

Supplemental Tables

Tab. S1. Duplications and larger expansions of chemosensory gene families.

Tab. S2. Homology of OR subfamily tandem arrays.

Tab. S3. Gene numbers per OR subfamily for all bee species examined.

Tab. S4. Patterns of selection in chemosensory genes between orchid bee species pairs

Tab. S5. Branches under selection.

Supplemental Datasets

Dataset S1. Contains detailed results of the selection analysis, homology of genomic locations of non-OR chemosensory gene families, and all chemosensory gene sequences annotated.

Tab. S1

Gene family	Honey bees	Bumble bees	Stingless bees	Orchid bees	within Orchid bees
ORs	27	32	25	16	31
GRs	2	3	1	1	2
IRs	0	0	0	0	1
CSPs	0	0	0	0	0
OBPs	3	1	0	1	4
Total	32	36	26	18	38

Tab. S2

Sub-family	<i>Eg. dilemma</i>	<i>Ef. mexicana</i>	Honey bee	Bumble bee	Stingless bee	Homolog
G11A	0	812	11.18	11.4	435748, 435971, (435874)	Y
G02A	29	2792	2.17	2.3	435794	Y
G09A-B	45	1523, 7050	9.10	9.4	435845	Y
G12A	61	221	12.4, 12.5	15.6	435908, 435704, 438518, 435897	Y
G13A	3	124	(13.5), 13.6	13.5	435896	Y
G13A out	NA	NA	10.26	Un980	435727	Y
G04A	30	2792	4.8, 4.7, 9.10*	4.5	435699, (435820)	Y
G12B	10	596	12.13, (12.11)	12.1, Un1054	435774	Y
G09C	15	2143, (4744748261), 11296, (54)	(9.10), 9.12	(9.1), 9.5	(435845), (435701), 435796, 435859	Y but OR73

G09C out	(2)	15773	1.27	1.3	435752	Y
GUnA	NA	NA	(7.19), Un26, (Un73), (Un132), (Un37)	10.4	435732, 435891, (435731)	N
G15A	5	1837	15.19	15.5	435821	Y
Orco	267	167	1.10	Un633	435750	Y
G07A	NA	2501	7.19	10.4	435732	Y
G09D	145	2143	9.10	9.1	435845	Y
G05A	14	(1653)	5.14	5.1	435863	Y
G14A	7	(4744748667), (4491), 422	14.1	(1.7), 14.7	(435834), 435970, (435938)	Y
G14B	56	(5018), (2888)	14.15, (14.14)	(14.2), 14.4, (14.5)	435711	Y
G15B	NA	NA	15.19	15.5	NA	Y
G05B	(388), (502), (200), (359)	(616), (2720), (2217)	(5.15), (5.20), 5.18	3.4	435827	Y
G11B	0	3780	11.18	(11.4), 11.1, (11.5)	435776	A+E Y B+M Y
G01A	19	(13082), 4744748268	1.31	1.8	435717	Y
GUnB	NA	NA	NA	NA	NA	NA
G01B	(40), (17), (26)	(572)	1.21	7.1	(435724), (435732)	Y
G02B	11	2332, (4744748507)	2.3, 2.11	2.1, 2.2	435692, 435794	Y
GUnC	NA	NA	NA	NA	NA	NA

Locations of tandem arrays corresponding to OR subfamilies are indicated by scaffold numbers for each species. In case the assembly was fragmented into multiple scaffolds, scaffolds are listed in order that matches homolog regions of the other species. Tandem arrays with homologous locations throughout the corbiculate bees are indicated by Y otherwise by N. Brackets indicate scaffolds that carried no ORs but were homologous to other species scaffolds carrying ORs. NA: not tested due to assembly fragmentation. *: Outgroup of G is only found in the honey bee and on a different chromosome. 'Out': Indicates the outgroup of a subfamily found in a different location than the rest of the ORs in the subfamily. A: Honey bee. E: Orchid bee. B: Bumble bee. M: Stingless bee.

