

**Signatures of repeated genomic selection associated with human-modified landscapes in
genetically independent populations of *Rhinella horribilis***

Supplementary material

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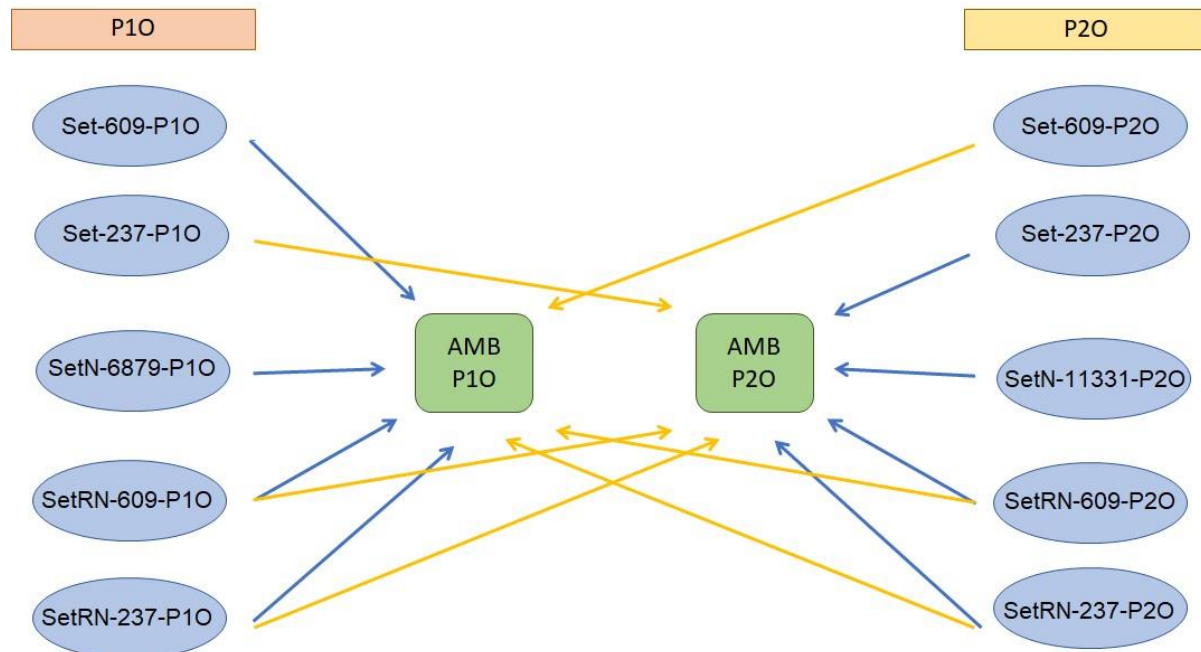


Figure S1. Redundancy analysis (RDA) scheme to test repeated signals of genomic selection and to identify if potentially adaptive genetic variation in the two landscapes responded similarly to the same landscape variables in *Rhinella horribilis* in two landscapes (P1O and P2O). On the left and right sides, the sets of SNPs obtained for P1O and P2O, respectively. The environmental variables of each landscape are schematized in the center (AMB; in green). Blue arrows indicate RDA tests to measure genetic x environmental relationships within the same landscape; yellow arrows indicate RDA tests to evaluate genetic x environmental relationships between landscapes (cross tests). See details in section Assessment of selection signals of the main text.

Tables

Table S1. Results of redundancy analysis (RDA) tests with different sets of SNPs to explain environmental variation within and between the two landscapes. P1O: landscape 1, P2O: landscape 2; Amb1: environmental variables of landscape 1; Amb2: environmental variables of landscape 2.

