the responses of ab3A neurons in wildtype *D. suzukii*, *DsuzOr22a*^{1}, and *DsuzOr22a*^{2} to a 10^{-4} dilution of isobutyl acetate.

(F) Example traces of the responses of ab3A neurons in wildtype *D. suzukii*, *DsuzOr22a*^{1}, and *DsuzOr22a*^{2} to a 10^{-4} dilution of β-cyclocitral.

(H) Responses of ab3A neurons in wildtype *D. suzukii*, *DsuzOr22a*$^{1/+}$, *DsuzOr22a*$^{2/+}$, *DsuzOr22a*^{1}, and *DsuzOr22a*^{2} to a battery of eleven odorants, each tested at a 10^{-4} dilution . One-way ANOVA followed by Tukey's multiple comparison test; n = 10. Values indicated with different letters are significantly different. Error bars represent SEM.

(I) Responses of wildtype *D. suzukii* ab3A neurons, *DsuzOr22a*$^{WT(D201A)}$, *DsuzOr22a*$^{(A201)}$, and wildtype *D. melanogaster* ab3A neurons to a battery of ten odorants, each tested at a 10^{-4} dilution. One-way ANOVA followed by Tukey's multiple comparison test; n = 10. Values indicated with different letters are significantly different. Error bars represent SEM.

(I) Responses of wildtype *D. suzukii* ab3A neurons, *DsuzOr22a*$^{WT(D201A)}$, *DsuzOr22a*$^{(A201)}$, and wildtype *D. melanogaster* ab3A neurons to different dilutions of isobutyl acetate. One-way ANOVA followed by Tukey's multiple comparison test; n = 10. Values indicated with different letters are significantly different. Error bars represent SEM.

Figure 4. Responses of *D. suzukii* Or67a paralogs to a battery of 119 odorants.

(A) Responses of *DsuzOr67a1*, *DsuzOr67a2*, and *DsuzOr67a1+2* to a battery of 119, each tested at a 10-4 dilution. n = 5. Error bars represent SEM.

(B) Responses of *DsuzOr67a3*, *DsuzOr67a4*, and *DsuzOr67a3+4* to a battery of 119, each tested at a 10-4 dilution. n = 5. Error bars represent SEM.

Figure 5. *Or67a4* is expressed in ab2B neurons.

(A) Schematic illustrating the generation of the *DsuzOr67a4*^{1} mutant using CRISPR/Cas9-mediated gene disruption.

779   (B) Example traces of the responses of ab2B neurons in wildtype *D. suzukii*,
780   *DsuzOr67a$^{1/+}$*, and *DsuzOr67a^{1}* to a 10^{-4} dilution of isoamyl acetate.
781
782   (C) Responses of ab2B neurons in wildtype *D. suzukii*, *DsuzOr67a$^{1/+}$*, and *DsuzOr67a^{1}*
783   to a panel of 15 odorants, each tested at a 10^{-4} dilution. One-way ANOVA followed by
784   Tukey's multiple comparison test; n = 10. Values indicated with different letters are
785   significantly different. Error bars represent SEM.
786
787
788   **Supplementary Tables and Figures**
789   **Table 1. List of odorants**
790

