

Supplementary Information for

**Extensive introgression among North American wild grapes (*Vitis*)
fuels biotic and abiotic adaptation**

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SUPPLEMENTAL FIGURES

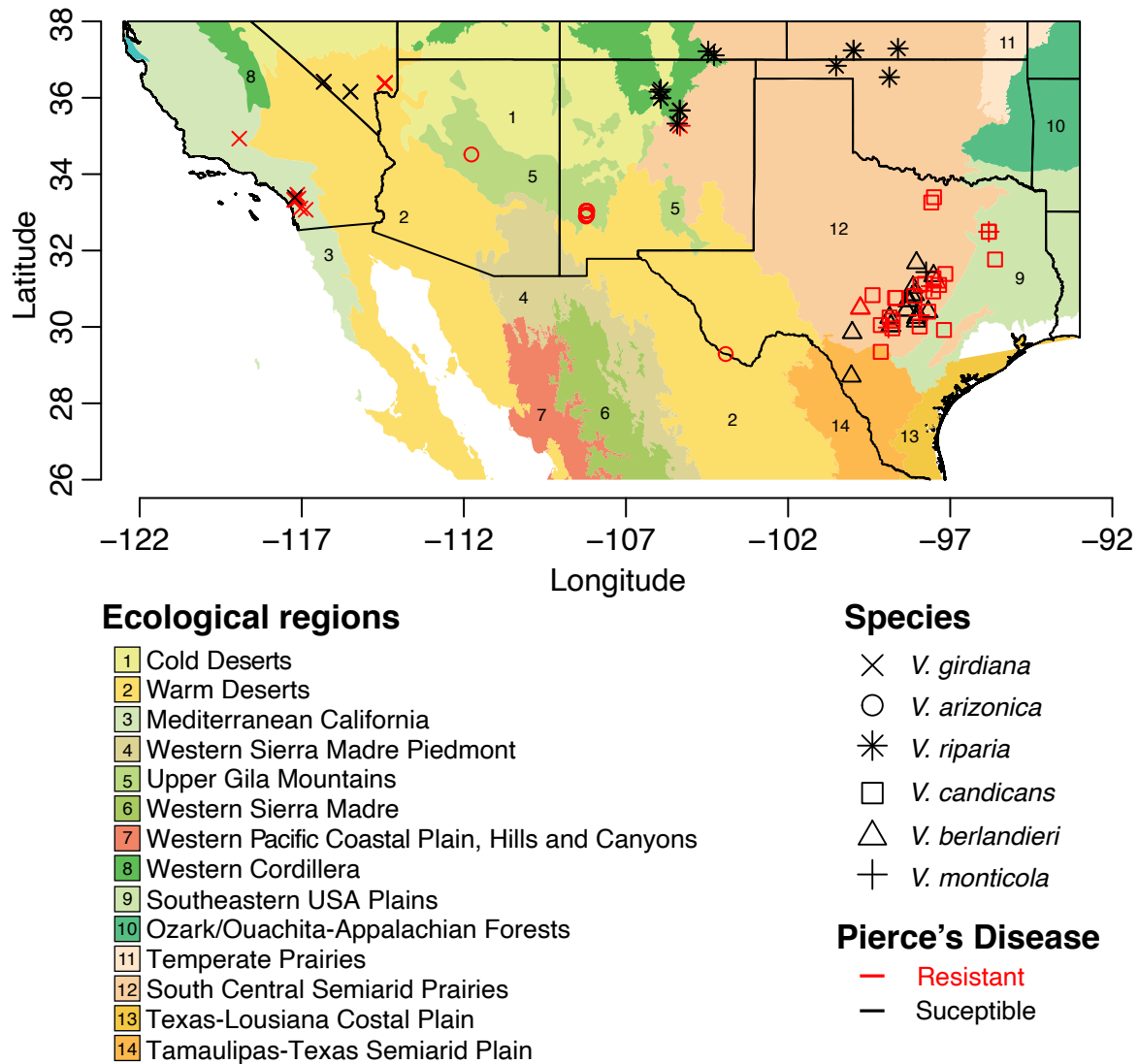


Figure S1. Geographic distribution and ecological diversity of sampled populations of wild grapes. Shapes correspond to different species, and samples colored red or black were classified as resistant or susceptible to Pierce's Disease, respectively. The numbers and colors of the regions correspond to the level II Ecological Regions defined by the United States Environmental Protection Agency (EPA), as shown in the legend.

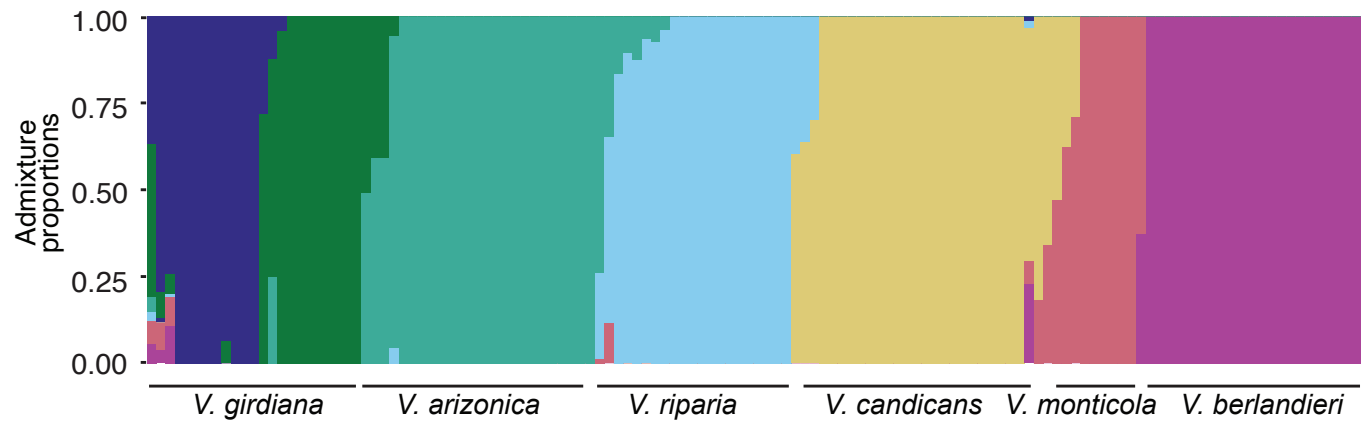


Figure S2. Genetic structure of all samples, including hybrid samples, with colors representing each cluster detected by the structure analysis (K=7).

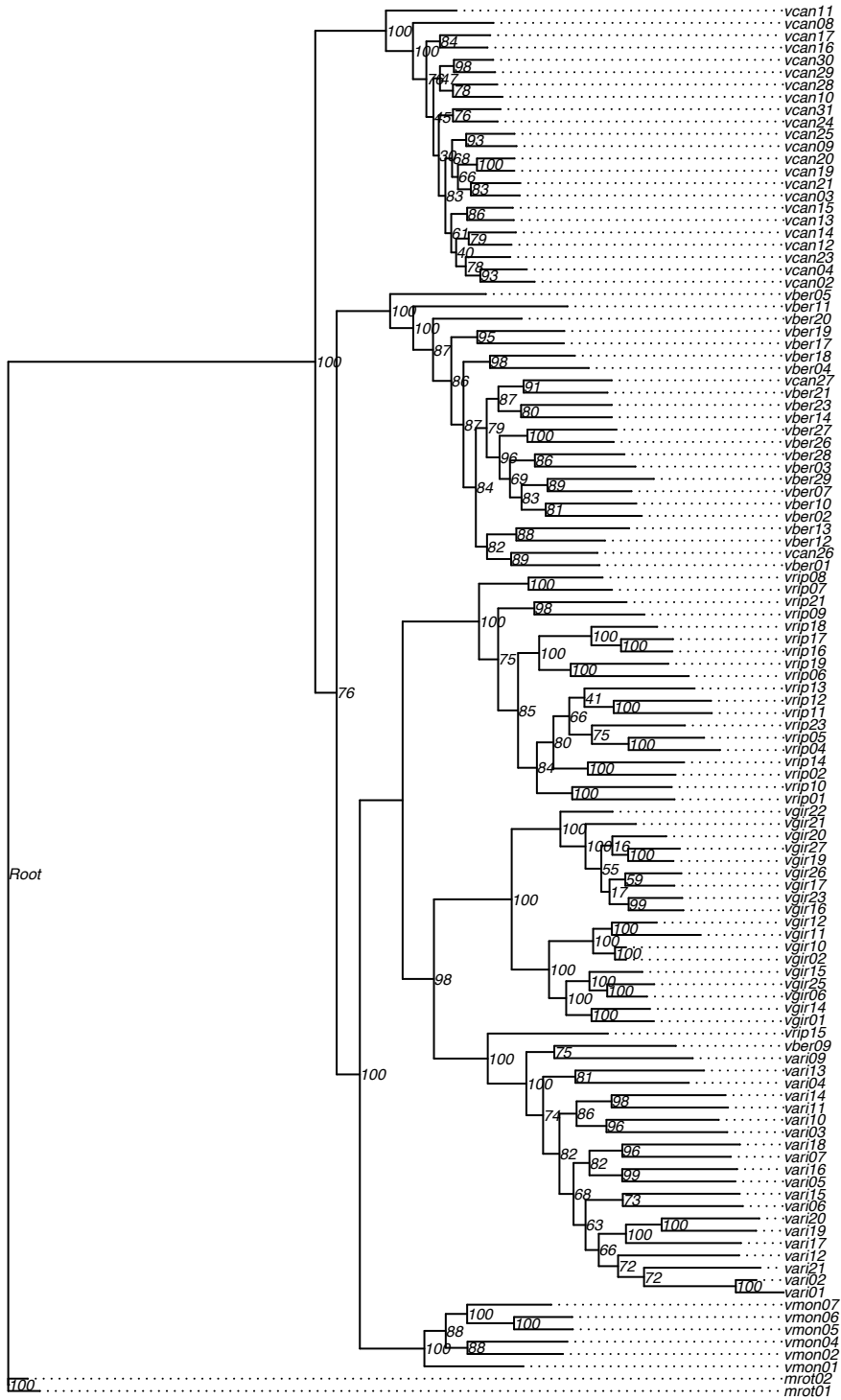


Figure S3. Consensus maximum likelihood phylogenetic tree created with IQtree. Numbers on the nodes correspond to bootstrap support values.