SNPs sets tested	R^2 (%)	p
(a) Set-609-P1O: 609 candidate SNPs P1O – Amb1	58.3	0.001
(b) Set-237-P2O: 237 candidate SNPs P2O – Amb2	85.7	0.001
(c) Set-609-P2O: 609 candidate SNPs P1O – Amb2	35.5	0.001
(d) Set-237-P1O: 237 candidate SNPs P2O – Amb1	51.8	0.001
(e) SetN-6879-P1O: neutral SNPs P1O – Amb1	6.3	0.001
(f) SetN-3494-P2O: neutral SNPs P2O – Amb2	19.4	0.001
(g) SetRN-609-P1O: 609 random neutral SNPs P1O – Amb1	6.7	0.001
(h) SetRN-237-P1O: 237 random neutral SNPs P1O – Amb1	7.1	0.001
(i) SetRN-609-P2O: 609 random neutral SNPs P2O – Amb2	26.0	0.001
(j) SetRN-237-P2O: 237 random neutral SNPs P2O – Amb2	24.4	0.001
(k) 609-P2O-P1O: 609 random neutral SNPs P2O – Amb1	14.0	0.001
(l) 237-P2O-P1O: 237 random neutral SNPs P2O – Amb1	14.6	0.001
(m) 609-P1O-P2O: 609 random neutral SNPs P1O – Amb2	26.1	0.001
(n) 237-P1O-P2O: 237 random neutral SNPs P1O – Amb2	27.2	0.001

Table S2. Sampling within each landscape. Eight sampling sites in landscape 1 (P1O) and seven in landscape 2 (P2O). n = number of individuals.

OP1	Sampling sites	n	Total
	Loc1	10	
	Loc2	15	
	Loc3	11	
	Loc4	23	
	Loc5	23	
	Loc6	10	
	Loc7	23	
	Loc8	10	
			125
OP2			
	Loc9	8	
	Loc10	4	
	Loc11	11	
	Loc12	3	
	Loc13	8	
	Loc14	10	
	Loc15	21	
			65

Table S3. Outlier loci detected for *Rhinella horribilis* by redundancy analysis (RDA), latent factor mixed model (LFMM) and PCAdapt methods. Number of SNPs associated with each variable (total for PCAdapt) and its percentage are indicated for landscape 1 (P1O) and landscape 2 (P2O).

P1O		Method			
Environmental variable	RDA	LFMM	PCAdapt	% RDA	% LFMM
Ambient temperature (AT)	56	412		8.5	10.6
Solar radiation (SR)	17	282		2.8	7.3
Relative humidity (RH)	0	201		0	5.2
Evapotranspiration (EVA)	141	1235		23.2	31.9
Potassium (K)	196	197		32.2	5.1
Sodium (Na)	27	551		4.4	14.2
Oxygen availability (OA)	0	215		0	5.6
Water temperature (WT)	171	772		28.1	19.9
Total (unique loci)	608	2389	109	100	100
Total (with duplicated loci)		3865			100
P2O		Method			
Environmental variable	RDA	LFMM	PCAdapt	%RDA	%LFMM
Solar radiation (SR)	45	1946		21.2	31.5
Relative humidity (RH)	107	936		50.5	15.2
Evapotranspiration (EVA)	21	755		9.9	12.2
Potassium (K)	0	1		0	0.01
Sodium (Na)	0	322		0	5.2
Nitrates (NO)	0	107		0	1.7
Oxygen availability (OA)	25	1081		11.8	15.5
Water temperature (WT)	14	1020		6.6	16.5
Total (unique loci)	212	2301	226	100	100
Total (with duplicated loci)		6168			100

Table S4. Hypergeometric test of the overlap of candidate SNPs associated with the same environmental variables in each landscape. P1O: landscape 1; P2O: landscape 2. CLI: climatic variables (evapotranspiration, solar radiation, ambient temperature, relative humidity); PHS: physicochemical variables (oxygen availability, water temperature, sodium, potassium). Between parentheses is the percentage of candidate SNPs in relation to the total in each case.

609 candidate SNPs identified in P1O				
	P1O-609	P2O-609	Overlap	<i>p</i> (hypergeometric test)
CLI	253 (41.5)	227 (37.2)	98 (16.1)	< 0.001
PHS	365 (59.9)	395 (64.9)	237 (38.9)	< 0.001
237 candidate SNPs identified in P2O				
	P1O-237	P2O-237	overlap	<i>p</i> (hypergeometric test)
CLI	184 (77.6)	138 (58.2)	112 (42.2)	< 0.001
PHS	43 (18.1)	87 (36.7)	17 (7.2)	< 0.001

Table S5. Gene annotation table for 385 regions associated with at least one gene in landscape 1 (P1O) and 248 in landscape 2 (P2O); 34 genes found in both landscapes are in bold (**available as an independent excel file**).

