Supplementary Table 1. Gene-based markers.

Marker Name	Gene Description	GenBank Accession Number	VS$_{07}$ Chromosome	VS$_{01}$ Chromosome	Forward Primer (5'-3')	Reverse Primer (5'-3')
Cp5$_{A}$	*H. virescens* partial mRNA for putative chemosensory receptor 5	AJ487480	not done	H01	GTTCATCAGCTTAATATGGAGCACTT	GAACGTATCGCTTCAGTATCAAAGAT
Vgcc	*Lepidoptera voltage-gated calcium channel*	DD345735	not done	H01	AACTGGATTTACTTTGTGCCTCTC	ACTTCCTCTGCTTTACAAATCCAC
Cp4	*H. virescens* mRNA for putative chemosensory receptor 4	AJ487479	not done	H04	TTATACTATAGCAGAGGGCAAAAGAA	CATAAATGACTAGAGCCGTTCAAT
Cr2$_{A}$	*H. virescens* mRNA for putative chemosensory receptor 2	AJ487477	not done	H04	AATTAGGGCAACTTGTTTGTGAT	TTATTTTTGCACCAGATTAAGAAATG
Ddc	*H. virescens* DOPA decarboxylase (DDC) gene, partial	U71428	not done	H05	CTATGATACGCGTGAAGAAACAAC	TGAGGTAACGATATTCAGGACAGA
Cp19	*H. virescens* mRNA for putative chemosensory receptor 19	AJ748334	not done	H06	TTCAAGGTGTTGGAACTGAACTAC	GAAGAAGTCCCTACAAACAACACA
Cp14$_{A}$	*H. virescens* mRNA for putative chemosensory receptor 14	AJ748329	not done	H07	GTTCACACTGTACCTCACTGG	GAACAACATTGGCCCGAATAC
Csp1	*H. virescens* chemosensory protein 1 (CSP1) gene	AY766374	not done	H08	CAAGTATGACAACGTAGACCTGGA	GTTCTCGAGAGCTTCAATGATGT
Cry1Ac	*H. virescens* cadherin-like Cry1Ac receptor	AY692445	not done	H10	TTGGTTTAAAGTCGCTCCAATAGACA	AAGTCCAGCATGTGATGGTTCTGCGT
Vatp	*Vacuolar (V-type) H(+)-ATPase B subunit gene*	S61797	not done	H17	AACTTCGCCATCGTGTTCGCCGCTAT	GTGTACATGTAACCTGGGAAACCACG
Hscp	*H. virescens* voltage-gated sodium channel alpha subunit (hscp) gene	AF072463	not done	H23	CTTATTCAACATCTGTCTGCTGCT	GATGTACATGTTGATGACGATGAG
Ryr	*H. virescens* ryanodine receptor (ryr)	AF009346	not done	H27	CTTCGTGTTCAACCTGTACAAGG	ACTGGTCACGCAGCTCTCCGA
Abp2	*H. virescens* mRNA for antennal binding protein (abp2) gene	AJ300654	not done	H28	CATTGATCCTTGTTTTATGAGCTG	TTTGCAGTTGATCTTCAATCATTT
RpL31	*H. virescens* mRNA for ribosomal protein L31 (rl31) gene	AJ298149	not done	H29	CAACGAAGTTGTAACTCGTG	TTCTTGGCTAGCGTCCACAT
Cp11	*H. virescens* mRNA for putative chemosensory receptor 11	AJ748326	H03	H03	CAGGCATTACGGGTCCAATGG	GGTCAAACATCGACACGCTGC
Cp14$_{B}$	*H. virescens* mRNA for putative chemosensory receptor 14	AJ748329	H07	not done	GTTCACACTGTACCTCACTGG	GTGGTCAGGTTTGCTGGCCTTGG
Cp5$_{B}$	*H. virescens* partial mRNA for putative chemosensory receptor 5	AJ487480	H01	not done	CTGTCCTGCTCATGCAACTTC	TGCATCATTGCCTTGATCATC
Cr12	*H. virescens* mRNA for putative chemosensory receptor 12	AJ748327	H18	not done	TGGCCTTGGGTGTATCTGCGACAG	CTCGATACAGTGTTTGAGCAATCG
Cr18	*H. virescens* mRNA for putative chemosensory receptor 18	AJ748333	H14	not done	TTACCATATCATCAAGGAGCGTG	AGGGCCCATAAACGTTCTGCAGCT
Cr2$_{B}$	*H. virescens* mRNA for putative chemosensory receptor 2	AJ487477	H04	not done	GAAGCGGCTTACTCCTGCCAGTGG	CATGAAGTAGGTTACCACGGCTCC
Csp2	*H. virescens* chemosensory protein 2 (CSP2) gene	AY766375	H08	not done	GAAATCTTGGAGTCTCAGCGCCT	AAAGCTTTGGTAACTGCGTCTG
Dd23	*Developed by the Gould lab (NCSU) from an AFLP marker; located on a chromosome involved in acetate production*	.	H06	not done	TCCAGGCTTTTCTAATACAACG	CCAAACTGACCTTAGGATCTTC
Ef1α	*H. virescens* elongation factor 1-alpha (EF-1α)gene, partial	U20135	H13	not done	GAATTCACAAACAAGGAGTGTG	Rev. #1: CAGGTTACAAAATCAGCTGCTA; Rev. #2: CAGGTAACAAAATCAGCTGCTA
Snmp	*H. virescens* mRNA for sensory neuron membrane protein-1 (snmp1) gene	AJ251959	H12	not done	GGACTGAATCCTGATGTCACCCAA	GACAAGTCCTTGAATAGGTCCAGC
δ9	*Developed by Mike Ward (NCSU), based on Helicoverpa zea* acyl-CoA delta-9 desaturase mRNA (FBDs) gene	AF272345	H28	not done	CAAGTACTCTGAAACGGATGCTG	TGATGTTCTTGTCGAAGGCTTGG
Jhbp	*H. virescens* juvenile hormone binding protein mRNA (JHBP) gene	U22515	not done	unlinked	GACTTCAAAATGGATACAGACAAGAA	GCAAGGCCTTTTGTAACTCTTCTC

