

Supplementary Table S11. Results of fitting logistic regression models for number of *Drosophila suzukii* when cultivars. Sonata, Skeena, Sweetheart, and Staccato are pooled. Models are symbolised by their highest-order terms. Thus, R (row) + H (height) + A (aspect) denotes a model with main effects, whereas R + H*A denotes a model with **main** effects plus an H*A interaction.

Model	Predictors	Deviance	df	AIC ^a	Models compared	Deviance difference	df difference
1	A*H*R	8552.88	1352	1805.2	.	.	.
2	A*H + H*R + R*A	8572.16	1354	1799.0	2_1	19.3	2
3a	A*H + H*R	8576.52	1356	1795.2	3a_2	4.4	2
3b	A*H + R*A	8595.40	1356	1795.3	3b_2	23.2	2
3c	H*R + R*A	8632.80	1355	1785.3	3c_2	60.6	1
4a	H*R + A	8635.57	1357	1781.9	4a_3a	59.0	1
4b	H*A + R	8598.01	1358	1792.1	4b_3a	21.5	2
4c	R*A + H	8653.19	1357	1782.9	4c_3a	76.7	1
5	H + R + A	8655.95	1359	1780.2	5_4b	57.9	1
6a	R + A	8702.97	1360	1798.2	6a_5	47.0	1
6b	R + H	8656.00	1360	1779.5	6b_5	0.1	1
6c	H + A	8744.19	1361	1764.9	6c_5	88.2	2
7a	H	8744.22	1362	1764.2	7a_6b	88.2	2
7b	A	8791.03	1362	1780.7	7b_6b	135.0	2
7c	R	8702.99	1361	1797.4	7c_6b	47.0	1
8	None	8791.04	1363	1779.9	8_7a	46.8	1

^a The bolded line is the lowest Akaike information criterion (AIC) value (and the best fit).

Supplementary Table S12. Results of fitting logistic regression models for number of *Drosophila suzukii* and cultivar Sonata only. Explanation of model as in Table S11.

Model	Predictors	Deviance	df	AIC ^a	Models compared	Deviance difference	df difference
1	A*H*R	1149.19	292	469.7	.	.	
2	A*H + H*R + R*A	1169.29	294	478.6	2_1	20.1	2
3a	A*H + H*R	1185.49	296	476.8	3a_2	16.2	2
3b	A*H + R*A	1173.28	296	474.1	3b_2	4.0	2
3c	H*R + R*A	1169.75	295	479.4	3c_2	0.5	1
4a	H*R + A	1185.86	297	477.2	4a_3c	16.1	2
4b	R*A + H	1173.81	297	474.8	4b_3c	4.1	2
5	R + A + H	1189.95	299	472.6	5_4b	16.1	2
6a	R + A	1191.52	300	476.3	6a_5	1.6	1
6b	R + H	1212.44	300	469.8^b	6b_5	22.5	1
6c	H + A	1221.91	301	475.2	6c_5	32.0	1
7a	R	1213.79	301	473.0	7a_6a	22.3	1
7b	A	1222.81	302	477.3	7b_6a	31.3	2
8	R = edge vs. centre + A	1221.50	301	475.8	8_6a	30.0	1
9	None	1245.38	303	477.0	9_6b	32.9	3

^a The bolded line is the lowest Akaike information criterion (AIC) value (and the best fit).

^b The simpler model (6b) was chosen over model 1 to better interpret emerging patterns.

Supplementary Table S13. Results of fitting logistic regression models for number of *Drosophila suzukii* and cultivar Skeena only. Explanation of model as in Table S11.

Model	Predictors	Deviance	df	AIC ^a	Models compared	Deviance difference	df difference
1	A*H*R	2547.58	312	411.6	.	.	.
2	A*H + H*R + R*A	2584.27	314	410.8	2_1	36.7	2
3a	A*H + H*R	2586.10	316	409.6	3a_2	1.8	2
3b	A*H + R*A	2637.10	316	414.3	3b_2	52.8	2
3c	H*R + R*A	2598.70	315	404.2	3c_2	14.4	1
4a	H*R + A	2602.41	317	403.5	4a_3a	16.3	1
4b	H*A + R	2640.93	318	413.4	4b_3a	54.8	2
5	H + R + A	2654.99	319	407.5	5_4a	52.6	2
6a	R + A	2655.41	320	405.8	6a_5	0.4	1
6b	R + H	2655.41	320	406.6	6b_5	0.4	1
6c	H + A	2693.46	321	396.1	6c_5	38.5	2
7a	H	2693.58	322	395.2	7a_6a	38.2	2.0
7b	A	2693.81	322	394.8	7b_6a	38.4	2.0
7c	R	2655.84	321	405.0	7c_6a	0.4	1.0
8	H*R	2602.48	318	402.7	8_4a	0.1	1
9	None	2693.94	323	394.0^b	9_7b	0.1	1

^a The bolded line is the lowest Akaike information criterion (AIC) value (and the best fit); in this case the null model.