Odorants	Source	Catalog number
1-Heptanol	Millipore Sigma	72954
1-Nonanol	Millipore Sigma	74280
1-Octen-3-ol	Millipore Sigma	O5284
1-Propanol	Millipore Sigma	34871
2,3-Butanediol	Millipore Sigma	B84904
2-Methyl-1-butanol	Millipore Sigma	133051
2-Methyl-1-propanol	Millipore Sigma	538132
3-Methyl-1-butanol	Millipore Sigma	77664
2-Phenylethanol	Millipore Sigma	77861
6-Methyl-5-hepten-2-ol	Millipore Sigma	W488401
Ethanol	Millipore Sigma	459828
Farnesol	Millipore Sigma	43348
trans-2-Hexen-1-ol	Millipore Sigma	W256218
Butyraldehyde	Millipore Sigma	538191
Hexanal	Millipore Sigma	18109
Phenylacetaldehyde	Millipore Sigma	W287407
trans-2-Hexen-1-al	Millipore Sigma	132659
trans-2-nonenal	TCI America	N04835ML
trans,trans-2,4-nonadienal	TCI America	N05215ML
2,3-Butanedione	Millipore Sigma	11038
2-Acetoxy-3-butanone	Millipore Sigma	W352623
2-Heptanone	Millipore Sigma	537683
2-Nonanone	Millipore Sigma	W278505
3-Nonanone	Millipore Sigma	
3-Octanone	Millipore Sigma	136913
4-Methyl-3-hepten-2-one	Millipore Sigma	49722
Acetone	Millipore Sigma	90872
Acetophenone	Millipore Sigma	42163
2-Ethylhexanoic acid	Millipore Sigma	538701
2-Methylbutyric acid	Millipore Sigma	193070
2-Oxovaleric acid	Millipore Sigma	75950
3-Butenoic acid	Millipore Sigma	134716

Acetic acid	Millipore Sigma	A6283
Butyric acid	Millipore Sigma	B103500
Heptanoic acid	Millipore Sigma	W334804
Hexanoic acid	Millipore Sigma	153745
Isobutyric acid	Millipore Sigma	W222208
Linoleic acid	Millipore Sigma	62230
Myristic acid	Millipore Sigma	W276413
Octanoic acid	Millipore Sigma	C2875
Oleic acid	Millipore Sigma	O1008
Pentanoic acid	Millipore Sigma	75054
Propionic acid	Millipore Sigma	402907
trans-3-Hexenoic acid	Millipore Sigma	W317004
Benzyl acetate	Millipore Sigma	50475
Benzyl butyrate	Millipore Sigma	W214000
Butyl acetate	Millipore Sigma	W217417
Butyl butyrate	Millipore Sigma	W218618
Butyl hexanoate	Millipore Sigma	W220108
Butyl isovalerate	Millipore Sigma	W221805
cis-3-hexenyl acetate	Millipore Sigma	74597
cis-3-hexenyl butyrate	Millipore Sigma	W340210
cis-3-hexenyl lactate	Millipore Sigma	W369020
Citronellyl acetate	Millipore Sigma	W231118
Diethyl succinate	Millipore Sigma	W237701
Ethyl (methylthio)acetate	Millipore Sigma	W383503
Ethyl 3-(methylthio)propionate	Millipore Sigma	W334308
Ethyl 3-hydroxybutyrate	Thermo Scientific Chemicals	AC118540250
Ethyl 3-hydroxyhexanoate	Millipore Sigma	W354503
Ethyl acetate	Millipore Sigma	L000325ML
Ethyl benzoate	Millipore Sigma	W242217
Ethyl butyrate	Millipore Sigma	75563
Ethyl decanoate	Millipore Sigma	148970
Ethyl Heptanoate	Millipore Sigma	W243728
Ethyl hexanoate	Millipore Sigma	148962
Ethyl isovalerate	Millipore Sigma	71607
Ethyl lactate	TCI America	L000325ML
Ethyl octanoate	Millipore Sigma	W244910
Ethyl salicylate	Millipore Sigma	68291
Ethyl *trans*-2-butenoate	TCI America	C0418
Ethyl *trans*-2-octenoate	Millipore Sigma	W364304
Geranyl acetate	Millipore Sigma	173495
Hexyl-2-methylbutanoate	Millipore Sigma	W349909
Hexyl hexanoate	Millipore Sigma	W257206
Isoamyl acetate	Millipore Sigma	W205532
Isoamyl butyrate	Millipore Sigma	W206008
Isobutyl acetate	Thermo Scientific Chemicals	AAB2570009