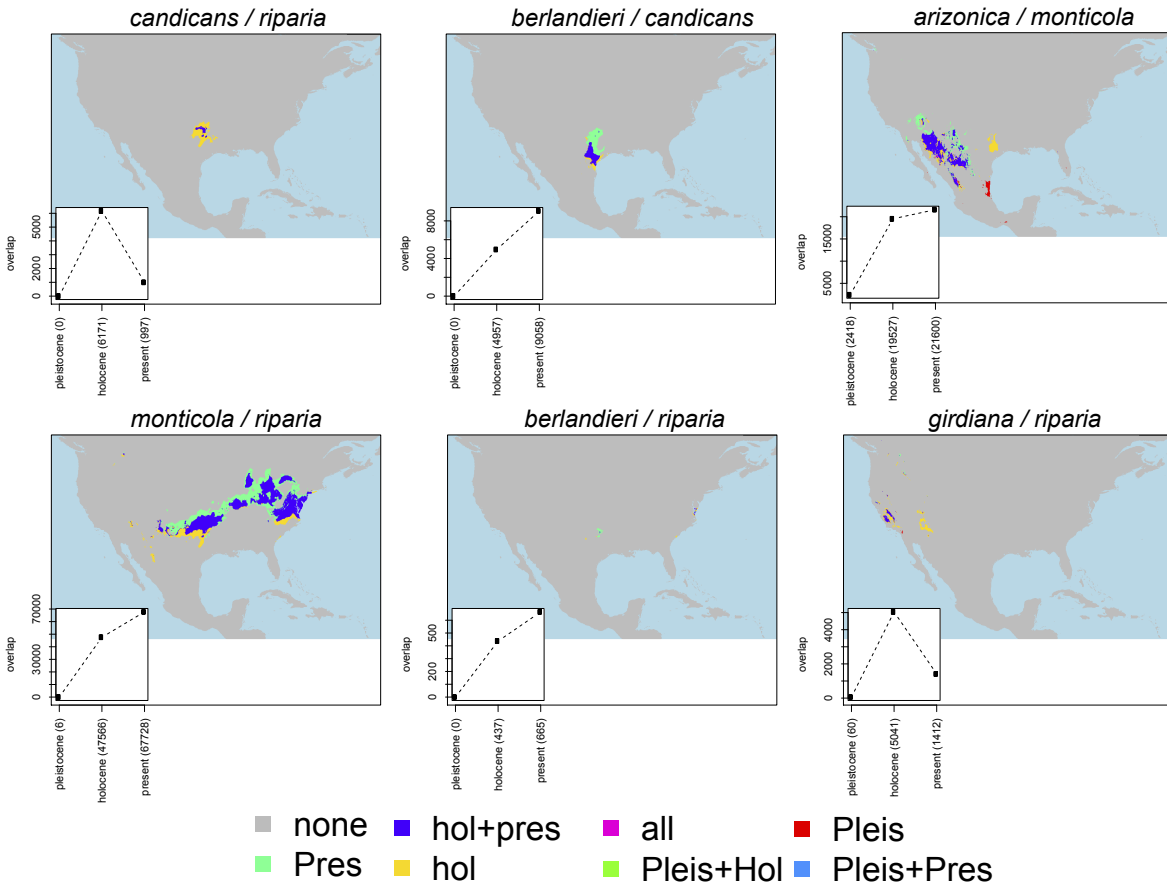


Figure S4. Pairs of species that show evidences of introgression present evidences of overlap at three periods, present, Holocene, Pleistocene.

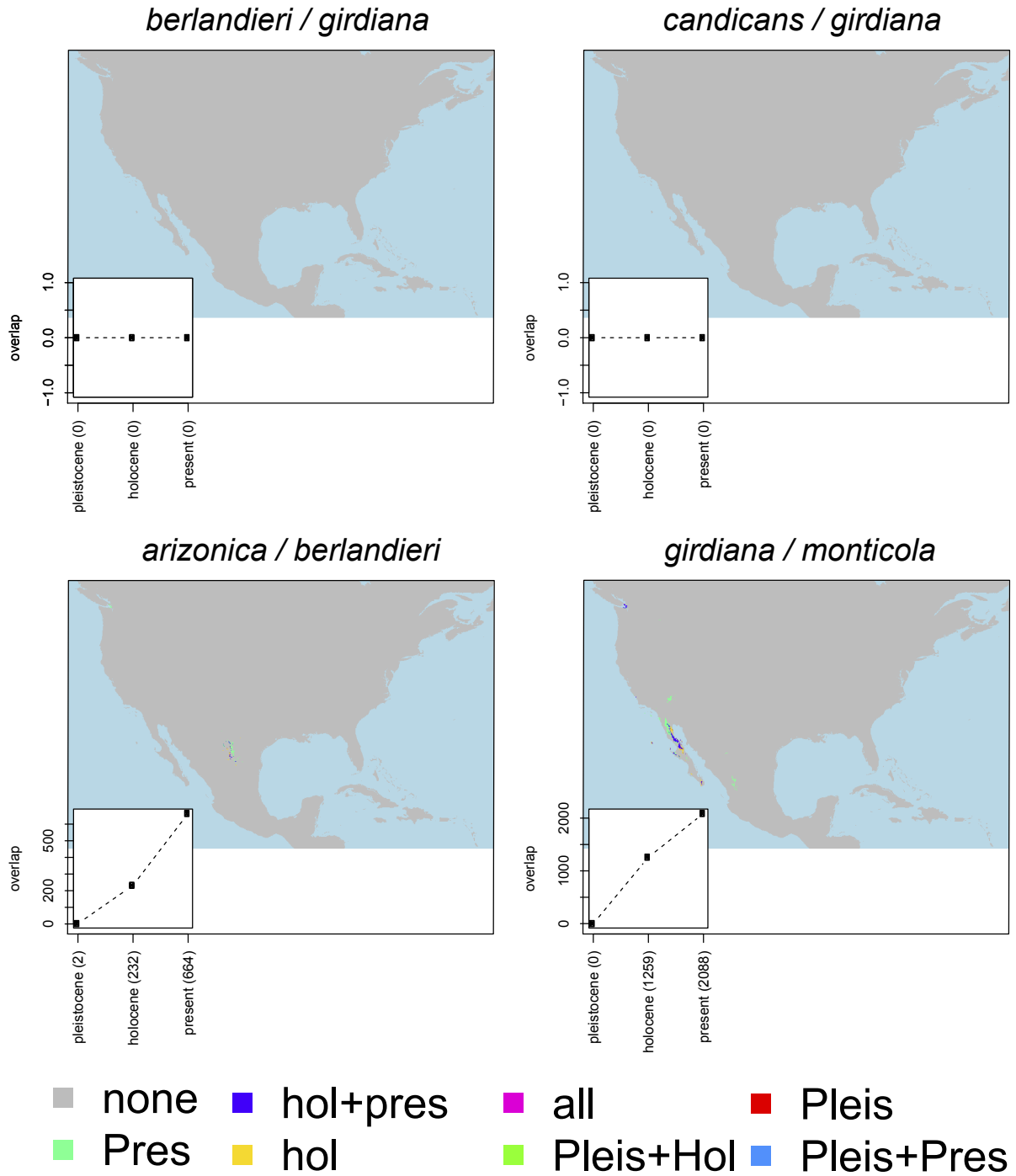


Figure S5. Pairs of species that do not show evidences of introgression present no or low overlap at three periods, present, Holocene, Pleistocene.

