Supplementary Material

Genome-scale data reveal deep lineage divergence and a complex demographic history in the Texas horned lizard (*Phrynosoma cornutum*) throughout the southwestern and central US

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Supplementary Tables

Table S1. Sampling data for all Texas horned lizards (*Phrynosoma cornutum*) and the outgroup (*P. solare*) used in this study. Raw total reads indicates the number of raw nGBS reads (total forward and reverse) for each sample. Loci in assembly shows the number of loci recovered from each sample after processing in ipyrad. Samples FHSM16593 and FHSM16898 were excluded from subsequent analyses due to a low number of reads. NA = Not Applicable.

Species	ID	Plate_ID	Assembly_ID	Country	State	County	Lat	Long	Raw total reads	Loci in assembly
Phrynosoma cornutum	CAS223566	A1	CAS223566	USA	Colorado	Otero Co.	37.70319	-103.41536	2,628,492	19,250
Phrynosoma cornutum	YPM18939	A2	YPM18939	USA	New Mexico	Hidalgo County	31.943009	-108.869931	3,139,608	27,496
Phrynosoma cornutum	MVZ238582	A3	MVZ238582	USA	Arizona	Cochise County	31.91259	-109.15076	2,557,172	17,713
Phrynosoma cornutum	FHSM9065	A4	FHSM9065	USA	Kansas	Ellis	39.1137	-99.42567	4,042,644	36,182
Phrynosoma cornutum	FHSM8954	A5	FHSM8954	USA	Kansas	Russell	39.0307	-99.00036	4,118,078	35,328
Phrynosoma cornutum	FHSM16593	A6	FHSM16593	USA	New Mexico	Hidalgo	32.61504	-108.98934	171,164	NA
Phrynosoma cornutum	CAS228870	B1	CAS228870	USA	New Mexico	Luna Co.	32.3675	-107.8428333	3,496,728	31,894
Phrynosoma cornutum	YPM18934	B2	YPM18934	USA	New Mexico	Hidalgo County	31.94322	-108.88875	3,113,348	28,861
Phrynosoma cornutum	MVZ269788	B3	MVZ269788	USA	Oklahoma	Harper County	36.9586	-99.9101	2,552,102	22,035
Phrynosoma cornutum	FHSM8541	B4	FHSM8541	USA	Kansas	Harper	37.02347	-97.83816	3,586,546	34,503
Phrynosoma cornutum	FHSM11180	B5	FHSM11180	USA	Kansas	Seward	37.13912	-100.78118	4,396,558	38,822
Phrynosoma cornutum	FHSM16233	B6	FHSM16233	USA	Oklahoma	Beckham	35.15165421	-99.85324662	4,135,670	38,433
Phrynosoma cornutum	CAS228873	C1	CAS228873	USA	Arizona	Cochise Co.	31.62443056	-109.2074889	3,026,500	25,894
Phrynosoma cornutum	YPM18947	C2	YPM18947	USA	Arizona	Cochise County	31.90903	-109.11222	3,097,846	29,694
Phrynosoma cornutum	FHSM9128	C3	FHSM9128	USA	Kansas	Meade	37.21475	-100.46707	4,976,888	42,652
Phrynosoma cornutum	FHSM8606	C4	FHSM8606	USA	Kansas	Kiowa	37.4661	-99.10786	4,211,224	36,869
Phrynosoma cornutum	FHSM11375	C5	FHSM11375	USA	Kansas	Seward	37.12771	-100.7822	3,992,240	37,881
Phrynosoma cornutum	FHSM16007	C6	FHSM16007	USA	Oklahoma	Cimarron	36.81620278	-102.8517467	3,662,888	35,591
Phrynosoma cornutum	CAS228872	D1	CAS228872	USA	Arizona	Cochise Co.	31.65231944	-109.1589694	3,050,294	27,856