Methyl benzoate	Millipore Sigma	18344
Methyl hexanoate	Millipore Sigma	259942
Methyl isobutyrate	Millipore Sigma	W269409
Methyl octanoate	Millipore Sigma	21719
Methyl salicylate	Millipore Sigma	76631
Pentyl acetate	Millipore Sigma	109584
Phenethyl propionate	Millipore Sigma	W286702
Phenyl acetate	Millipore Sigma	108723
trans-2-Hexenyl acetate	Millipore Sigma	W256404
α-Terpinyl acetate	Millipore Sigma	W304799
4-Ethylguaiacol	Millipore Sigma	39774
4-Methyl veratrole	Millipore Sigma	ALNH9A9DBBB4
Guaiacol	Millipore Sigma	W253200
Indole	TCI America	I002125G
p-Cresol	Millipore Sigma	42429
Veratrole	Millipore Sigma	W379905
Eugenol	Millipore Sigma	35995
Methyl Eugenol	Millipore Sigma	04607
1,4-Diaminobutane	Millipore Sigma	D13208
2-Phenylethylamine	Millipore Sigma	8073340005
Ammonia hydroxide	Millipore Sigma	338818
Cadaverine	Millipore Sigma	33211
Spermidine	Millipore Sigma	S2626
Pyridine	Millipore Sigma	27040
Pyrrolidine	Millipore Sigma	W352316
(+)-Limonene oxide	Millipore Sigma	218324
(R)-(+)-Limonene	Millipore Sigma	62118
(S)-(-)-Limonene	Millipore Sigma	62128
(-)-Menthone	Millipore Sigma	63677
(-)-*trans*-Caryophyllene	Millipore Sigma	75541
Farnesene	Millipore Sigma	W383902
Sabinene	Millipore Sigma	W530597
Terpinolene	Millipore Sigma	W304603
Valencene	Millipore Sigma	W344303
α-Ionone	Millipore Sigma	03642
α-Phellandrene	Millipore Sigma	W285611
α-Pinene	Millipore Sigma	147524
α-Terpineol	Millipore Sigma	04899
β-Citronellol	Millipore Sigma	C83201
β-Cyclocitral	Thermo Scientific Chemicals	AAB2570009
β-Ionone	Millipore Sigma	W259525
γ-Terpinene	Millipore Sigma	223190
γ-Decalactone	Millipore Sigma	93738
γ-Hexalactone	Millipore Sigma	68554
1-Heptadecene	Millipore Sigma	H1108

DEET	Millipore Sigma	36542
Diallyl disulfide	Millipore Sigma	30648

791
792
793 **Table 2. List of primers for UAS constructs**

	Forward primer (5' to 3')	Reverse primer (5' to 3')
DsuzO r22a	ATGTTAGCCAAATTTTTTCCGC	CTATTTAAACTTTTCGGCTAAG
DsuzO r23a-1	ATGAAACTCAGCAAGATTTCCG	TTATTTAAATGAAACTTGAGTTGGATG
DsuzO r23a-2	ATGAAACTCAGCAAGATCTTTG	TTACAAAAAAGAACCTTGGCCATC
DsuzO r23a-3	ATGGAACTCACCAAGATCCTTG	TTAAGTCCTCCGGTTTAGGGAG
DsuzO r23a-4	ATGGAACTCACCAAGATCCATG	TTATTTAAATGAAACTTGAGTTGGATG
DsuzO r23a-1+4	Or23a1 part: ATGAAACTCAGCAAGATTTCCG	Or23a1 part: tgttctttcactgactgagtttttgcagatggctgg aaatgaaacttgagctggatggtc
	Or23a4 part: tcagtcagtgaaagaacaaaaccagacaggatg gaactcaccaagatccttgagattgac	Or23a4 part: ttaaaatgaaactttagttggatg
DsuzO r67a-1	ATGATTGATTTAATAAAACAAAAAAT TTTTG	TTACTTGTACATCATTCGAACGG
DsuzO r67a-2	ATGAGCATTGACTTAAAAAAGAAG	CTACTGATACATCATTCGAATGG
DsuzO r67a-3	ATGGCTATTAACTTGTTTAGAAAGG	TTACTGATACATTGTTCGAATGG
DsuzO r67a-4	ATGAGTGTCCAGTTTATCAAAAAAC	TTATTGACACACTGTTTTTATAG C
DsuzO r67a-5	ATGAGGGTCGACTCCTTGAAG	CTACTGATACATAGTTCGAAGA GC
Note: flanking regions were added to the forward (5'-CAACTTAAAAAAAAAATCAAA-3') and reverse (5'-TAAAAACGATTCATTCTAGA-3') primers.		