Table S6. Redundancy analysis (RDA) for the association between the 34 shared genes and environmental (AT, SR, RH, EVA) and water physicochemical (K, NA, OA, WT) variables in landscape 1 (P10) and landscape 2 (P20). The best predictor (BP), correlation value (Cor), and gene symbol (Gen S) are indicated. The enriched genes are shown in bold.

Environmental predictor												
P10												
SNP ID	RDA loading	AT	SR	RH	EVA	K	NA	OA	WT	BP	Cor	Gen S
5940_5	0.310	0.135	-0.144	-0.070	0.175	-0.024	0.440	-0.260	0.527	WT	0.527	U2AF2
5941_108	0.190	0.121	-0.150	-0.040	0.169	-0.026	0.433	-0.236	0.473	WT	0.473	ZCCHC3
												SP3
												ANKRD45
												ZFR
												NFYC
10330_89	0.407	-0.030	0.550	-0.499	0.014	0.663	-0.554	-0.428	-0.401	K	0.663	TCIM
29533_38	-1.219	-0.529	0.135	0.200	-0.162	0.258	0.155	-0.071	-0.208	AT	0.529	TGFBRAP1
												EMC8
												HELZ
												CBX6
34934_85	0.334	-0.178	0.521	-0.393	-0.062	0.736	-0.533	-0.583	-0.431	K	0.736	MAPK13
37417_115	0.214	0.103	-0.036	-0.119	0.197	0.058	0.401	-0.332	0.451	WT	0.451	STK39
												ZNF451
												TRAF2
												PRKCD
												SPNS1
												RABIF
												FRZB2
43017_23	0.427	-0.011	0.550	-0.558	0.040	0.710	-0.485	-0.487	-0.319	K	0.710	USP45
43325_96	-0.120	-0.055	0.383	0.210	0.370	-0.206	0.065	-0.078	-0.040	SR	0.383	RPS28P9
43325_95	-0.125	-0.097	0.446	0.125	0.320	-0.202	0.064	-0.044	0.002	SR	0.446	RPS18