Supplementary Table 2. AFLP primer pairs used for linkage mapping and the number of informative markers generated by each pair across years and families.

Primers		**Informative Loci**							
Eco RI	*Mse* I	Total Markers from Primer Pair	VS$_{07}$C$_1$	VS$_{07}$A	VS$_{07}$B	VS$_{07}$C$_2$	VS$_{07}$C$_3$	VS$_{01}$A	VS$_{01}$B
AAA	CGA	29	23	22	13	13	18	14	15
	CTG	46	41	38	18	15	17	12	10
AAC	CCC	17	9	9	5	6	7	7	6
	CCT	31	21	18	18	15	13	17	18
AAg	CAG	26	14	13	11	10	12	10	8
	CGA	15	11	8	6	7	9	8	7
AAT	CAG	32	23	23	14	15	11	9	20
ACC	CAG	10	7	5	5	7	7	6	8
	CTT	17	16	16	11	12	11	12	13
ACg	CAG	11	8	8	5	8	5	5	5
	CTT	17	10	7	9	4	8	8	6
ACT	CCT	29	16	15	15	12	13	5	15
AgA	CGG	12	9	9	10	10	10	8	11
AgC	CCA	24	14	14	17	11	13	8	12
ATA	CTA	32	18	18	18	19	17	17	20
ATC	CAA	29	22	21	19	19	15	11	14
	CAG	20	11	9	10	10	10	9	11
	CAT	33	23	22	19	18	22	15	11
	CCT	23	17	16	18	16	18	6	19
Total Markers		453	313	291	241	227	236	187	229

Supplementary Table 3. Chromosomes identified in all seven VS backcross families. Linkage groups that shared at least two markers across families were considered homologous.