Table 3. Primers for CRISPR

	Forward primer (5' to 3')	Reverse primer (5' to 3')
DsuzOr22a gRNA synthesize	TAATACGACTCACTATAGcactttcctctgaccaagca	TTCTAGCTCTAAAACtgcttggtcagaggaaagtg
DsuzOr22a screen	tgccaatatcgattgtcgtg	atactgaccgtgggacaaaca
DsuzOr67a4 gRNA synthesize	TAATACGACTCACTATAGATCGATGCCATACGTTGAGT	TTCTAGCTCTAAAACACTCAACGTATGGCATCGAT
DsuzOr67a4 screen	CGAGTCCTCGAAACCTGAAG	ATGCCGAACACCACGTTTAT

Figure S1. Responses of ORNs housed in D. suzukii and *D. melanogaster* antennal Basiconic, and intermediate, and trichoid sensilla.

(A,B) Heatmap of responses of ORNs housed in *D. suzukii* (A) and *D. melanogaster* (B) antennal basiconic, intermediate, and trichoid sensilla to 113 odorants. Each odorant was diluted in hexane and tested at a 10^{-2} dilution. Odorants are color coded by functional group.

Figure S2. Responses of large basiconic sensilla in *DsuzOrco³* to β-cyclocitral.

Figure S3. A single amino acid substitution alters the architecture of the ligand-binding pocket of Or22a in *D. suzukii*.

(A) Alignment of *D. melanogaster*, *D. suzukii*, and *D. biarmipes Or22a* orthologs.

(B) the location of the ligand-binding pocket with docked isobutyl acetate.