^b Backwards elimination showed that a model with no effects (the null model) was the best fit, neither canopy location nor orchard row influenced *D. suzukii* distribution.

Supplementary Table S14. Results of fitting logistic regression models for number of *Drosophila suzukii* and cultivar Sweetheart only. Explanation of model as in Table S11.

Model	Predictors	Deviance	df	AIC ^a	Models compared	Deviance difference	df difference
1	A*H*R	2497.58	357	489.4	.	.	.
2	A*H + H*R + R*A	2613.85	359	478.9	2_1	116.3	2
3a	A*H + H*R	2615.56	361	476.5	3a_2	1.7	2
3b	A*H + R*A	2618.61	361	475.8	3b_2	4.8	2
3c	H*R + R*A	2634.74	360	472.4	3c_2	20.9	1
4a	H*R + A	2636.05	362	470.0	4a_3a	20.5	1
4b	H*A + R	2619.84	363	473.5	4b_3a	4.3	2
4c	R*A + H	2638.79	362	469.8	4c_3a	23.2	1
5	H + R + A	2640.12	364	467.6	5_4b	20.3	1
6a	R + A	2649.19	365	470.0	6a_5	9.1	1
6b	R + H	2658.97	365	465.4	6b_5	18.9	1
6c	H + A	2665.35	366	457.0	6c_5	25.2	2
7a	H	2684.66	367	454.4	7a_6a	35.5	2
7b	A	2674.65	367	459.9	7b_6a	25.5	2
7c	R	2667.94	366	466.7	7c_6a	18.8	1
8	None	2693.90	368	456.3	8_7a	9.2	1

^a The bolded line is the lowest Akaike information criterion (AIC) value (and the best fit).

Supplementary Table S15. Results of fitting logistic regression models for number of *Drosophila suzukii* and cultivar Staccato only. Explanation of model as in Table S11.

Model	Predictors	Deviance	df	AIC ^a	Models compared	Deviance difference	df difference
1	A*H*R	1788.56	355	547.2	.	.	.
2	A*H + H*R + R*A	1792.70	357	543.9	2_1	4.14	2
3a	A*H + H*R	1812.64	359	541.5	3a_2	19.94	2
3b	A*H + R*A	1794.10	359	542.8	3b_2	1.40	2
3c	H*R + R*A	1866.80	358	545.7	3c_2	74.10	1
4a	H*R + A	1886.31	360	543.5	4a_3b	92.21	1
4b	H*A + R	1812.74	361	539.7	4b_3b	18.64	2
4c	R*A + H	1866.89	360	543.9	4c_3b	72.79	1
5	H + R + A	1886.45	362	541.5	5_4b	73.71	1
6a	R + A	1979.97	363	543.4	6a_5	93.52	1
6b	R + H	1952.36	363	535.7	6b_5	65.91	1
6c	H + A	1928.32	364	542.1	6c_5	41.88	2
7a	H	1992.98	365	531.8	7a_6c	64.66	1
7b	A	2019.04	365	543.4	7b_6c	90.72	1
7c	R	2047.34	364	549.3	7c_6c	119.02	0
8	None	2085.79	366	545.2	8_7a	92.81	1

^a The bolded line is the lowest Akaike information criterion (AIC) value (and the best fit).

Supplementary Table S16. Results of one-way analysis of variance of the intraspecific aggregated egg distribution of *Drosophila suzukii*.

Source	df	Sum of squares	Mean square	F-Ratio	P-value
Sector	3	0.762	0.254	0.4773	0.7039
Error	12	6.382	0.532		
Corrected total	15	7.144			

$R^2 = 0.11$.

Supplementary Table S17. Results of one-way analysis of variance of the intraspecific aggregated egg distribution of native *Drosophila* species.

Source	df	Sum of squares	Mean square	F-Ratio	P-value
Sector	3	1.252	0.417	0.4845	0.6993
Error	12	10.341	0.862		
Corrected total	15	11.593			

$R^2 = 0.11$.

Supplementary Table S18. Results of one-way analysis of variance of the interspecific aggregated egg distribution of *Drosophila suzukii* and of native *Drosophila* species.

Source	df	Sum of squares	Mean square	F-Ratio	P-value
Sector	3	6.157	2.052	0.8268	0.5042
Error	12	29.787	2.482		
Corrected Total	15	35.943			

$R^2 = 0.17$.