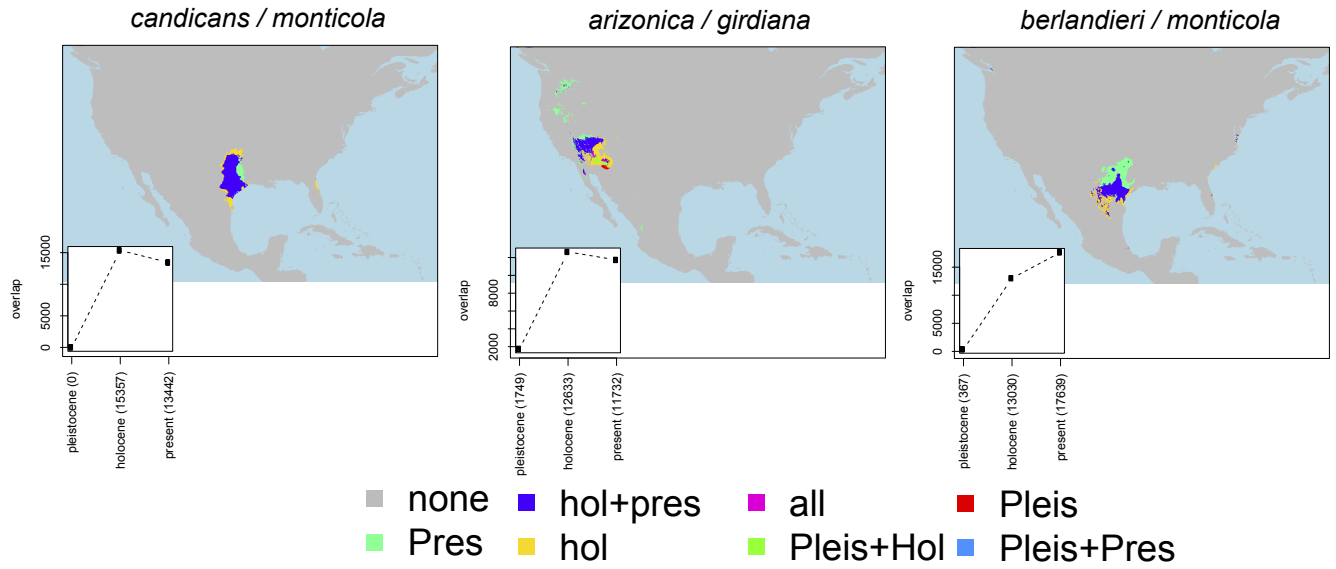


Figure S6. Pairs of species that do not show evidences of introgression but have overlapping distributions at three periods, present, Holocene, Pleistocene

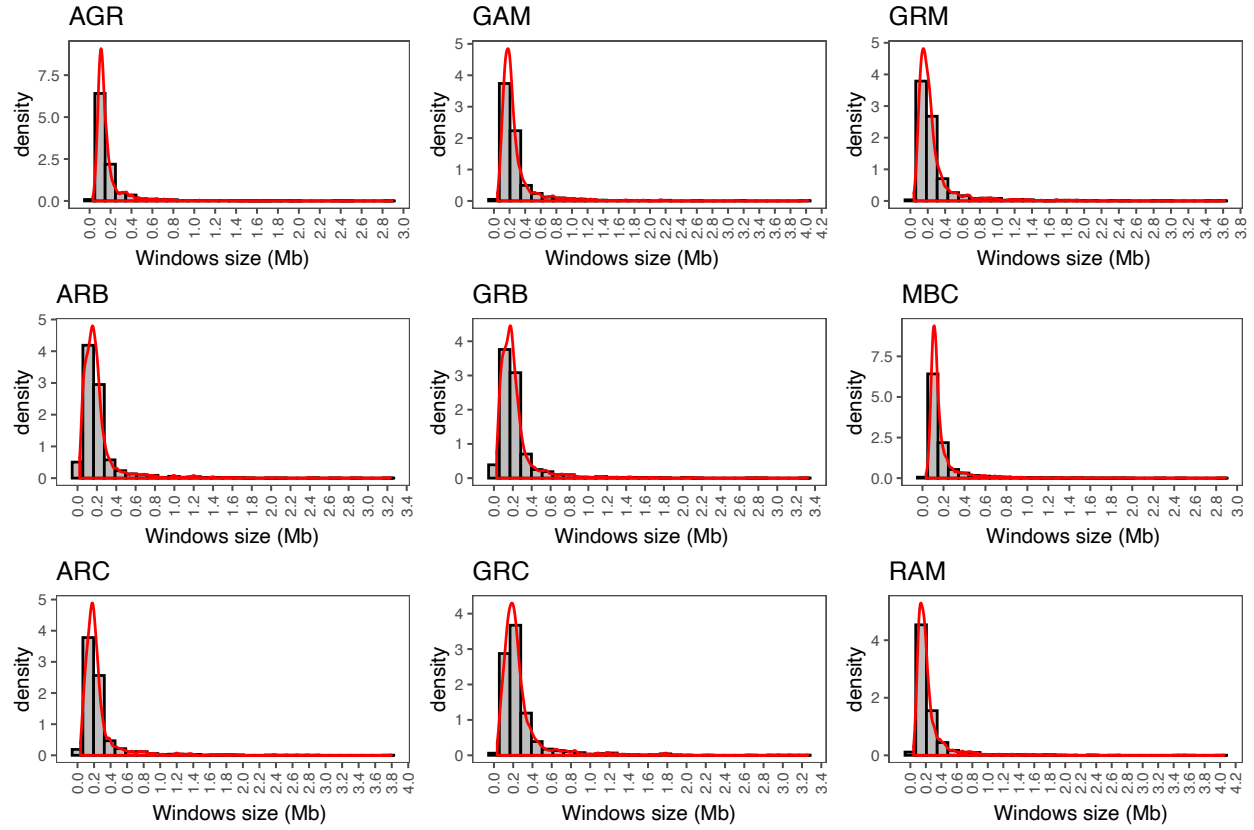


Figure S7. Genomic size distribution of the windows used to calculate the ABBA-BABA statistics per trio.

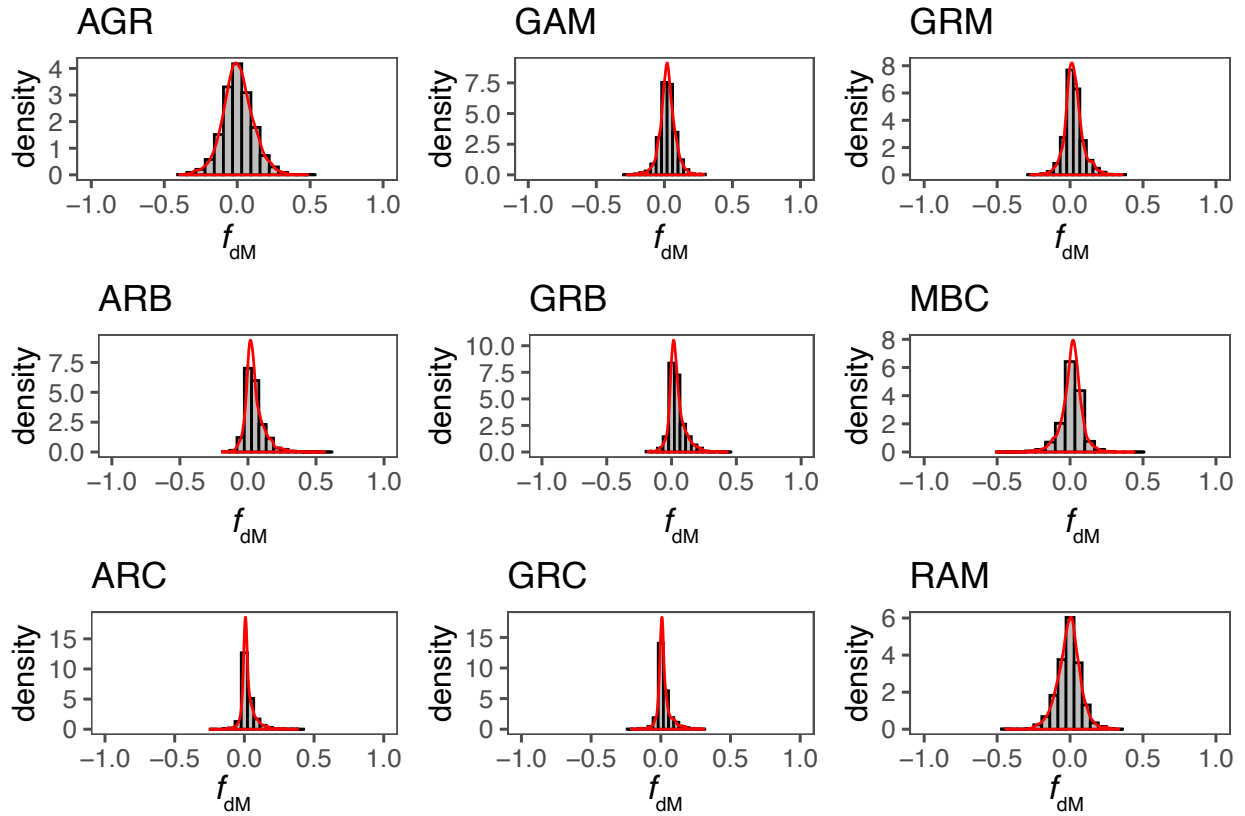


Figure S8. Distribution the f_{dM} statistic values across windows per trio.