References

References

1   Benton, R. *Drosophila* olfaction: past, present and future. *Proc Biol Sci* **289**, 20222054
(2022). https://doi.org:10.1098/rspb.2022.2054
2   Hansson, B. S. & Stensmyr, M. C. Evolution of insect olfaction. *Neuron* **72**, 698-711 (2011).
https://doi.org:10.1016/j.neuron.2011.11.003
3   Joseph, R. M. & Carlson, J. R. *Drosophila* Chemoreceptors: A Molecular Interface Between
the Chemical World and the Brain. *Trends Genet* **31**, 683-695 (2015).
https://doi.org:10.1016/j.tig.2015.09.005
4   Montell, C. Drosophila sensory receptors-a set of molecular Swiss Army Knives. *Genetics*
217, 1-34 (2021). https://doi.org:10.1093/genetics/iyaa011
5   Andersson, M. N., Löfstedt, C. & Newcomb, R. D. Insect olfaction and the evolution of
receptor tuning. *Frontiers in Ecology and Evolution* **Volume 3 - 2015** (2015).
https://doi.org:10.3389/fevo.2015.00053
6   Auer, T. O., Shahandeh, M. P. & Benton, R. *Drosophila sechellia*: A Genetic Model for
Behavioral Evolution and Neuroecology. *Annu Rev Genet* **55**, 527-554 (2021).
https://doi.org:10.1146/annurev-genet-071719-020719
7   Keesey, I. W. Sensory neuroecology and multimodal evolution across the genus
Drosophila. *Frontiers in Ecology and Evolution* **Volume 10 - 2022** (2022).
https://doi.org:10.3389/fevo.2022.932344
8   Nozawa, M. & Nei, M. Evolutionary dynamics of olfactory receptor genes in *Drosophila*
species. *Proc Natl Acad Sci U S A* **104**, 7122-7127 (2007).
https://doi.org:10.1073/pnas.0702133104
9   Peláez, J. N. *et al.* Evolution of chemosensory and detoxification gene families across
herbivorous Drosophilidae. *G3 Genes|Genomes|Genetics* **13** (2023).
https://doi.org:10.1093/g3journal/jkad133
10   Sánchez-Gracia, A., Vieira, F. G. & Rozas, J. Molecular evolution of the major chemosensory
gene families in insects. *Heredity* **103**, 208-216 (2009). https://doi.org:10.1038/hdy.2009.55
11   Eyun, S. I. *et al.* Evolutionary history of chemosensory-related gene families across the
Arthropoda. *Mol Biol Evol* **34**, 1838-1862 (2017). https://doi.org:10.1093/molbev/msx147
12   McBride, C. S., Arguello, J. R. & O'Meara, B. C. Five Drosophila genomes reveal nonneutral
evolution and the signature of host specialization in the chemoreceptor superfamily.
Genetics **177**, 1395-1416 (2007). https://doi.org:10.1534/genetics.107.078683
13   Dweck, H. K., Talross, G. J., Wang, W. & Carlson, J. R. Evolutionary shifts in taste coding in
the fruit pest *Drosophila suzukii*. *Elife* **10** (2021). https://doi.org:10.7554/eLife.64317
14   Karageorgi, M. *et al.* Evolution of Multiple Sensory Systems Drives Novel Egg-Laying
Behavior in the Fruit Pest *Drosophila suzukii*. *Curr Biol* **27**, 847-853 (2017).
https://doi.org:10.1016/j.cub.2017.01.055
15   Yeh, D. A., Drummond, F. A., Gómez, M. I. & Fan, X. The economic impacts and
management of spotted wing *Drosophila* (*Drosophila Suzukii*): The case of wild blueberries
in Maine. *Journal of Economic Entomology* **113**, 1262-1269 (2020).
https://doi.org:10.1093/jee/toz360
16   Auer, T. O., Álvarez-Ocaña, R., Cruchet, S., Benton, R. & Arguello, J. R. Copy number
changes in co-expressed odorant receptor genes enable selection for sensory differences
in *drosophilid* species. *Nat Ecol Evol* **6**, 1343-1353 (2022). https://doi.org:10.1038/s41559-
022-01830-y
17   Goldman-Huertas, B. *et al.* Evolution of herbivory in *Drosophilidae* linked to loss of
behaviors, antennal responses, odorant receptors, and ancestral diet. *Proc Natl Acad Sci U*
S A **112**, 3026-3031 (2015). https://doi.org:10.1073/pnas.1424656112