Chromosome	**# AFLP Loci**	**# AFLP Primer Pairs**	**Gene-Based Markers**	**# Loci Present in Each Family**							**Percent of Individuals with Chromosome Present**
				VS$_{07}$A	**VS$_{07}$B**	**VS$_{07}$C$_{1}$**	**VS$_{07}$C$_{2}$**	**VS$_{07}$C$_{3}$**	**VS$_{01}$A**	**VS$_{01}$B**	
H01	13	9	*Cp5*$_{A\&B}$, *Vgcc*	12	10	12	11	11	7	8	48
H02	25	14		20	14	19	11	15	16	11	44
H03	18	10	*Cp11*	14	13	11	12	12	10	12	52
H04	12	6	*Cr2*$_{A\&B}$, *Cp4*	9	9	10	8	9	5	10	50
H05	15	10	*Ddc*	10	6	8	7	8	6	8	48
H06	22	9	*Dd23, Cp19*	11	9	13	10	8	13	8	48
H07	16	10	*Cp14*$_{A\&B}$	10	10	9	11	7	7	8	50
H08	15	7	*Csp2, Csp1*	5	2	7	3	9	8	4	50
H09	16	9		9	11	8	7	6	5	9	50
H10	28	15	*Cry1Ac*	15	8	14	9	9	9	12	50
H11	12	8		9	10	8	11	11	4	6	50
H12	9	5	*Snmp*	7	5	8	4	4	5	4	47
H13	17	12	*Jhbp, Ef1α*	8	5	6	4	6	7	7	49
H14	13	11	*Cr18*	5	6	7	4	4	4	7	47
H15	13	9		8	9	7	8	8	4	5	50
H16	12	9		8	8	8	8	8	5	7	48
H17	11	7	*Vatp*	7	8	6	4	3	5	6	50
H18	14	9	*Cr12*	9	7	7	7	8	6	5	49
H19	17	13		8	12	8	6	6	5	9	50
H20	9	6		6	6	5	7	6	3	6	45
H21	9	6		4	4	4	5	6	6	7	49
H22	7	7		3	5	3	3	5	3	3	49
H23	17	8	*Hscp*	9	11	8	11	11	9	12	50
H24	10	8		7	5	4	5	7	3	2	45
H25	15	11		4	5	6	4	7	5	10	49
H26	14	10		6	6	7	7	6	9	7	50
H27	12	8	*Ryr*	6	6	8	6	4	6	7	48
H28	17	10	*δ9, Abp2*	10	9	12	8	7	7	10	48
H29	10	7	*RpL31*	8	7	6	4	6	2	2	48

Supplementary Table 4. Phenotypic means for the seven backcross families used in this study. Values shown are $\bar{x}$ ± 95% CI.

Trait	**Units**	**$VS_{01}A$**	**$VS_{01}B$**	**$VS_{07}A$**	**$VS_{07}B$**	**$VS_{07}C_1$**	**$VS_{07}C_2$**	**$VS_{07}C_3$**
Larval Start Weight	mg	1.54 ± 0.08	1.85 ± 0.06	1.28 ± 0.07	1.22 ± 0.06	1.02 ± 0.05	1.33 ± 0.07	1.25 ± 0.09
Larval Feeding	percent	83.33 ± 5.46	83.2 ± 6.58	76.1 ± 5.29	72.51 ± 6.04	65.3 ± 6.32	65.43 ± 5.99	69.76 ± 5.73
Change in Fruit Weight	g	1.6 ± 0.16	2.06 ± 0.12	3 ± 0.07	3.14 ± 0.07	2.99 ± 0.08	3.06 ± 0.08	2.89 ± 0.07
Percent Change in Larval Weight	percent	8.2 ± 8.63	83.35 ± 22.69	66.31 ± 6.29	59.03 ± 6.3	59.01 ± 6.59	59.86 ± 7.5	54.35 ± 6.11
Number of Holes in Calyx	number of holes	1.77 ± 0.22	2.4 ± 0.33	2.24 ± 0.29	1.49 ± 0.2	2.48 ± 0.38	1.67 ± 0.23	2.12 ± 0.3
Assimilation Efficiency	mg change in larval weight per g *Physalis* fruit consumed	1.96 ± 2.5	5.68 ± 1.84	2.83 ± 0.37	2.58 ± 0.33	2.03 ± 0.25	2.68 ± 0.36	2.29 ± 0.3

Supplementary Table 5. Chromosomes affecting willingness to feed on *Physalis* in VS_{07} backcross insects.