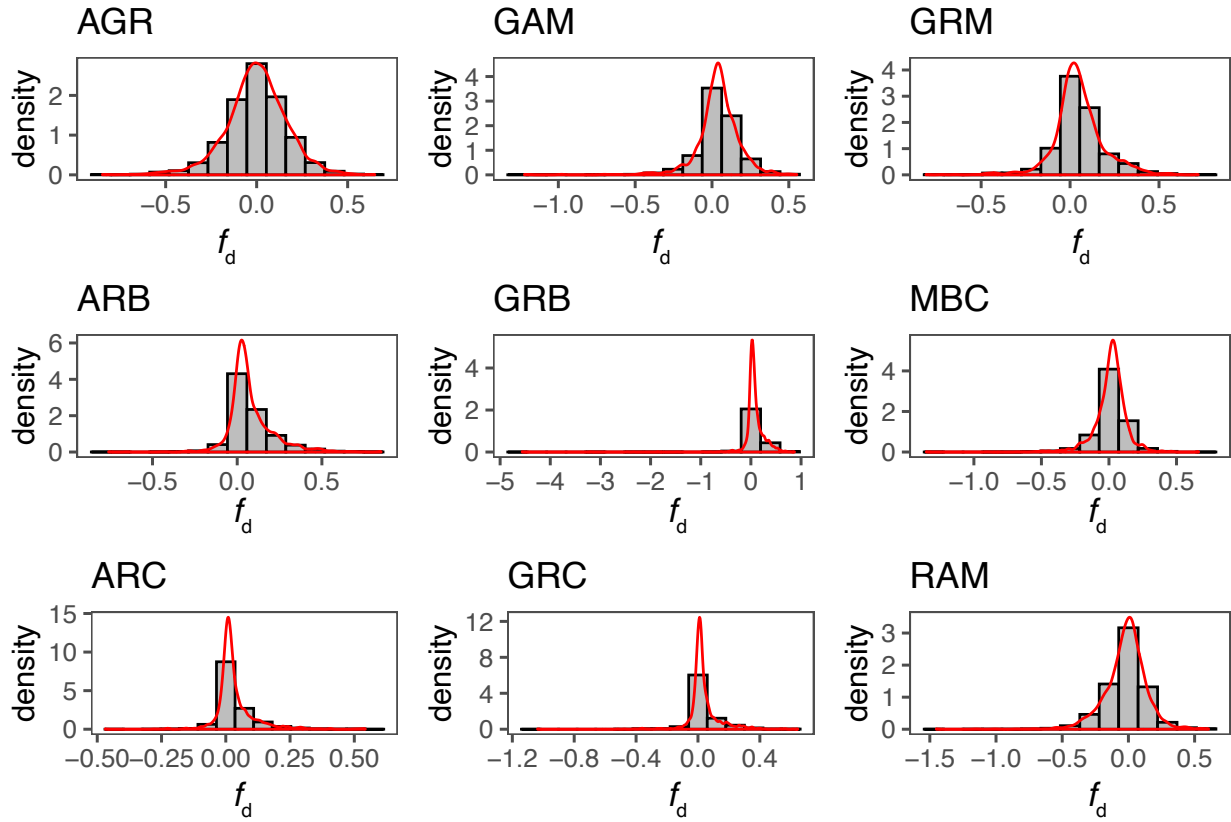


Figure S9. Distribution the f_d statistic values across windows per trio.

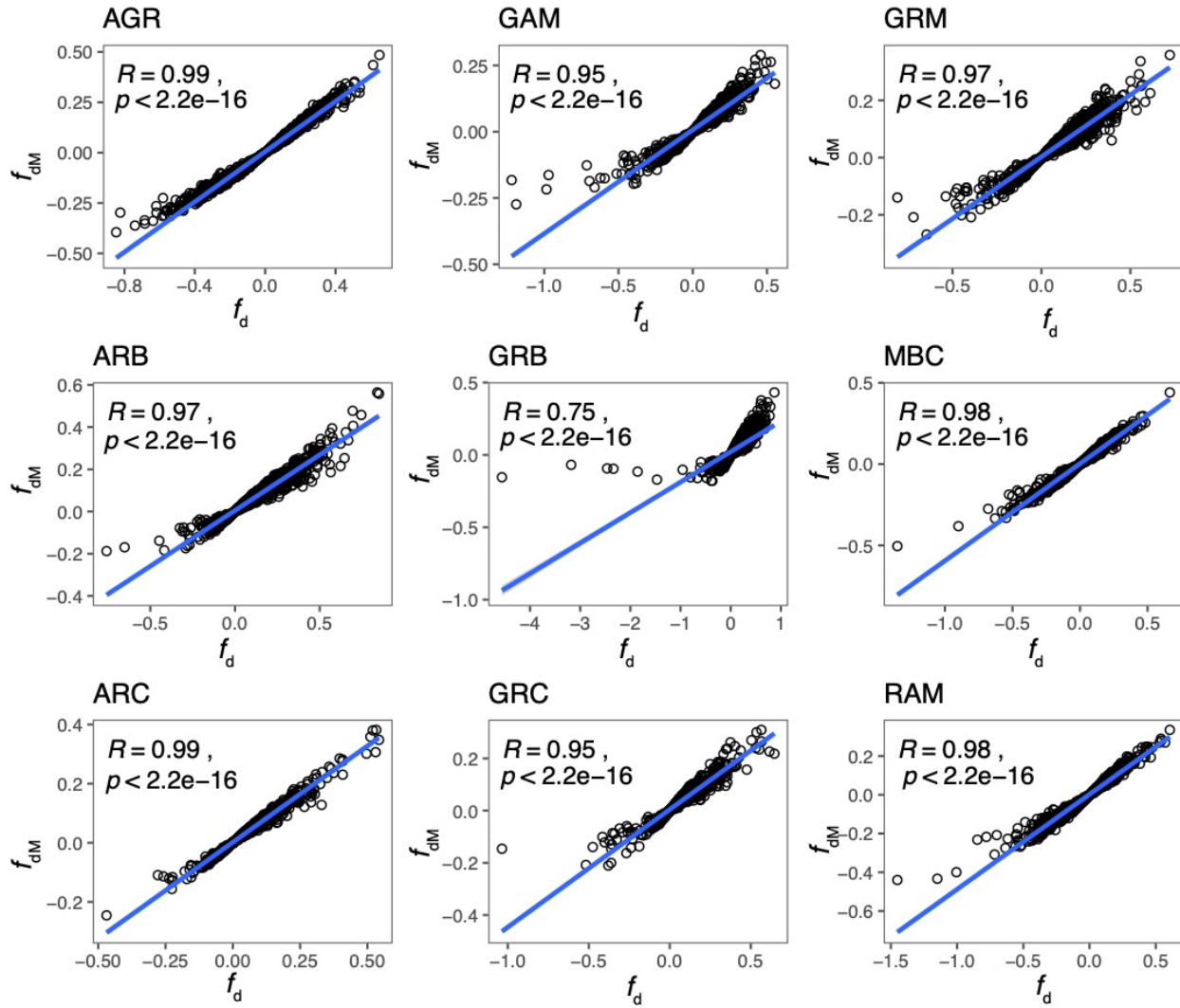


Figure S10. Scatterplot showing correlations between the f_{dM} and f_d statistics across all windows in the genome.

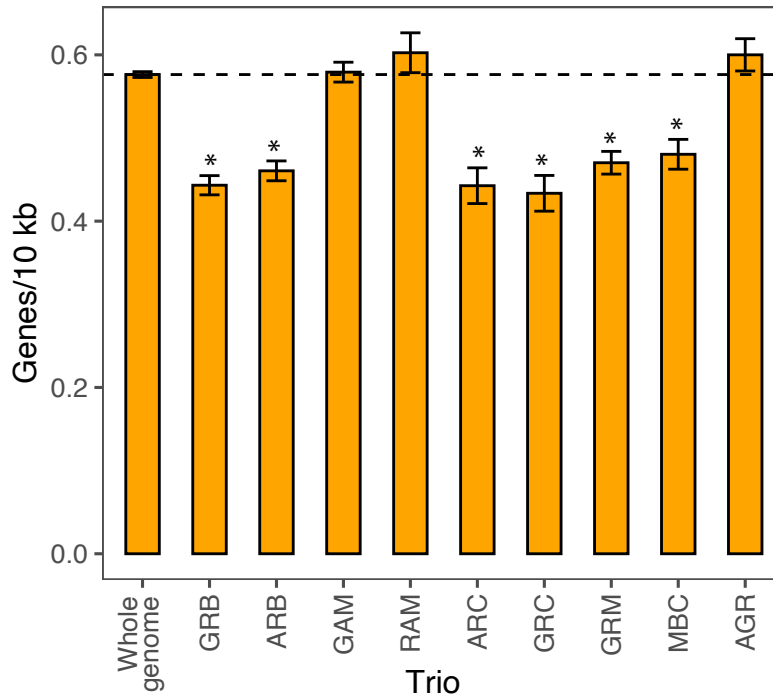


Figure S11. Mean gene density of across the whole genome and within the pIRs of all the trios. Error bars correspond to 1 SD. Dotted line corresponds the mean gene density of the whole genome. Asterisks denote trios with significantly lower gene density than the genome-wide average (t-test, $p < 0.001$).