18 Matsunaga, T. *et al.* Evolution of Olfactory Receptors Tuned to Mustard Oils in Herbivorous
Drosophilidae. *Mol Biol Evol* **39** (2022). https://doi.org:10.1093/molbev/msab362
19 Matsunaga, T. *et al.* Odorant receptors mediating avoidance of toxic mustard oils in
Drosophila melanogaster are expanded in herbivorous relatives. *bioRxiv* (2025).
https://doi.org:10.1101/2024.10.08.617316
20 Shaw, K. H., Johnson, T. K., Anderson, A., de Bruyne, M. & Warr, C. G. Molecular and
Functional Evolution at the Odorant Receptor Or22 Locus in *Drosophila melanogaster*.
Molecular Biology and Evolution **36**, 919-929 (2019).
https://doi.org:10.1093/molbev/msz018
21 Durkin, S. M. *et al.* Behavioral and Genomic Sensory Adaptations Underlying the Pest
Activity of *Drosophila suzukii*. *Mol Biol Evol* **38**, 2532-2546 (2021).
https://doi.org:10.1093/molbev/msab048
22 Hickner, P. V. *et al.* The making of a pest: Insights from the evolution of chemosensory
receptor families in a pestiferous and invasive fly, *Drosophila suzukii*. *BMC Genomics* **17**,
648 (2016). https://doi.org:10.1186/s12864-016-2983-9
23 Ramasamy, S. *et al.* The Evolution of olfactory gene families in *Drosophila* and the genomic
basis of chemical-Ecological adaptation in *Drosophila suzukii*. *Genome Biol Evol* **8**, 2297-
2311 (2016). https://doi.org:10.1093/gbe/evw160
24 Walker, W. B., 3rd *et al.* Comparative transcriptomic assessment of the chemosensory
receptor repertoire of *Drosophila suzukii* adult and larval olfactory organs. *Comp Biochem*
Physiol Part D Genomics Proteomics **45**, 101049 (2023).
https://doi.org:10.1016/j.cbd.2022.101049
25 Benton, R. *et al.* An integrated anatomical, functional and evolutionary view of the
Drosophila olfactory system. *EMBO reports* **0**, 1-22 (2025).
https://doi.org:https://doi.org/10.1038/s44319-025-00476-8
26 Dweck, H. K. M. *et al.* The Olfactory Logic behind Fruit Odor Preferences in Larval and Adult
Drosophila. *Cell Rep* **23**, 2524-2531 (2018). https://doi.org:10.1016/j.celrep.2018.04.085
27 Hallem, E. A. & Carlson, J. R. Coding of odors by a receptor repertoire. *Cell* **125**, 143-160
(2006). https://doi.org:10.1016/j.cell.2006.01.050
28 Dweck, H. K. *et al.* Olfactory channels associated with the *Drosophila* maxillary palp
mediate short- and long-range attraction. *Elife* **5** (2016).
https://doi.org:10.7554/eLife.14925
29 Xue, Q., Hasan, K. S., Dweck, O., Ebrahim, S. A. M. & Dweck, H. K. M. Functional
characterization and evolution of olfactory responses in coeloconic sensilla of the global
fruit pest *Drosophila suzukii*. *BMC Biol* **23**, 50 (2025). https://doi.org:10.1186/s12915-025-
02151-9
30 Depetris-Chauvin, A. *et al.* Evolution at multiple processing levels underlies odor-guided
behavior in the genus *Drosophila*. *Curr Biol* **33**, 4771-4785 e4777 (2023).
https://doi.org:10.1016/j.cub.2023.09.039
31 Chiu, J. C. *et al.* Genome of Drosophila suzukii, the spotted wing drosophila. *G3 (Bethesda)*
3, 2257-2271 (2013). https://doi.org:10.1534/g3.113.008185
32 Ometto, L. *et al.* Linking genomics and ecology to investigate the complex evolution of an
invasive *Drosophila* pest. *Genome Biol Evol* **5**, 745-757 (2013).
https://doi.org:10.1093/gbe/evt034
33 Keesey, I. W., Knaden, M. & Hansson, B. S. Olfactory specialization in *Drosophila suzukii*
supports an ecological shift in host preference from rotten to fresh fruit. *J Chem Ecol* **41**,
121-128 (2015). https://doi.org:10.1007/s10886-015-0544-3