	Factor		**H01**	**H10**	**H15**	**H19**	**H25**	**H26**	**H28**	**H29**
1) Genome-wide significance[a]	Observed *F*		ns	ns	ns	13.957	ns	ns	8.77	ns
2) Mixed model analysis of chromosome by environment interactions[b]	Chromosome		ns	$F_{1,1136}=5.41$; $p=0.02$	$F_{1,1135}=5.02$; $p=0.03$	$F_{1,1136}=12.66$; $p=0.0004$	$F_{1,1136}=7.92$; $p=0.005$	$F_{1,1132}=3.61$; $p=0.06$	$F_{1,1132}=7.71$; $p=0.006$	$F_{1,1132}=7.21$; $p=0.007$
	Sex		$F_{1,1132}=5.5$; $p=0.02$	$F_{1,1136}=5.91$; $p=0.02$	$F_{1,1135}=5.32$; $p=0.02$	$F_{1,1136}=5.79$; $p=0.02$	$F_{1,1136}=5.32$; $p=0.02$	$F_{1,1132}=4.82$; $p=0.03$	$F_{1,1132}=7.07$; $p=0.008$	$F_{1,1132}=6.35$; $p=0.01$
	Family		ns	$F_{4,1136}=2.33$; $p=0.05$	$F_{4,1135}=2.6$; $p=0.03$	$F_{4,1136}=2.43$; $p=0.05$	$F_{4,1136}=2.58$; $p=0.04$	$F_{4,1132}=2.86$; $p=0.02$	ns	ns
	Chromosome × Sex		ns	ns	ns	ns	ns	ns	ns	ns
	Chromosome × Family		$F_{5,1132}=4.49$; $p=0.0005$	ns	ns	ns	ns	$F_{4,1132}=2.77$; $p=0.03$	$F_{4,1132}=2.62$; $p=0.03$	$F_{4,1132}=2.22$; $p=0.02$
	Chromosome × Sex × Family		ns	ns	ns	ns	ns	ns	ns	ns
3) Partitioned analysis of chromosome effects[c]	Sex	♂VS_{07}	$F_{1,1131}=3.15$; $p=0.08$	$F_{1,1131}=3.12$; $p=0.08$	$F_{1,1131}=7.36$; $p=0.007$	$F_{1,1131}=3.22$; $p=0.07$	$F_{1,1131}=8.84$; $p=0.003$	$F_{1,1131}=2.92$; $p=0.09$	ns	ns
		♀VS_{07}	ns	ns	ns	$F_{1,1131}=9.58$; $p=0.002$	ns	ns	$F_{1,1131}=5.86$; $p=0.02$	$F_{1,1131}=5.52$; $p=0.02$
	Family	$VS_{07}A$	ns	ns	ns	ns	$F_{1,1131}=4.46$; $p=0.04$	ns	ns	$F_{1,1131}=4.51$; $p=0.03$
		$VS_{07}B$	ns	ns	$F_{1,1131}=3.7$; $p=0.05$	ns	ns	$F_{1,1131}=9.2$; $p=0.003$	ns	ns
		$VS_{07}C_1$	$F_{1,1131}=10.28$; $p=0.001$	ns	ns	ns	ns	$F_{1,1131}=3.38$; $p=0.07$	$F_{1,1131}=9.72$; $p=0.002$	$F_{1,1131}=7.2$; $p=0.007$
		$VS_{07}C_2$	$F_{1,1131}=2.93$; $p=0.09$	$F_{1,1131}=7.44$; $p=0.007$	ns	$F_{1,1131}=11.06$; $p=0.0009$	ns	ns	ns	$F_{1,1131}=4.22$; $p=0.04$
		$VS_{07}C_3$	$F_{1,1131}=8.47$; $p=0.004$	ns	ns	ns	ns	ns	$F_{1,1131}=6.62$; $p=0.01$	ns

[a] Empirical significance thresholds for chromosome-phenotype association were determined by 1,000 permutations of phenotypic values among chromosomal genotypes in a model that included all chromosomes as the independent variables and a given phenotypic trait as the dependent variable (Churchill and Doerge 1994). *F* thresholds for the trait "occurence of larval feeding" in VS_{07}: $p < 0.05 = 9.708$; $p < 0.1 = 8.546$.

[b] Chromosome by environment interactions were evaluated by conducting a mixed-model analysis of variance for each chromosome and trait. We used Proc GlimMix (SAS 9.2) to examine the effect of chromosome, sex, family, and the interaction among these on the observed phenotypes. The SIMULATE option was used to obtain p-values corrected for the number of tests performed.

[c] Phenotypic differences associated with chromosome state within each level of sex and family were examined using the SLICE option in GLIMMIX to perform a partitioned analysis of the LS-means for each interaction. The SIMULATE option was used to obtain *p*-values corrected for the number of tests performed.

Supplementary Table 6a. Chromosomes affecting the percent change in larval weight after 48 hours of feeding on *Physalis* by VS_{07} backcross insects.