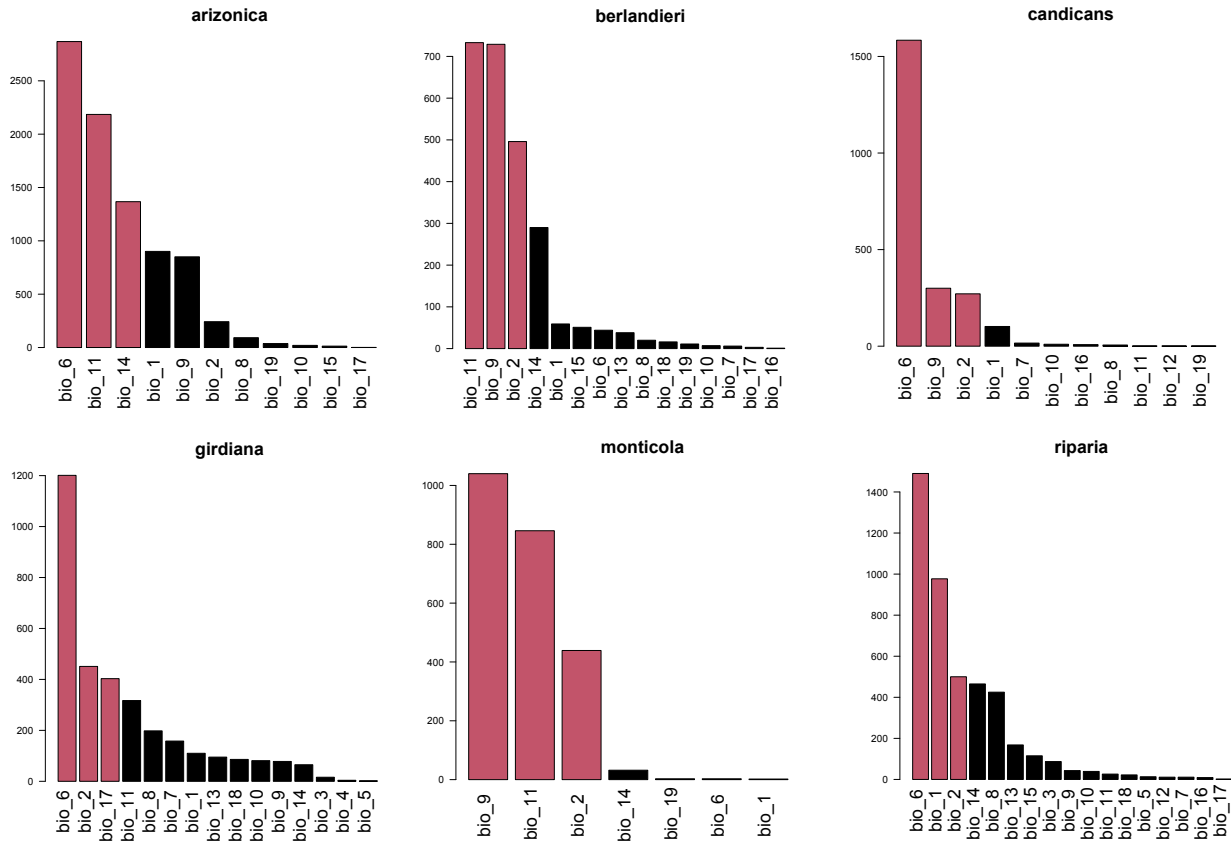


Figure S12. Number of associated candidate SNPs per bioclimatic variables per species. Red bars indicate the three Bioclimatic variables with the higher number of associated SNPs.

SUPPLEMENTAL TABLES**Table S1.** Accession identifiers and geographical coordinates of the 130 accessions used in this study. Coordinates correspond to the original collection site of the accession.

Accession	Sample ID	Species after phylogeny	Latitude	Longitude
NM11-048	vari12	<i>V. arizonica</i>	33.03475	-108.20006
NM11-031	vari11	<i>V. arizonica</i>	32.91086	-108.22894
NM11-047	vari21	<i>V. arizonica</i>	33.03644	-108.20619
NM11-040	vari16	<i>V. arizonica</i>	33.03514	-108.22894
NM11-034	vari14	<i>V. arizonica</i>	32.91928	-108.21964
NM11-033	vari13	<i>V. arizonica</i>	32.91944	-108.21933
NM11-046	vari07	<i>V. arizonica</i>	33.03928	-108.22067
NM11-035	vari03	<i>V. arizonica</i>	32.92264	-108.21567
NM11-026	vari09	<i>V. arizonica</i>	32.89156	-108.23436
TXNM088	vber09	<i>V. arizonica</i>	29.28985	-103.92507
NM11-044f	vari20	<i>V. arizonica</i>	33.03994	-108.22264
NM11-044a	vari19	<i>V. arizonica</i>	33.03994	-108.22264
NM11-042	vari17	<i>V. arizonica</i>	33.03503	-108.22875
NM11-038	vari15	<i>V. arizonica</i>	32.94819	-108.20100
NM11-027	vari10	<i>V. arizonica</i>	32.90675	-108.23219
NM11-039	vari06	<i>V. arizonica</i>	32.94953	-108.20667
ANU58	vrip15	<i>V. arizonica</i>	34.51501	-111.76801
NM11-043	vari18	<i>V. arizonica</i>	33.03994	-108.22264
NM11-037	vari05	<i>V. arizonica</i>	32.93492	-108.20075
NM11-036	vari04	<i>V. arizonica</i>	32.92881	-108.21033
NM11-045	vari02	<i>V. arizonica</i>	33.03961	-108.22000
NM11-049	vari01	<i>V. arizonica</i>	33.03500	-108.20050
TX16-022	vber21	<i>V. berlandieri</i>	30.84407	-98.09657
TX16-032	vber14	<i>V. berlandieri</i>	30.43791	-98.34980
TX16-064	vcan26	<i>V. berlandieri</i>	30.24638	-98.04376
TX16-018	vber18	<i>V. berlandieri</i>	31.03509	-98.14784
TX16-065	vber28	<i>V. berlandieri</i>	30.14990	-98.05138
TX16-026	vber12	<i>V. berlandieri</i>	30.79163	-98.16845
TX15-003	vber10	<i>V. berlandieri</i>	29.84893	-100.02290
TX16-034	vber26	<i>V. berlandieri</i>	30.03024	-98.83222
TX16-035	vber27	<i>V. berlandieri</i>	30.02967	-98.83170

TX16-016	vber17	<i>V. berlandieri</i>	31.33896	-97.51378
TX15-059	vber11	<i>V. berlandieri</i>	30.43829	-98.34963
T21	vber02	<i>V. berlandieri</i>	30.48940	-99.77200
T18	vber29	<i>V. berlandieri</i>	30.48940	-99.77200
TX15-063	vber23	<i>V. berlandieri</i>	30.68166	-98.31197
C 8-93	vber20	<i>V. berlandieri</i>	31.67678	-98.04191
C 5-93	vber19	<i>V. berlandieri</i>	31.16966	-97.42910
TX16-030	vber13	<i>V. berlandieri</i>	30.68943	-98.27036
T 03-05 S03	vber07	<i>V. berlandieri</i>	30.24687	-98.87010
TX9722	vber05	<i>V. berlandieri</i>	28.70910	-100.04950
T38	vber04	<i>V. berlandieri</i>	30.40020	-97.67910
T23	vber03	<i>V. berlandieri</i>	30.04740	-99.14030
TX43-01	vber01	<i>V. berlandieri</i>	30.31996	-97.99865
T45	vcan02	<i>V. candicans</i>	30.75930	-98.67500
T64	vcan17	<i>V. candicans</i>	31.13000	-97.78000
TX9715	vcan15	<i>V. candicans</i>	29.34750	-99.14140
candicans 9003	vcan29	<i>V. candicans</i>	32.49250	-95.80917
candicans 9005	vcan30	<i>V. candicans</i>	32.49250	-95.80917
T62	vcan16	<i>V. candicans</i>	31.27230	-97.51570
T36	vcan13	<i>V. candicans</i>	30.40020	-97.67570
TX12-003	vcan09	<i>V. candicans</i>	33.39661	-97.50039
TX32-01	vcan04	<i>V. candicans</i>	30.04743	-99.14032
T48	vcan03	<i>V. candicans</i>	30.75620	-98.70030
T46	vcan14	<i>V. candicans</i>	30.75930	-98.67500
T2	vcan10	<i>V. candicans</i>	33.25760	-97.58324
T56	vcan08	<i>V. candicans</i>	31.09820	-97.34280
candicans 9039	vcan31	<i>V. candicans</i>	29.91972	-97.19306
candicans 9001	vcan28	<i>V. candicans</i>	31.76583	-95.61667
TX16-024	vcan27	<i>V. candicans</i>	30.81022	-98.10594
TX16-006	vcan25	<i>V. candicans</i>	31.10614	-97.91810
TX16-001	vcan24	<i>V. candicans</i>	30.93038	-97.52800
TX14-081	vcan23	<i>V. candicans</i>	30.00979	-97.94384
T 03-13	vcan21	<i>V. candicans</i>	30.83118	-99.39540
T 03-08	vcan20	<i>V. candicans</i>	30.16750	-98.77183
T 03-05	vcan19	<i>V. candicans</i>	30.24687	-98.87010
TX9703	vcan12	<i>V. candicans</i>	29.96270	-98.78630
T73	vcan11	<i>V. candicans</i>	31.38660	-97.15040
SC37	vgir19	<i>V. girdiana</i>	33.33007	-117.23638
NV12-040	vgir01	<i>V. girdiana</i>	36.16128	-115.49850
SC11	vgir25	<i>V. girdiana</i>	36.41840	-116.31895