34   Versace, E. *et al.* Physiological and behavioral responses in *Drosophila melanogaster* to
odorants present at different plant maturation stages. *Physiol Behav* **163**, 322-331 (2016).
https://doi.org:10.1016/j.physbeh.2016.05.027
35   Cha, D. H., Adams, T., Rogg, H. & Landolt, P. J. Identification and field evaluation of
fermentation volatiles from wine and vinegar that mediate attraction of spotted wing
Drosophila, Drosophila suzukii. *J Chem Ecol* **38**, 1419-1431 (2012).
https://doi.org:10.1007/s10886-012-0196-5
36   Chahda, J. S. *et al.* The molecular and cellular basis of olfactory response to tsetse fly
attractants. *PLoS Genet* **15**, e1008005 (2019).
https://doi.org:10.1371/journal.pgen.1008005
37   Shaw, K. H., Johnson, T. K., Anderson, A., de Bruyne, M. & Warr, C. G. Molecular and
Functional Evolution at the Odorant Receptor *Or22* Locus in *Drosophila melanogaster*. *Mol
Biol Evol* **36**, 919-929 (2019). https://doi.org:10.1093/molbev/msz018
38   Butterwick, J. A. *et al.* Cryo-EM structure of the insect olfactory receptor Orco. *Nature* **560**,
447-452 (2018). https://doi.org:10.1038/s41586-018-0420-8
39   Dekker, T., Ibba, I., Siju, K. P., Stensmyr, M. C. & Hansson, B. S. Olfactory shifts parallel
superspecialism for toxic fruit in *Drosophila melanogaster* sibling, *D. sechellia*. *Curr Biol
16, 101-109 (2006). https://doi.org:10.1016/j.cub.2005.11.075
40   Stensmyr, M. C., Dekker, T. & Hansson, B. S. Evolution of the olfactory code in the
Drosophila melanogaster subgroup. *Proc Biol Sci* **270**, 2333-2340 (2003).
https://doi.org:10.1098/rspb.2003.2512
41   Auer, T. O. *et al.* Olfactory receptor and circuit evolution promote host specialization.
Nature **579**, 402-408 (2020). https://doi.org:10.1038/s41586-020-2073-7
42   Shaw, K. H. *et al.* Natural variation at the *Drosophila melanogaster Or22* odorant receptor
locus is associated with changes in olfactory behaviour. *Open Biol* **11**, 210158 (2021).
https://doi.org:10.1098/rsob.210158
43   Mansourian, S. *et al.* Wild African *Drosophila melanogaster* Are Seasonal Specialists on
Marula Fruit. *Curr Biol* **28**, 3960-3968 e3963 (2018).
https://doi.org:10.1016/j.cub.2018.10.033
44   Crowley-Gall, A. *et al.* Olfactory variation among closely related cactophilic *Drosophila*
species. *J Comp Physiol A Neuroethol Sens Neural Behav Physiol* (2025).
https://doi.org:10.1007/s00359-025-01744-7
45   de Bruyne, M., Smart, R., Zammit, E. & Warr, C. G. Functional and molecular evolution of
olfactory neurons and receptors for aliphatic esters across the *Drosophila* genus. *J Comp
Physiol A Neuroethol Sens Neural Behav Physiol* **196**, 97-109 (2010).
https://doi.org:10.1007/s00359-009-0496-6
46   Keesey, I. W. *et al.* Functional olfactory evolution in *Drosophila* suzukii and the subgenus
Sophophora. *iScience* **25**, 104212 (2022). https://doi.org:10.1016/j.isci.2022.104212
47   Silbering, A. F. *et al.* Complementary function and integrated wiring of the evolutionarily
distinct *Drosophila* olfactory subsystems. *J Neurosci* **31**, 13357-13375 (2011).
https://doi.org:10.1523/jneurosci.2360-11.2011
48   Jumper, J. *et al.* Highly accurate protein structure prediction with AlphaFold. *Nature* **596**,
583-589 (2021). https://doi.org:10.1038/s41586-021-03819-2
49   O'Boyle, N. M. *et al.* Open Babel: An open chemical toolbox. *J Cheminform* **3**, 33 (2011).
https://doi.org:10.1186/1758-2946-3-33
974

Figure 2

Figure 3

A

B

Dsuz-CT

ab2

DsuzOr67a4[1/+]

DsuzOr67a4[1]

Isoamyl acetate

C

Isoamyl acetate
Pentyl acetate
Butyl acetate
6-Methyl-5-hepten-2-ol
Benzyl acetate
2-Heptanone
trans-2-Hexenyl acetate
Isoamyl butyrate
3-Methyl-1-butanol
3-Octanone
cis-3-Hexenyl acitate
1-Octen-3-ol
Methyl hexanoate
3-Nonanone
Citronellyl acetate

Dsuz-ab2B   *DsuzOr67a4*[1]/+   *DsuzOr67a4*[1]