	Factor		**H01**	**H06**	**H08**	**H13**	**H15**	**H18**	**H19**	**H28**	**H29**
1) Genome-wide significance[a]	Observed F		ns	ns	$F=14.82$	ns	$F=15.047$	ns	$F=9.15$	ns	ns
2) Mixed model analysis of chromosome by environment interactions	Chromosome		$F_{1,789}=6.43$; $p=0.01$	$F_{1,793}=4.32$; $p=0.04$	$F_{1,793}=12.29$; $p=0.0005$	$F_{1,789}=4.86$; $p=0.03$	$F_{1,789}=13.50$; $p=0.0003$	$F_{1,793}=3.30$; $p=0.07$	$F_{1,789}=7.05$; $p=0.008$	$F_{1,789}=2.95$; $p=0.09$	$F_{1,793}=5.37$; $p=0.02$
	Sex		ns	ns	ns	ns	ns	ns	ns	ns	ns
	Family		$F_{4,789}=2.02$; $p=0.09$	ns	ns	$F_{4,789}=2.07$; $p=0.08$	$F_{4,789}=2.00$; $p=0.09$	ns	$F_{4,789}=2.00$; $p=0.09$	$F_{4,789}=2.01$; $p=0.09$	ns
	Chromosome × Sex		ns	ns	ns	ns	ns	ns	ns	ns	ns
	Chromosome × Family		ns	ns	ns	ns	ns	ns	ns	ns	ns
	Chromosome × Sex × Family		ns	ns	ns	ns	ns	ns	ns	ns	ns
3) Partitioned analysis of chromosome effects	Sex	♂VS_{07}	ns	ns	$F_{1,783}=8.51$; $p=0.004$	$F_{1,783}=3.93$; $p=0.05$	ns	$F_{1,783}=3.74$; $p=0.05$	ns	$F_{1,783}=4.11$; $p=0.04$	$F_{1,783}=5.14$; $p=0.02$
		♀VS_{07}	$F_{1,783}=7.17$; $p=0.008$	ns	$F_{1,783}=3.53$; $p=0.06$	ns	$F_{1,783}=12.91$; $p=0.0003$	ns	$F_{1,783}=5.77$; $p=0.02$	ns	ns
	Family	$VS_{07}A$	$F_{1,783}=4.36$; $p=0.04$	ns	ns	ns	ns	ns	ns	ns	ns
		$VS_{07}B$	$F_{1,783}=2.67$; $p=0.10$	$F_{1,783}=4.21$; $p=0.04$	ns	ns	ns	ns	ns	ns	ns
		$VS_{07}C_1$	ns	ns	ns	ns	ns	ns	$F_{1,783}=3.42$; $p=0.07$	ns	ns
		$VS_{07}C_2$	ns	ns	$F_{1,783}=4.67$; $p=0.03$	ns	$F_{1,783}=6.66$; $p=0.01$	$F_{1,783}=4.02$; $p=0.05$	ns	ns	$F_{1,783}=4.98$; $p=0.03$
		$VS_{07}C_3$	ns	ns	$F_{1,783}=5.70$; $p=0.02$	ns	$F_{1,783}=3.09$; $p=0.08$	ns	ns	ns	$F_{1,783}=3.73$; $p=0.05$

[a] F thresholds for the trait "percent change in larval weight" in VS_{07}: $p < 0.05 = 10.174$; $p < 0.1 = 8.633$.

Supplementary Table 6b. Chromosomes affecting the percent change in larval weight after 48 hours of feeding on *Physalis* by VS_{01} backcross insects.

	Factor		**H05**	**H19**	**H29**
1) Genome-wide significance[a]	Observed F		ns	11.2	ns
2) Mixed model analysis of chromosome by environment interactions	Chromosome		$F_{1,213}=5.03$; $p=0.03$	$F_{1,213}=22.02$; $p<0.0001$	ns
	Sex		$F_{1,213}=17.11$; $p<0.0001$	$F_{1,213}=16.79$; $p<0.0001$	$F_{1,213}=10.03$; $p=0.002$
	Family		$F_{1,213}=52.42$; $p<0.0001$	$F_{1,213}=42.41$; $p<0.0001$	$F_{1,213}=40.99$; $p<0.0001$
	Chromosome × Sex		$F_{1,213}=4.84$; $p=0.03$	ns	ns
	Chromosome × Family		$F_{1,213}=9.16$; $p=0.003$	ns	$F_{1,213}=4.79$; $p=0.009$
	Chromosome × Sex × Family		$F_{4,213}=5.72$; $p=0.004$	$F_{4,213}=2.29$; $p=0.07$	$F_{4,213}=2.35$; $p=0.07$
3) Partitioned analysis of chromosome effects	Sex	♂VS_{01}	ns	$F_{1,215}=7.08$; $p=0.008$	ns
		♀VS_{01}	$F_{1,215}=6.83$; $p=0.01$	$F_{1,215}=12.30$; $p=0.0006$	ns
	Family	$VS_{01}A$	ns	$F_{1,215}=12.33$; $p=0.0005$	ns
		$VS_{01}B$	$F_{1,215}=8.48$; $p=0.004$	$F_{1,215}=7.33$; $p=0.007$	$F_{1,215}=8.32$; $p=0.004$

[a] F thresholds for the trait "percent change in larval weight" in VS_{01}: $p < 0.05 = 9.463$; $p < 0.1 = 8.362$.