Phrynosoma cornutum	OCGR14021	D2	OCGR14021	USA	Oklahoma	Canadian	38.696014	-98.0207	3,532,950	31,258
Phrynosoma cornutum	FHSM8542	D3	FHSM8542	USA	Kansas	Barber	37.13965	-98.69531	3,786,694	36,435
Phrynosoma cornutum	FHSM8607	D4	FHSM8607	USA	Kansas	Kiowa	37.51368	-99.15667	4,440,656	39,848
Phrynosoma cornutum	FHSM9010	D5	FHSM9010	USA	Kansas	Stanton	37.51959	-102.01588	4,660,100	40,689
Phrynosoma cornutum	FHSM16232	D6	FHSM16232	USA	Oklahoma	Greer	35.0942235	-99.78271819	3,620,344	35,256
Phrynosoma cornutum	CAS223567	E1	CAS223567	USA	Colorado	Las Animas Co.	37.589185	-103.329031	2,790,664	24,773
Phrynosoma cornutum	OCGR9297	E2	OCGR9297	USA	Oklahoma	Cimarron	36.6629	-102.78673	2,127,180	12,266
Phrynosoma cornutum	FHSM11825	E3	FHSM11825	USA	Kansas	Barber	37.09546	-98.96539	3,577,724	30,615
Phrynosoma cornutum	FHSM9111	E4	FHSM9111	USA	Kansas	Lincoln	39.0794	-98.1511	3,620,426	33,438
Phrynosoma cornutum	FHSM16492	E5	FHSM16492	USA	Kansas	Stanton	37.486559	-102.041782	1,129,208	4,757
Phrynosoma cornutum	FHSM16223	E6	FHSM16223	USA	Oklahoma	Harmon	34.95179125	-99.9145693	3,717,844	35,981
Phrynosoma cornutum	CAS223561	F1	CAS223561	USA	Colorado	Otero Co.	37.76283333	-103.5785	3,254,194	31,438
Phrynosoma cornutum	OCGR6643	F2	OCGR6643	USA	Oklahoma	Ellis	35.8934	-99.6637	2,534,122	21,926
Phrynosoma cornutum	FHSM16898	F3	FHSM16898	USA	Kansas	Chautauqua	37.09865	-96.26519	482,518	NA
Phrynosoma cornutum	FHSM8605	F4	FHSM8605	USA	Kansas	Meade	37.0531	-100.10749	3,626,724	34,054
Phrynosoma cornutum	FHSM11371	F5	FHSM11371	USA	Kansas	Stevens	37.07085	-101.4834	3,299,466	28,957
Phrynosoma cornutum	FHSM16024	F6	FHSM16024	USA	Oklahoma	Harper	36.64099493	-99.4764639	4,042,414	36,568
Phrynosoma cornutum	YPM18957	G1	YPM18957	USA	New Mexico	Hidalgo County	31.932925	-108.969717	3,248,856	30,276
Phrynosoma cornutum	MVZ161507	G2	MVZ161507	USA	New Mexico	Dona Ana County	32.312222	-106.777779	3,031,026	26,703
Phrynosoma cornutum	FHSM8581	G3	FHSM8581	USA	Kansas	Clark	37.19376	-99.87469	3,273,952	31,369
Phrynosoma cornutum	FHSM11559	G4	FHSM11559	USA	Kansas	Osborne	39.17528	-98.8996	3,779,880	36,322
Phrynosoma cornutum	FHSM16889	G5	FHSM16889	USA	Kansas	Stevens	37.054774	-101.483188	3,696,916	34,764
Phrynosoma cornutum	FHSM17437	G6	FHSM17437	USA	Kansas	Elk	37.567365	-96.495885	2,717,418	24,535
Phrynosoma cornutum	YPM18933	H1	YPM18933	USA	Arizona	Cochise County	31.90903	-109.11222	3,058,390	27,171
Phrynosoma cornutum	MVZ252854	H2	MVZ252854	USA	New Mexico	Dona Ana County	32.53023333	-106.7740167	2,624,244	20,976
Phrynosoma cornutum	FHSM9126	H3	FHSM9126	USA	Kansas	Comanche	37.25453	-99.11038	4,300,416	37,922
Phrynosoma cornutum	FHSM8038	H4	FHSM8038	USA	Kansas	Russell	38.7994	-99.0196	3,826,740	34,920
Phrynosoma cornutum	FHSM16814	H5	FHSM16814	USA	New Mexico	Grant	32.558056	-107.984478	3,275,088	29,636