43325_93	0.002	-0.038	0.408	0.138	0.337	-0.238	0.041	-0.055	0.000	SR	0.408	
43326_87	0.203	-0.193	0.006	-0.195	-0.524	-0.172	-0.213	0.012	-0.063	EVA	0.524	
43326_60	0.148	-0.181	-0.073	-0.218	-0.569	-0.215	-0.135	0.084	0.022	EVA	0.569	
57470_27	-1.239	-0.455	0.161	0.124	-0.127	0.247	0.136	0.018	-0.215	AT	0.455	LOC100497432
63686_91	-1.087	-0.439	0.075	0.158	-0.191	0.189	0.100	0.041	-0.207	AT	0.439	SLC7A9 PECAM1
112556_67	0.176	0.042	-0.173	0.002	0.084	-0.071	0.444	-0.257	0.484	WT	0.484	MAP3K4 NAB2
114880_71	0.403	-0.048	0.499	-0.451	0.011	0.701	-0.531	-0.483	-0.398	K	0.701	PIK3R1 SOX11
156350_66	-1.190	-0.496	0.031	0.246	-0.178	0.151	0.211	0.074	-0.121	AT	0.496	SLAMF8 MANSC1
623828_63	-1.162	-0.439	0.130	0.153	-0.131	0.210	0.123	0.044	-0.205	AT	0.439	TNIK
624633_21	-1.040	-0.403	0.044	0.157	-0.148	0.145	0.205	-0.017	-0.098	AT	0.403	NEUROD1
879041_124	0.516	-0.055	0.493	-0.376	0.015	0.655	-0.591	-0.458	-0.434	K	0.655	KMT2C
P2O												
34934_22	-0.109	-0.589	0.339	-0.481	-0.732	-0.225	0.234	0.301	-0.395	EVA	0.732	MAPK13
72018_43	-0.139	-0.182	0.271	0.220	-0.051	-0.253	-0.323	0.228	-0.459	WT	0.459	U2AF2
92393_74	-0.297	0.535	-0.617	0.751	0.231	-0.121	0.427	0.654	0.488	RH	0.751	FRZB2
126617_49	1.082	-0.385	0.535	-0.073	-0.449	-0.261	0.232	-0.245	0.346	SR	0.535	RPS28P9 RPS18
142202_127	1.092	-0.434	0.552	-0.074	-0.451	-0.338	0.294	-0.270	0.356	SR	0.552	NEUROD1
290084_106	1.086	-0.378	0.533	-0.051	-0.464	-0.357	0.322	-0.221	0.304	SR	0.533	MAP3K4
444250_65	-0.437	0.218	-0.427	0.466	-0.165	-0.295	0.560	0.832	0.136	OA	0.832	NAB2
444251_58	-0.437	0.218	-0.427	0.466	-0.165	-0.295	0.560	0.832	0.136	OA	0.832	PIK3R1
582279_123	-0.467	0.235	-0.472	0.469	-0.142	-0.239	0.552	0.836	0.205	OA	0.836	ZCCHC3
689120_38	1.085	-0.390	0.537	-0.079	-0.458	-0.267	0.242	-0.244	0.345	SR	0.537	PECAM1
698786_122	-0.194	-0.381	0.224	-0.320	-0.577	-0.283	0.254	0.354	-0.484	EVA	0.577	BLTP3B
721346_50	-0.302	0.544	-0.627	0.746	0.237	-0.119	0.437	0.648	0.490	RH	0.746	ZNF451
721346_46	-0.302	0.544	-0.627	0.746	0.237	-0.119	0.437	0.648	0.490	RH	0.746	TCIM
722973_16	1.078	-0.324	0.528	-0.044	-0.498	-0.350	0.316	-0.157	0.223	SR	0.528	
750597_88	-0.272	0.563	-0.645	0.802	0.230	-0.163	0.498	0.688	0.531	RH	0.802	KMT2C

750598_12	-0.272	0.563	-0.645	0.802	0.230	-0.163	0.498	0.688	0.531	RH	0.802	
766025_53	1.007	-0.285	0.481	-0.009	-0.452	-0.299	0.266	-0.127	0.240	SR	0.481	SP3
786001_57	1.080	-0.398	0.537	-0.077	-0.472	-0.277	0.256	-0.227	0.347	SR	0.537	ANKRD45
786000_75	1.081	-0.398	0.546	-0.067	-0.499	-0.358	0.325	-0.197	0.289	SR	0.546	ZFR
												NFYC
												TRAF2
813406_90	1.086	-0.384	0.532	-0.062	-0.435	-0.281	0.248	-0.256	0.352	SR	0.532	TNIK
												PRKCD
												SPNS1
												RABIF
827236_55	0.886	-0.561	0.571	-0.155	-0.814	-0.428	0.447	0.137	0.145	EVA	0.814	SLAMF8
												MANSC1
869295_44	-0.251	0.499	-0.604	0.743	0.242	-0.189	0.503	0.595	0.527	RH	0.743	USP45
												LOC100497432
876016_76	1.097	-0.427	0.544	-0.067	-0.437	-0.356	0.318	-0.283	0.365	SR	0.544	SOX11
876016_46	1.085	-0.380	0.524	-0.061	-0.435	-0.272	0.250	-0.252	0.367	SR	0.524	
891384_74	1.150	-0.415	0.571	-0.052	-0.484	-0.332	0.286	-0.239	0.357	SR	0.571	STK39
952796_10	1.074	-0.335	0.515	-0.062	-0.436	-0.179	0.159	-0.225	0.351	SR	0.515	TGFBRAP1
												CBX6
												SLC7A9
												EMC8
												HELZ