-50   250   -50   250   -50   250
Spikes/s   Spikes/s   Spikes/s

Figure S2

A

	pid		
DmelOr22a	100.0%	MLSKFFPHIKEKPLSERVKSRDAFIYLDRVMWSFGWTEPENKRWILPYKLWLAFVNIVML	60
DsuzOr22a	69.8%	MLAKFFPLIKERPLNERVQSRDAFIYLDRVMWTLGWTEPYEKRWAAVYKVFCFLTTMVCF	60
DbiaOr22a	69.0%	MLIKFFPLIKEKPLNELVQSRDAFIYLERVMWTLGWTEPYEKRWAVVYKVFSFMTSIGFF	60

TM1

DmelOr22a	100.0%	ILLPISISIEYLHRFKTFSAGEFLSSLEIGVNMYGSSFKCAFTLIGFKKRQEAKVLLDQL	120
DsuzOr22a	69.8%	ILVPISIVVEYVRRFKSFSAGEFLSSLEIGVNMYGCSFKNTYTLLGQRKVRKAKLILDRL	120
DbiaOr22a	69.0%	ILLPLSICVEYVNRFKSFSAGEFLSSLEIGVNMCGCSFKNTYTLLGRRKVRKAKLILDRL	120

TM2

DmelOr22a	100.0%	DKRCLSDKERSTVHRYVAMGNFFDILYHIFYSTFVVMNFPYFLLERRHAWRMYFPYIDSD	180
DsuzOr22a	69.8%	DERCLRDEEKSLVHRYVALGNFSYVVYHTCYWVFVITNFIGFLLIGHHAWRMFIPLLKSD	180
DbiaOr22a	69.0%	DERCLRDEEKSLVHRYVALGNFSYTVYHTCYWVFVITNFIGFLLIGHHAWRMYIPLLKSD	180

TM3

DmelOr22a	100.0%	EQFYISSIAECFLMTEAIYMDLCTDVCPLISMLMARCHISLLKQRLRNLRSKPGRTEDEY	240
DsuzOr22a	69.8%	EHFLISSVAEFLLMLYVVTMAQCSDVCPTVSMLMARCHILLLQKRVLRLRSDPGKGDDED	240
DbiaOr22a	69.0%	EHFLISSVAEFLLMLYVVTMAQCSDVCPTISMLMARCHIILLRNRMMRLRSDPEKGDDED	240

TM4

DmelOr22a	100.0%	LEELTECIRDHRLLLDYVDALRPVFSGTIFVQFLLIGTVLGLSMINLMFFSTFWTGVATC	300
DsuzOr22a	69.8%	LEELAKCIQDHHLILDYVNTLRPVFSGVIFVQFLLIGVVLGLSMINVMFFLSFWTGLGTC	300
DbiaOr22a	69.0%	LEELTKCIQDHRLILDYVNTLRPVFSGVIFVQFLLIGVVLGLSMINVMFFLSFWTGLGTC	300

TM5   TM6

DmelOr22a	100.0%	LFMFDVSMETFPFCYLCNMIIDDCQEMSNCLFQSDWTSADRRYKSTLVYFLHNLQQPITL	360
DsuzOr22a	69.8%	LFMFDVCMETFPFCYLCNMIIDDCQDLSDSLFQSNWTSASRRYKSTLVYFLHNLQQPIIL	360
DbiaOr22a	69.0%	LFMFDVCMETFPFCYLCNIIIDDCQDLADSLFQSNWTSASRRYKSTLVYFLHNLQQPIIL	360

TM7

DmelOr22a	100.0%	TAGGVFPISMQTNLAMVKLAFSVVTVIKQFNLAERFQ	397
DsuzOr22a	69.8%	TAGGVFPICMQTNLSMVKLAFSVVTIIKQFNLAEKFK	397
DbiaOr22a	69.0%	TAGGIFPICMQTNLSMVKLAFSVVTIIKQFNLADKFK	397

B

DsuzOr22a$^{WT(D201A)}$

DsuzOr22a$^{(A201D)}$