SC9	vgir06	<i>V. girdiana</i>	36.41840	-116.31895
SC26	vgir23	<i>V. girdiana</i>	34.93163	-118.92795
SC39	vgir26	<i>V. girdiana</i>	33.31813	-117.19465
NV12-041	vgir14	<i>V. girdiana</i>	36.15642	-115.49542
NV11-118	vgir12	<i>V. girdiana</i>	36.37539	-114.44308
NV11-115	vgir10	<i>V. girdiana</i>	36.38999	-114.42996
ANU78	vgir02	<i>V. girdiana</i>	36.38925	-114.42955
NV12-050	vgir15	<i>V. girdiana</i>	36.41986	-116.32050
NV11-116	vgir11	<i>V. girdiana</i>	36.37678	-114.44361
SC53	vgir17	<i>V. girdiana</i>	33.10527	-117.04198
SC36	vgir27	<i>V. girdiana</i>	33.33007	-117.23638
SC30	vgir22	<i>V. girdiana</i>	33.46235	-117.13700
SC33	vgir21	<i>V. girdiana</i>	33.39145	-117.21640
SC40	vgir20	<i>V. girdiana</i>	33.36293	-117.10158
SC51	vgir16	<i>V. girdiana</i>	33.06660	-116.87915
C20-93-A	vmon05	<i>V. monticola</i>	31.06623	-97.57890
T 03-02 S01	vmon04	<i>V. monticola</i>	29.98305	-98.90348
monticola 9040	vmon07	<i>V. monticola</i>	32.49250	-95.80917
C20-93	vmon06	<i>V. monticola</i>	31.06623	-97.57890
T40	vmon02	<i>V. monticola</i>	30.30610	-97.95240
TX67-03	vmon01	<i>V. monticola</i>	31.43516	-97.74391
NM12-119	vrip21	<i>V. riparia</i>	36.21283	-105.92722
NM12-114	vrip07	<i>V. riparia</i>	35.98822	-105.93197
NM12-108	vrip19	<i>V. riparia</i>	35.32289	-105.41953
NM12-117	vrip09	<i>V. riparia</i>	36.15992	-105.97272
NM12-116	vrip08	<i>V. riparia</i>	35.98911	-105.93036
KS14-036	vrip12	<i>V. riparia</i>	37.24091	-99.98147
CO12-103	vrip02	<i>V. riparia</i>	37.11083	-104.28486
KS14-043	vrip23	<i>V. riparia</i>	37.29012	-98.61109
NM12-104	vrip18	<i>V. riparia</i>	35.66897	-105.34619
TXNM0824	vrip17	<i>V. riparia</i>	35.66893	-105.33610
TXNM0823	vrip16	<i>V. riparia</i>	35.66893	-105.33610
CO12-102	vrip14	<i>V. riparia</i>	37.21572	-104.46469
OK14-064	vrip13	<i>V. riparia</i>	36.53865	-98.87695
KS14-035	vrip11	<i>V. riparia</i>	37.24038	-99.98163
OK14-027	vrip10	<i>V. riparia</i>	36.83688	-100.51925
NM12-111	vrip06	<i>V. riparia</i>	35.26753	-105.33447
V28-96	vrip05	<i>V. riparia</i>	41.14871	-73.27039
V23-98	vrip04	<i>V. riparia</i>	41.71946	-72.57670
OK14-026	vrip01	<i>V. riparia</i>	36.83703	-100.51897

T39	vcan06	hybrid	30.30610	-97.95240
UT12-094	vgir05	hybrid	37.29369	-113.41414
OK12-025	vcan22	hybrid	34.10983	-98.53114
OK12-027	vcan07	hybrid	34.11075	-98.53250
OK12-019	vcan05	hybrid	34.12075	-98.52269
T42	vcan01	hybrid	30.32000	-97.99860
TXNM083	vber08	hybrid	30.53358	-103.78433
SC12	vgir09	hybrid	37.03228	-117.32460
NV11-119 (GVC)	vgir13	hybrid	35.22736	-114.68964
PC96-C	vrip22	hybrid	NA	NA
TX9714	vmon03	hybrid	29.34750	-99.14140
SC23	vgir24	hybrid	35.66705	-118.25247
SC27	vgir08	hybrid	34.93163	-118.92795
SC42	vgir07	hybrid	33.28781	-116.87448
UT12-084	vgir04	hybrid	37.30861	-113.42914
UT12-075	vgir03	hybrid	37.31033	-113.43553
candicans x aestivalis 9012	vcan32	hybrid	31.76583	-95.61667
T74	vcan18	hybrid	31.38660	-97.15040
T 03-01 S01	vber06	hybrid	29.98305	-98.90348

Table S2. Statistics of the *V. arizonica* b40-14 genome assembly

Metric	Number
Total number of bases	503291318
Number of sequences	19
Average length of sequences	2.65E+07
Minimum length of sequences	17755125
Maximum length of sequences	47005314
N10 length	35285526
N20 length	33926803
N30 length	30932466
N40 length	30043575
N50 length	25930761
N60 length	25085101
N70 length	23233325
N80 length	22502345
N90 length	19267294
N10 index	2
N20 index	3
N30 index	5
N40 index	6
N50 index	8
N60 index	10
N70 index	12
N80 index	14
N90 index	17
Number of sequences \geq 100bp	19
Average length of sequences \geq 100bp	2.65E+07
N50 sequences \geq 100bp	25930761

Table S3. Summary table of the BUSCO genes of both haplotypes detected in the *V. arizonica* genome assembly

Metric	Count	Percentage
Complete BUSCOs (C)	1389	96.40%
Complete and single-copy BUSCOs (S)	493	34.20%
Complete and duplicated BUSCOs (D)	896	62.20%
Fragmented BUSCOs (F)	14	1.00%
Missing BUSCOs (M)	37	2.60%
Total BUSCO groups searched	1440	

Table S4. Chromosome size, raw number of predicted SNPs and number of SNPs after filtering across all 130 samples

Chromosome	Size (bp)	Size (Mbp)	SNPs raw biallelic	SNPs after filtering
Vari_b40-14_v1.hap1.chr01	33,926,803	33.9	2,782,419	1,375,689
Vari_b40-14_v1.hap1.chr02	22,787,875	22.8	1,955,943	920,414
Vari_b40-14_v1.hap1.chr03	17,755,125	17.8	1,542,440	767,980
Vari_b40-14_v1.hap1.chr04	30,932,466	30.9	2,566,482	1,169,772
Vari_b40-14_v1.hap1.chr05	25,930,761	25.9	2,311,363	1,188,958
Vari_b40-14_v1.hap1.chr06	23,233,325	23.2	1,759,313	968,551
Vari_b40-14_v1.hap1.chr07	35,285,526	35.3	2,852,943	1,378,311
Vari_b40-14_v1.hap1.chr08	19,150,580	19.2	1,496,299	612,688
Vari_b40-14_v1.hap1.chr09	25,085,101	25.1	2,036,641	931,494
Vari_b40-14_v1.hap1.chr10	23,682,995	23.7	2,032,387	1,089,722
Vari_b40-14_v1.hap1.chr11	19,267,294	19.3	1,355,229	665,031
Vari_b40-14_v1.hap1.chr12	32,374,331	32.4	2,849,773	1,316,433
Vari_b40-14_v1.hap1.chr13	30,043,575	30.0	2,576,413	1,324,160
Vari_b40-14_v1.hap1.chr14	27,053,463	27.1	2,430,724	1,229,304
Vari_b40-14_v1.hap1.chr15	22,502,345	22.5	1,999,980	836,821
Vari_b40-14_v1.hap1.chr16	25,629,229	25.6	2,132,614	916,236
Vari_b40-14_v1.hap1.chr17	19,376,636	19.4	1,776,932	918,695
Vari_b40-14_v1.hap1.chr18	47,005,314	47.0	3,832,273	1,639,733
Vari_b40-14_v1.hap1.chr19	22,268,574	22.3	1,807,138	741,236
Total	503,291,318	503	42,097,306	19,991,228

Table S5. Genome-wide calculation of nucleotide diversity (π) within per species

Species	π
<i>V. monticola</i>	0.00353
<i>V. riparia</i>	0.00312
<i>V. candicans</i>	0.00304
<i>V. arizonica</i>	0.00270
<i>V. girdiana</i>	0.00255
<i>V. berlandieri</i>	0.00211

Table S6. Results from genome-wide estimates of introgressions across all combination of trios tested.

Trio	P1	P2	P3	D	Z-score	p-value	f4-ratio	BBA	ABBA	BABA
GAM	<i>girdiana</i>	<i>arizonica</i>	<i>monticola</i>	0.086	15.764	0.00E+00	8.03%	312836	147982	124492
GRM	<i>girdiana</i>	<i>riparia</i>	<i>monticola</i>	0.062	10.308	0.00E+00	6.08%	294631	151684	133908
ARC	<i>arizonica</i>	<i>riparia</i>	<i>candicans</i>	0.091	21.944	0.00E+00	2.43%	411536	126061	105037
MBC	<i>monticola</i>	<i>berlandieri</i>	<i>candicans</i>	0.071	9.224	0.00E+00	3.24%	231272	189653	164656
GRC	<i>girdiana</i>	<i>riparia</i>	<i>candicans</i>	0.087	17.202	0.00E+00	2.30%	417236	124661	104798
ARB	<i>arizonica</i>	<i>riparia</i>	<i>berlandieri</i>	0.116	27.752	0.00E+00	7.40%	350794	140344	111062
GRB	<i>girdiana</i>	<i>riparia</i>	<i>berlandieri</i>	0.119	23.024	0.00E+00	7.47%	357161	139597	110007
AGR	<i>arizonica</i>	<i>girdiana</i>	<i>riparia</i>	0.021	2.961	1.54E-03	3.32%	204334	176756	169492
RAM	<i>riparia</i>	<i>arizonica</i>	<i>monticola</i>	0.019	2.737	3.10E-03	2.07%	281783	151658	145974
AGC	<i>arizonica</i>	<i>girdiana</i>	<i>candicans</i>	0.005	1.256	1.05E-01	0.13%	446358	106248	105140
GAB	<i>girdiana</i>	<i>arizonica</i>	<i>berlandieri</i>	0.001	0.358	3.60E-01	0.09%	388298	113818	113480

Table S7. Gene density averages per 10 kb and relative enrichment as presented in Table 1.