Supplementary Table 7a. Chromosomes affecting the number of holes bored in the calyx of *Physalis* by VS_{07} backcross insects.

	Factor		**H05**	**H06**	**H11**	**H17**	**H19**	**H22**	**H26**	**H28**	**H29**
1) Genome-wide significance[a]	Observed *F*		ns	ns	ns	ns	ns	ns	ns	ns	ns
2) Mixed model analysis of chromosome by environment interactions	Chromosome		$F_{1,1137}=18.38$; $p<0.0001$	$F_{1,1137}=11.33$; $p=0.0008$	ns	ns	$F_{1,1137}=13.21$; $p=0.0003$	ns	$F_{1,1137}=17.23$; $p<0.0001$	$F_{1,1137}=12.49$; $p=0.0004$	$F_{1,1135}=19.23$; $p<0.0001$
	Sex		ns	ns	ns	ns	ns	ns	ns	ns	ns
	Family		$F_{4,1137}=17.04$; $p<0.0001$	$F_{4,1137}=18.28$; $p<0.0001$	$F_{4,1133}=18.5$; $p<0.0001$	$F_{4,1133}=16.3$; $p<0.0001$	$F_{4,1137}=18.29$; $p<0.0001$	$F_{4,1131}=18.16$; $p<0.0001$	$F_{4,1137}=18.98$; $p<0.0001$	$F_{4,1137}=17.4$; $p<0.0001$	$F_{4,1135}=17.83$; $p<0.0001$
	Chromosome × Sex		ns	ns	ns	ns	ns	$F_{2,1131}=4.9$; $p=0.008$	ns	ns	$F_{2,1135}=5.58$; $p=0.004$
	Chromosome × Family		ns	$F_{4,1133}=6.3$; $p<0.0001$	$F_{5,1133}=4.23$; $p=0.0008$	$F_{5,1133}=4.5$; $p=0.0005$	ns	ns	ns	ns	ns
	Chromosome × Sex × Family		ns	ns	ns	ns	ns	ns	ns	ns	ns
3) Partitioned analysis of chromosome effects	Sex	♂VS_{07}	ns	$F_{1,1131}=7.09$; $p=0.008$	ns	ns	ns	$F_{1,1131}=7.78$; $p=0.005$	$F_{1,1131}=10.46$; $p=0.001$	$F_{1,1131}=15.96$; $p<0.0001$	ns
		♀VS_{07}	$F_{1,1131}=21.42$; $p<0.0001$	ns	ns	ns	$F_{1,1131}=9.3$; $p=0.002$	ns	$F_{1,1131}=6.09$; $p=0.01$	ns	$F_{1,1131}=30.7$; $p<0.0001$
	Family	$VS_{07}A$	ns	$F_{1,1131}=13.03$; $p=0.0003$	ns	$F_{1,1131}=4.12$; $p=0.04$	$F_{1,1131}=8.4$; $p=0.004$	ns	ns	ns	ns
		$VS_{07}B$	ns	ns	$F_{1,1131}=2.98$; $p=0.08$	ns	$F_{1,1131}=3.14$; $p=0.08$	ns	ns	$F_{1,1131}=6.92$; $p=0.009$	ns
		$VS_{07}C_1$	$F_{1,1131}=7.97$; $p=0.005$	$F_{1,1131}=7.88$; $p=0.005$	ns	$F_{1,1131}=10.94$; $p=0.001$	ns	ns	$F_{1,1131}=12.18$; $p=0.0005$	$F_{1,1131}=8.67$; $p=0.003$	$F_{1,1131}=17.18$; $p<0.0001$
		$VS_{07}C_2$	$F_{1,1131}=3.19$; $p=0.07$	$F_{1,1131}=12.27$; $p=0.0005$	ns	$F_{1,1131}=2.89$; $p=0.09$	$F_{1,1131}=16.87$; $p<0.0001$	ns	ns	ns	$F_{1,1131}=7.52$; $p=0.006$
		$VS_{07}C_3$	$F_{1,1131}=4.89$; $p=0.03$	$F_{1,1131}=3.12$; $p=0.08$	$F_{1,1131}=13.88$; $p=0.0002$	$F_{1,1131}=3.52$; $p=0.06$	ns	ns	$F_{1,1131}=3.38$; $p=0.07$	$F_{1,1131}=9.67$; $p=0.002$	$F_{1,1131}=3.17$; $p=0.08$