Tab. S3

Sfamily	Edil	Evir†	Eimp†	Efla†	Emer†	Ebom†	Emex	Amel	Bter	Mqua	Sum
G13A	5	4	5	5	5	5	4[1]	7	12	8	60
G07A	2	2	2	2	2	2	2	3	1	3[1]	21
G09B	1	1	1	1	1	1	1	1	2	1	11
GUnC	18(4)[1]	8	11	11	7	8(1)	8(1)	12[1]	9	20	112
G02B	2[1]	1	1	1	1	1	1	1	1	1	11
G09A	3	2	3	2	1	2	10(1)[1]	3	1	1	28
G04A	8(3)	1	0	2(1)	2	0	8(2)[2]	25[2]	11	1	58
G05B	0	0	1	1	1	1	0	1	1	1	7
G11B	1	1	1	1	1	1	1	1	3	2	13
G12B	5	3	4(1)	5	5	3	8	8	10	12(1)	63
G11A	12(3)	7	8	7	9	10	11	9[1]	12	13(1)[1]	98
9Exon	26(6)	12	14(1)	16 (1)	18	15	28(2)[2]	44[3]	37	29(2)[1]	239
G01A	1	1	1	1	1	1	1	1	1	1	10
GUnB	2(1)	1	1	1	1	1	0	0	0	1	8
G09C	5(1)	4	4	4	5[1]*	5[1]*	4[2]	3	11[3]	24(3)[1]	69
G15A	2	2	2	2	2	2	2	6	11	2	33
G02A	35[2]	22	26	29	27(1)	33(2)[1]*	36[4]	60[1]	46	66(9)[5]	380
GUnA	23(7)	8	12	13 (1)	7	7	12(4)[1]	6	7	5	100
G09D	1	1	1	1	1	1	1	1	1	1	10
G05A	1	1	1	1	1	1	0	1	1	1	9
G14A	1	1	1	1	1	1	1	1	4	7[2]	19
G14B	1	1	1	1	1	1	0	1	1	1	9
G15B	0	0	0	0	1	1	0	1	1	0	4

G12A	53(16)[10]	12	20(4)	22 (2)	25	26 (2)	30[1]	23[2]	17[1]	20(3)	248
Orco	1	1	1	1	1	1	1	1	1	1	10
G01B	0	0	0	0	1	0	0	1	1	0	3
Sum	183(41) [14]	85	108(6)	115(5)	110(1)[1]*	115(5)[2]*	142(10) [14]	177[10]	166[4]	193(19) [11]	1394

9Exon corresponds to OR Subfamilies G05B, G04A, G11B, G12A, and G11A. †indicates species with transcriptome information only. * indicates expressed ORs with nonsense stop codon that were defined as pseudogenes. Numbers in () indicate incomplete ORs of length<300AA and [] indicates OR pseudogenes of total number.

Tab. S4

Gene family	<i>Eg. dilemma - Eg. viridissima</i>	<i>Eg. flammea - Eg. imperialis</i>	<i>El. bombiformis - El. meriana</i>
ORs	2 (1 1)	7 (5 3)	3 (3 0)
GRs	0	1 (0 1)	1 (1 0)
IRs	1 (1 0)	0	0
OBPs	0	1 (0 1)	0
CSPs	0	0	0

Orthologous chemosensory genes under positive selection between a species pair are indicated. Chemosensory genes under selection detected with the branch-site model approach and the pairwise approach, respectively, are shown in brackets.

Tab. S5

Gene family	All Species			Species with genomes*		
	Branches under selection	Thereof duplicated branches†	Thereof non-duplicated branches	Branches under selection	Thereof duplicated branches†	Thereof non-duplicated branches
ORs	69	26 (0.38)	43	53	25 (0.47)	28
GRs	28	9 (0.32)	19	21	9 (0.43)	12
IRs	6	0 (0)	6	5	0 (0)	5
OBPs	7	3 (0.43)	4	6	3 (0.5)	3
CSPs	1	0 (0)	1	0	0 (0)	0
Total§	111	38 (0.32)	73	85	37 (0.41)	48

* *Apis mellifera*, *Bombus terrestris*, *Melipona quadrifasciata*, *Euglossa dilemma* and *Eufriesea mexicana*. † The proportion of duplicated branches of all branches under selection is given in brackets. § A total of 2513 branches of which 638 were duplication branches and 1875 were non-duplication branches were tested.