Trio	Avg. gene density	Relative. Enrichment
Genome-wide	0.5762719	-
ARC	0.4417671	0.77
GRC	0.4383202	0.76
GRB	0.433835	0.75
ARB	0.4343598	0.75
GAM	0.5551546	0.96
RAM	0.5276498	0.92
GRM	0.4581006	0.79
MBC	0.4706927	0.82
AGR	0.5678322	0.99

Table S8. GO terms significantly enriched ($p < 0.05$) in pIRs

Trio	GO ID	GO Description	p-value
AGR	GO:0005575	C:cellular_component	8.87E-04
ARB	GO:0005575	C:cellular_component	5.46E-03
ARB	GO:0030246	F:carbohydrate binding	1.81E-09
GRB	GO:0030246	F:carbohydrate binding	9.54E-06
GRC	GO:0030246	F:carbohydrate binding	5.34E-05
GRM	GO:0030246	F:carbohydrate binding	5.12E-25
ARB	GO:0016301	F:kinase activity	7.01E-07
GRB	GO:0016301	F:kinase activity	3.82E-02
GRM	GO:0016301	F:kinase activity	4.99E-12
AGR	GO:0008289	F:lipid binding	9.83E-03
AGR	GO:0003674	F:molecular_function	9.58E-03
ARB	GO:0003674	F:molecular_function	4.59E-02
ARB	GO:0000166	F:nucleotide binding	6.68E-07
GRB	GO:0000166	F:nucleotide binding	2.48E-05
GRC	GO:0000166	F:nucleotide binding	1.57E-02
GRM	GO:0000166	F:nucleotide binding	1.07E-10
ARC	GO:0004872	F:receptor activity	4.37E-02
ARC	GO:0038023	F:signaling receptor activity	1.55E-02
GRM	GO:0007154	P:cell communication	6.06E-04
ARC	GO:0007267	P:cell-cell signaling	2.21E-07
GRM	GO:0007267	P:cell-cell signaling	1.03E-03
GRM	GO:0006464	P:cellular protein modification process	1.45E-05
RAM	GO:0009790	P:embryo development	3.43E-02
RAM	GO:0009908	P:flower development	6.48E-04
GAM	GO:0006139	P:nucleobase-containing compound metabolic process	4.81E-02
GRM	GO:0009856	P:pollination	5.40E-05

Table S9. Recombination rates per trio and values relative to the genome-wide estimated rate of recombination as presented in Table 1.

Trio	Avg. cM/Kb	Relative to genome-wide
Genome-wide	0.0092	-
AGR	0.0148	1.61
ARB	0.0166	1.80
ARC	0.0113	1.23
GAM	0.0208	2.27
GRB	0.0132	1.43
GRC	0.0134	1.45
GRM	0.0111	1.21
MBC	0.0139	1.52
RAM	0.0101	1.10

Table S10. Quantitative measurements of Pierce's Disease evaluations.

Accession	Sample ID	Species	Category	Least Sq Mean	Std Error	Mean	Study ¹
ANU58	vrip15	<i>V. arizonica</i>	R	12.485003	0.9391245	11.628	This study
NM11-026	vari09	<i>V. arizonica</i>	R	8.773918	0.9660364	9.424	This study
NM11-027	vari10	<i>V. arizonica</i>	R	10.759918	0.9660364	11.41	This study
NM11-031	vari11	<i>V. arizonica</i>	R	7.942103	0.9478225	7.376	This study
NM11-033	vari13	<i>V. arizonica</i>	R	10.741918	0.9660364	11.392	This study
NM11-034	vari14	<i>V. arizonica</i>	R	12.762103	0.9478225	12.196	This study
NM11-035	vari03	<i>V. arizonica</i>	R	10.931406	1.0575963	9.8675	This study
NM11-036	vari04	<i>V. arizonica</i>	R	7.707725	0.9528475	7.626	Riaz et al 2020
NM11-037	vari05	<i>V. arizonica</i>	R	10.211003	0.6692616	9.354	This study
NM11-038	vari15	<i>V. arizonica</i>	R	8.845087	1.0666604	9.5825	This study
NM11-039	vari06	<i>V. arizonica</i>	R	12.227725	0.9528475	12.146	Riaz et al 2020
NM11-040	vari16	<i>V. arizonica</i>	R	11.457918	0.9660364	12.108	This study
NM11-042	vari17	<i>V. arizonica</i>	R	11.349918	0.9660364	12	This study
NM11-043	vari18	<i>V. arizonica</i>	R	9.465918	0.9660364	10.116	This study
NM11-044a	vari19	<i>V. arizonica</i>	R	9.235918	0.9660364	9.886	This study
NM11-044f	vari20	<i>V. arizonica</i>	R	7.889725	0.9528475	7.808	Riaz et al 2020
NM11-045	vari02	<i>V. arizonica</i>	R	11.181725	0.9528475	11.1	Riaz et al 2020
NM11-046	vari07	<i>V. arizonica</i>	R	10.871003	0.9391245	10.014	This study
NM11-047	vari21	<i>V. arizonica</i>	R	11.534918	1.0724963	12.185	This study
NM11-048	vari12	<i>V. arizonica</i>	R	8.603603	1.0561199	8.0375	This study
NM11-049	vari01	<i>V. arizonica</i>	R	9.553725	0.9528475	9.472	Riaz et al 2020
TXNM088	vber09	<i>V. arizonica</i>	R	10.723725	0.9528475	10.642	Riaz et al 2020
C 5-93	vber19	<i>V. berlandieri</i>	R	13.102103	0.9478225	12.536	This study
C 8-93	vber20	<i>V. berlandieri</i>	S	14.021906	0.9494672	12.958	This study
T 03-05 S03	vber07	<i>V. berlandieri</i>	S	14.782248	0.9503933	14.754	This study
T18	vber29	<i>V. berlandieri</i>	R	11.807725	0.9528475	11.726	This study
T21	vber02	<i>V. berlandieri</i>	R	14.156103	1.2153569	13.59	This study
T38	vber04	<i>V. berlandieri</i>	S	15.851725	1.060632	15.77	This study
TX15-003	vber10	<i>V. berlandieri</i>	S	13.205996	0.9645934	14.906	Riaz et al 2020
TX15-059	vber11	<i>V. berlandieri</i>	S	14.269906	0.9494672	13.206	This study
TX15-063	vber23	<i>V. berlandieri</i>	S	16.171996	0.9645934	17.872	Riaz et al 2020
TX16-016	vber17	<i>V. berlandieri</i>	S	16.345996	0.9645934	18.046	Riaz et al 2020
TX16-018	vber18	<i>V. berlandieri</i>	S	15.284996	1.0711966	16.985	Riaz et al 2020
TX16-022	vber21	<i>V. berlandieri</i>	S	16.657496	1.0711966	18.3575	Riaz et al 2020
TX16-026	vber12	<i>V. berlandieri</i>	S	17.015996	0.9645934	18.716	Riaz et al 2020