[a] *F* thresholds for the trait "number of holes" in VS_{07}: $p < 0.05 = 10.222$; $p < 0.1 = 8.697$.

Supplementary Table 7b. Chromosomes affecting the number of holes bored in the calyx of *Physalis* by VS$_{01}$ backcross insects.

	Factor		H01	H05	H17	H18	H19
1) Genome-wide significance[a]	Observed F		ns	ns	ns	ns	ns
2) Mixed model analysis of chromosome by environment interactions	Chromosome		$F_{1,286}=7.64$; $p=0.006$	ns	ns	$F_{1,286}=4.43$; $p=0.04$	$F_{1,286}=7.7$; $p=0.006$
	Sex		ns	ns	ns	ns	ns
	Family		$F_{1,286}=12.04$; $p=0.0006$	$F_{1,284}=12.17$; $p=0.0006$	$F_{1,285}=9.12$; $p=0.003$	$F_{1,286}=11.56$; $p=0.0008$	$F_{1,286}=12.07$; $p=0.0006$
	Chromosome × Sex		ns	$F_{3,284}=3.45$; $p=0.02$	ns	ns	ns
	Chromosome × Family		ns	ns	$F_{2,285}=6.24$; $p=0.02$	ns	ns
	Chromosome × Sex × Family		ns	ns	ns	ns	ns
3) Partitioned analysis of chromosome effects	Sex	♂VS$_{01}$	ns	$F_{1,283}=6.17$; $p=0.01$	ns	$F_{1,283}=3.29$; $p=0.07$	ns
		♀VS$_{01}$	$F_{1,283}=5.35$; $p=0.02$	$F_{1,283}=4.45$; $p=0.04$	ns	ns	$F_{1,283}=5.46$; $p=0.02$
	Family	VS$_{01}$A	$F_{1,283}=6.56$; $p=0.01$	ns	$F_{1,283}=4.32$; $p=0.04$	ns	$F_{1,283}=5.33$; $p=0.02$
		VS$_{01}$B	ns	ns	$F_{1,283}=7.79$; $p=0.006$	$F_{1,283}=4.35$; $p=0.04$	ns

[a]F thresholds for the trait "number of holes" in VS$_{01}$: $p < 0.05 = 9.895$; $p < 0.1 = 8.291$.

Supplementary Table 8a. Chromosomes affecting assimilation efficiency of VS_{07} backcross insects on *Physalis* .

	Factor		**H01**	**H03**	**H08**	**H10**	**H13**	**H14**	**H15**	**H16**	**H18**
1) Genome-wide significance[a]	Observed *F*		ns	ns	ns	F=8.62	ns	ns	F=14.76	ns	ns
2) Mixed model analysis of chromosome by environment interactions	Chromosome		$F_{1,785}=6.86$; $p=0.01$	$F_{1,785}=5.75$; $p=0.02$	$F_{1,785}=5.08$; $p=0.02$	$F_{1,783}=6.16$; $p=0.01$	$F_{1,785}=4.06$; $p=0.01$	$F_{4,785}=4.07$; $p=0.04$	$F_{4,785}=11.76$; $p=0.0006$	ns	$F_{1,785}=5.26$; $p=0.02$
	Sex		ns	ns	ns	ns	ns	ns	ns	ns	ns
	Family		$F_{4,785}=3.24$; $p=0.01$	$F_{4,785}=3.24$; $p=0.01$	$F_{4,785}=2.79$; $p=0.03$	$F_{4,783}=2.89$; $p=0.02$	$F_{4,785}=3.28$; $p=0.01$	$F_{4,785}=2.97$; $p=0.02$	$F_{4,785}=3.05$; $p=0.02$	$F_{4,783}=2.88$; $p=0.02$	$F_{4,785}=3.1$; $p=0.02$
	Chromosome × Sex		ns	ns	ns	$F_{2,783}=2.92$; $p=0.05$	ns	ns	ns	$F_{3,783}=3.11$; $p=0.03$	ns
	Chromosome × Family		ns	ns	ns	ns	ns	ns	ns	ns	ns
	Chromosome × Sex × Family		ns	ns	ns	ns	ns	ns	ns	ns	ns
3) Partitioned analysis of chromosome effects	Sex	♂VS_{07}	ns	ns	$F_{1,779}=7.10$; $p=0.008$	ns	ns	ns	ns	$F_{1,779}=6.18$; $p=0.01$	ns
		♀VS_{07}	$F_{1,779}=5.20$; $p=0.02$	$F_{1,779}=3.16$; $p=0.08$	ns	$F_{1,779}=12.90$; $p=0.0003$	$F_{1,779}=2.85$; $p=0.09$	$F_{1,779}=5.07$; $p=0.02$	$F_{1,779}=10.34$; $p=0.001$	ns	$F_{1,779}=3.40$; $p=0.07$
	Family	$VS_{07}A$	$F_{1,779}=6.91$; $p=0.009$	ns	ns	ns	$F_{1,779}=3.62$; $p=0.06$	ns	ns	ns	ns
		$VS_{07}B$	ns	ns	ns	$F_{1,779}=4.31$; $p=0.04$	ns	ns	ns	ns	ns
		$VS_{07}C_1$	ns	$F_{1,779}=3.19$; $p=0.07$	ns	ns	ns	ns	ns	ns	ns
		$VS_{07}C_2$	ns	$F_{1,779}=4.20$; $p=0.04$	ns	ns	ns	ns	ns	ns	$F_{1,779}=3.92$; $p=0.05$
		$VS_{07}C_3$	ns	ns	ns	ns	ns	ns	$F_{1,779}=4.48$; $p=0.03$	ns	ns

[a] *F* thresholds for the trait "assimilation efficiency" in VS_{07}: $p < 0.05 = 9.832$; $p < 0.1 = 8.348$.

Supplementary Table 8b. Chromosomes affecting assimilation efficiency of VS_{01} backcross insects on *Physalis* .

	Factor		**H03**	**H19**	**H20**
1) Genome-wide significance[a]	Observed F		ns	14.55	ns
2) Mixed model analysis of chromosome by environment interactions	Chromosome		$F_{1,216}=4.79$; $p=0.03$	$F_{1,216}=18.86$; $p<0.0001$	$F_{1,216}=3.34$; $p=0.07$
	Sex		$F_{1,216}=4.41$; $p=0.04$	$F_{1,216}=4.86$; $p=0.03$	ns
	Family		$F_{1,216}=5.50$; $p=0.02$	$F_{1,216}=7.32$; $p=0.007$	$F_{1,216}=7.84$; $p=0.006$
	Chromosome × Sex		ns	$F_{1,216}=3.81$; $p=0.05$	ns
	Chromosome × Family		$F_{1,785}=2.88$; $p=0.09$	ns	ns
	Chromosome × Sex × Family		ns	ns	ns
3) Partitioned analysis of chromosome effects	Sex	♂VS_{01}	ns	ns	ns
		♀VS_{01}	$F_{1,215}=5.50$; $p=0.02$	$F_{1,215}=19.40$; $p<0.0001$	ns
	Family	$VS_{01}A$	$F_{1,215}=9.97$; $p=0.002$	$F_{1,215}=19.83$; $p<0.0001$	$F_{1,215}=3.17$; $p=0.08$
		$VS_{01}B$	ns	ns	ns

[a] F thresholds for the trait "assimilation efficiency" in VS_{01}: $p < 0.05 = 9.655$; $p < 0.1 = 8.429$.

Supplementary Table 9. Kendall correlation coefficients between two measures of QTL effect size: 1) PVE = percent of variation explained in the backcross population; 2) Interspecific = percent of the phenotypic gap between *Hs* and *Hv* explained.

QTL Category	**Correlation**
All QTL	0.46***
QTL affecting willingness to feed on *Physalis*	0.94***
QTL affecting percent change in larval weight	0.81***
QTL affecting number of holes in calyx	0.61*
QTL affecting assimilation efficiency	0.74***
QTL with *Hs*-like effects	0.47***
QTL with *Hv*-like effects	0.43†

*** $p \leq 0.0001$; ** $p \leq 0.001$; *$p \leq 0.05$

†Correlation not significant