TX16-030	vber13	<i>V. berlandieri</i>	S	17.053996	0.9645934	18.754	Riaz et al 2020
TX16-032	vber14	<i>V. berlandieri</i>	S	15.362496	1.0711966	17.0625	Riaz et al 2020
TX16-034	vber26	<i>V. berlandieri</i>	S	12.471996	0.9645934	14.172	Riaz et al 2020
TX16-035	vber27	<i>V. berlandieri</i>	S	13.961996	0.9645934	15.662	Riaz et al 2020
TX16-064	vcan26	<i>V. berlandieri</i>	S	14.997239	1.21664	13.9333	This study
TX16-065	vber28	<i>V. berlandieri</i>	S	16.885996	0.9645934	18.586	Riaz et al 2020
TX43-01	vber01	<i>V. berlandieri</i>	S	16.148392	1.2192798	16.0667	This study
TX9722	vber05	<i>V. berlandieri</i>	S	17.903725	0.9528475	17.822	Riaz et al 2020
ANU78	vgir02	<i>V. girdiana</i>	R	13.300498	0.8790632	13.6867	Riaz et al 2020
NV11-115	vgir10	<i>V. girdiana</i>	R	12.263725	0.9528475	12.182	This study
NV11-116	vgir11	<i>V. girdiana</i>	R	10.339725	0.9528475	10.258	This study
NV11-118	vgir12	<i>V. girdiana</i>	R	9.753725	0.9528475	9.672	This study
NV12-040	vgir01	<i>V. girdiana</i>	S	16.535725	0.9528475	16.454	This study
NV12-041	vgir14	<i>V. girdiana</i>	S	16.669225	1.060632	16.5875	This study
NV12-050	vgir15	<i>V. girdiana</i>	S	16.813906	1.0575963	15.75	This study
SC11	vgir25	<i>V. girdiana</i>	R	14.202165	0.8790632	14.5883	Riaz et al 2020
SC26	vgir23	<i>V. girdiana</i>	R	12.232165	0.8790632	12.6183	Riaz et al 2020
SC30	vgir22	<i>V. girdiana</i>	R	10.857165	0.8790632	11.2433	Riaz et al 2020
SC33	vgir21	<i>V. girdiana</i>	S	14.543906	1.21664	13.48	This study
SC36	vgir27	<i>V. girdiana</i>	R	9.368118	0.5385843	8.8462	Riaz et al 2020
SC39	vgir26	<i>V. girdiana</i>	R	11.460498	0.8790632	11.8467	Riaz et al 2020
SC40	vgir20	<i>V. girdiana</i>	R	14.673003	0.9391245	13.816	This study
SC51	vgir16	<i>V. girdiana</i>	R	11.351906	0.9494672	10.288	This study
SC53	vgir17	<i>V. girdiana</i>	R	10.727906	0.9494672	9.664	This study
SC9	vgir06	<i>V. girdiana</i>	S	16.425906	0.9494672	15.362	This study
CO12-102	vrip14	<i>V. riparia</i>	S	18.289725	0.9528475	18.208	This study
CO12-103	vrip02	<i>V. riparia</i>	S	15.681003	0.9391245	14.824	This study
KS14-035	vrip11	<i>V. riparia</i>	S	15.404103	0.9478225	14.838	This study
KS14-036	vrip12	<i>V. riparia</i>	S	15.754103	0.9478225	15.188	This study
KS14-043	vrip23	<i>V. riparia</i>	S	18.979003	0.9391245	18.122	This study
NM12-104	vrip18	<i>V. riparia</i>	S	14.587725	0.9528475	14.506	This study
NM12-108	vrip19	<i>V. riparia</i>	S	15.833906	0.9494672	14.77	This study
NM12-111	vrip06	<i>V. riparia</i>	R	14.243003	0.9391245	13.386	This study
NM12-114	vrip07	<i>V. riparia</i>	S	17.899003	0.9391245	17.042	This study
NM12-116	vrip08	<i>V. riparia</i>	S	16.71867	0.8586463	15.8617	This study
NM12-117	vrip09	<i>V. riparia</i>	S	17.079725	0.9528475	16.998	This study
NM12-119	vrip21	<i>V. riparia</i>	S	15.079725	0.9528475	14.998	This study
OK14-026	vrip01	<i>V. riparia</i>	S	16.903906	1.0575963	15.84	This study
OK14-027	vrip10	<i>V. riparia</i>	S	17.109254	1.2245275	17.8467	This study
OK14-064	vrip13	<i>V. riparia</i>	S	15.501906	0.9494672	14.438	This study

TXNM0823	vrip16	<i>V. riparia</i>	R	12.131003	0.9391245	11.274	This study
TXNM0824	vrip17	<i>V. riparia</i>	S	17.139003	0.9391245	16.282	This study
V23-98	vrip04	<i>V. riparia</i>	S	17.477104	1.4921791	16.565	This study
V28-96	vrip05	<i>V. riparia</i>	S	17.282104	1.4921791	16.37	This study

¹ The citation Riaz et al 2020 refers to Ref (Riaz et al., 2020)

Table S11. Number of SNPs across the genome and their association with genes for the receptor species tested in this study

Species	PD-SNPs	N. genes with PD-SNPs	N. PD-SNPs in genes	% PD-SNPs in genes
<i>V. arizonica</i>	527	66	129	24.5%
<i>V. berlandieri</i>	5424	842	2756	50.8%
<i>V. girdiana</i>	356	43	108	30.3%
<i>V. riparia</i>	1690	208	625	37.0%

Table 12. Genes with SNPs associated to PD detected in more than one species. The trio is denoted if the gene was inside pIRs.

Chr	Gene ID	Description	PRG annotation	Assoc. Species	Trio detected
chr19	g270290	LRR receptor-like kinase	RLK	vber, vrip	ARB, ARC, GRB
chr04	g046570	zinc finger FYVE domain	-	vber, vrip	MBC
chr12	g171820	EI24 homolog	-	vber, vrip	ARB
chr12	g167550	Diacylglycerol kinase 5-like	CNL	vber, vgir	-
chr01	g003720	Histone chaperone ASF1B	-	vber, vrip	-
chr01	g014200	iron-sulfur cluster co-chaperone mitochondrial	-	vber, vrip	-
chr04	g045340	Ribosomal S5 domain 2-like superfamily	-	vber, vrip	-
chr06	g078540	E3 ubiquitin ligase BIG BROTHER-like	-	vber, vrip	-
chr08	g115260	eukaryotic translation initiation factor	-	vber, vgir	-
chr10	g133570	L-ascorbate oxidase homolog	-	vber, vrip	-
chr11	g155590	pentatricopeptide repeat-containing At5g52630	-	vber, vrip	-
chr12	g160220	probable S-acyltransferase 7	-	vari,vber	-
chr12	g168300	SNF7 family	-	vari,vber	-
chr14	g196910	nucleolar coiled-body phospho	-	vber, vrip	-
chr15	g212860	MADS-box SOC1-like	-	vber, vrip	-
chr15	g213680	probable plastid-lipid-associated chloroplastic	-	vber, vrip	-
chr15	g217180	Remorin family	-	vber, vrip	-
chr18	g249790	pesticidal crystal cry8Ba	-	vber, vrip	-
chr18	g254900	Cytochrome P450 734A1	-	vari, vrip	-

Table S13. Number of SNPs across within pIRs and their association with genes per trio

Trio	Receptor species	PD-SNPs in pIRs	N. genes with PD-SNPs in pIRs	N. PD-SNPs in genes & pIRs	% PD-SNPs in genes & pIRs
MBC	<i>V. berlandieri</i>	323	34	92	28%
ARB	<i>V. riparia</i>	190	15	48	25%
GRB	<i>V. riparia</i>	117	13	48	41%
GRM	<i>V. riparia</i>	110	7	7	6%
GAM	<i>V. arizonica</i>	50	8	14	28%
ARC	<i>V. riparia</i>	18	3	6	33%
GRC	<i>V. riparia</i>	18	3	3	17%
RAM	<i>V. arizonica</i>	16	3	6	38%
AGR	<i>V. girdiana</i>	0	0	0	0%

Table S14. Comparison of number of SNPs significantly associated with PD with the expected value calculated by window permutations. P-values correspond to a t-test comparing the observed value with the whole distribution of results by random permutations.

Trio	Observed	Expected	Relative Enrichment	p-value
ARB	190	122.71	1.5484	< 2.2e-16
GAM	50	39.98	1.2506	< 2.2e-16
MBC	323	163.74	1.9726	< 2.2e-16
RAM	16	10.16	1.5748	< 2.2e-16
AGR	0	11.73	0	1
ARC	18	39.34	0.4575	1
GRB	117	124.81	0.9374	1
GRC	18	36.94	0.4873	1
GRM	100	100.74	0.9927	1

Table S15. Relative enrichment of the top three bioclimatic variables per trio. p-values correspond to a t-test comparing the observed value with the whole distribution of results by random permutations.

Trio	Sp. Assoc	BIO	Relative enrich.	p-value
ARC	V. riparia	1	1.05	< 2.2e-16
ARC	V. riparia	2	1.27	< 2.2e-16
ARC	V. riparia	6	1.05	< 2.2e-16
GRC	V. riparia	1	1.35	< 2.2e-16
GRC	V. riparia	2	1.48	< 2.2e-16
GRC	V. riparia	6	1.24	< 2.2e-16
GRB	V. riparia	1	1.07	< 2.2e-16
GRB	V. riparia	2	1.21	< 2.2e-16
GRB	V. riparia	6	1.07	< 2.2e-16
ARB	V. riparia	1	1.33	< 2.2e-16
ARB	V. riparia	2	1.30	< 2.2e-16
ARB	V. riparia	6	1.18	< 2.2e-16
GAM	V. arizonica	6	0.25	1
GAM	V. arizonica	11	0.56	1
GAM	V. arizonica	14	0.15	1
RAM	V. arizonica	6	1.34	< 2.2e-16
RAM	V. arizonica	11	1.05	< 2.2e-16
RAM	V. arizonica	14	1.34	< 2.2e-16
AGR	V. girdiana	2	1.90	< 2.2e-16
AGR	V. girdiana	6	1.07	< 2.2e-16
AGR	V. girdiana	17	1.51	< 2.2e-16
GRM	V. riparia	1	0.44	1
GRM	V. riparia	2	0.59	1
GRM	V. riparia	6	0.24	1
MBC	V. berlandieri	2	1.77	< 2.2e-16
MBC	V. berlandieri	9	2.09	< 2.2e-16
MBC	V. berlandieri	11	2.11	< 2.2e-16

DATASETS

Datasets are available in Figshare: <https://doi.org/10.6084/m9.figshare.13912178>

Dataset legends

Dataset S1. Genomic windows identified as putative introgressed regions (pIRs) across nine trios.

Dataset S2. Gene functional annotation for the genome reference of *Vitis arizonica*.

Dataset S3. Significant SNPs (Bonferroni adjusted $p < 0.05$) from whole genome associations with bacterial levels after infection with the causative agent of Pierce's Disease for four receptor species of introgression.

Dataset S4. Significant SNPs (Bayes' Factor > 10) from whole genome associations with the top three bioclimatic variables per species.

SI REFERENCES

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