Phrynosoma cornutum	10R2L8L	P1-10R2L8L	10R2L8L	USA	Texas	Dimmit/La Salle	28.32603	-99.407555	3,633,126	20,955
Phrynosoma cornutum	5R7R6L	P1-5R7R6L	5R7R6L	USA	Texas	Potter	35.419743	-101.947293	4,030,164	23,331
Phrynosoma cornutum	7R10L	P1-7R10L	7R10L	USA	Texas	Dimmit/La Salle	28.32603	-99.407555	2,858,336	18,544
Phrynosoma cornutum	ABGF01	P1-AGBF01	ABGF01	USA	Texas	Brisco	34.547778	-100.950556	9,410,592	33,297
Phrynosoma cornutum	ABGF11	P1-AGBF11	ABGF11	USA	Texas	Motley	34.1525	-100.704444	4,842,856	23,150
Phrynosoma cornutum	BL2	P1-BL2	BL2	USA	Texas	Midland	31.912383	-102.069583	2,614,366	16,903
Phrynosoma cornutum	BS2	P1-BS2	BS2	USA	Texas	Nolan	32.15489916	-100.4307774	12,423,608	30,309
Phrynosoma cornutum	CO14	P1-CO14	CO14	USA	Colorado	Prowers	37.659408	-102.544595	4,349,506	28,893
Phrynosoma cornutum	CO2	P1-CO2	CO2	USA	Colorado	Baca	37.235833	-102.724035	5,879,784	35,553
Phrynosoma cornutum	K10	P1-K10	K10	USA	Texas	Karnes	28.888123	-97.898467	5,758,698	24,942
Phrynosoma cornutum	K24	P1-K24	K24	USA	Texas	Karnes	28.890415	-97.897358	5,409,790	24,584
Phrynosoma cornutum	K71	P1-K71	K71	USA	Texas	Karnes	28.810068	-97.845914	5,032,512	26,854
Phrynosoma cornutum	KK104	P1-KK104	KK104	USA	Texas	Brewster	30.0032	-103.488	4,900,104	23,031
Phrynosoma cornutum	KL05	P1-KL05	KL05	USA	Texas	Midland	31.893113	-102.327828	4,283,458	23,307
Phrynosoma cornutum	MA123	P1-MA123	MA123	USA	Texas	Cottle	34.117351	-100.344618	8,468,242	29,485
Phrynosoma cornutum	MA133	P1-MA133	MA133	USA	Texas	Cottle	34.117351	-100.344618	2,460,288	14,402
Phrynosoma cornutum	MA166	P1-MA166	MA166	USA	Texas	Cottle	34.117351	-100.344618	4,695,164	24,657
Phrynosoma cornutum	MA182	P1-MA182	MA182	USA	Texas	Cottle	34.117351	-100.344618	10,111,700	30,331
Phrynosoma cornutum	PhCo1	P1-Pc1	Pc1	USA	New Mexico	Tucumcari	35.1833	-103.663	5,216,602	25,629
Phrynosoma cornutum	PhCo2	P1-Pc2	Pc2	USA	New Mexico	Tucumcari	35.1833	-103.663	6,503,754	25,430
Phrynosoma cornutum	PhCo3	P1-Pc3	Pc3	USA	New Mexico	Tucumcari	35.1833	-103.663	7,872,410	28,340
Phrynosoma cornutum	PhCo4	P1-Pc4	Pc4	USA	New Mexico	Tucumcari	35.1833	-103.663	7,185,118	27,746
Phrynosoma cornutum	PhCo5	P1-Pc5	Pc5	USA	New Mexico	Carlsbad	32.28549	-104.63	3,531,324	20,257
Phrynosoma cornutum	PhCo6	P1-Pc6	Pc6	USA	New Mexico	Carlsbad	32.28812	-104.608	4,705,198	23,426
Phrynosoma cornutum	UTA R-65008	P1-UTA65008	UTA65008	USA	Texas	Briscoe	34.4	-101.05	5,747,492	26,158
Phrynosoma cornutum	MA227	P1-MA227	MA227	USA	Texas	Cottle	34.117351	-100.344618	11,323,318	34,095
Phrynosoma cornutum	MA230	P1-MA230	MA230	USA	Texas	Cottle	34.117351	-100.344618	5,139,164	25,251
Phrynosoma cornutum	MA69	P1-MA69	MA69	USA	Texas	Cottle	34.117351	-100.344618	8,680,360	27,959
Phrynosoma solare	FHSM9405	H6	FHSM9405	USA	Arizona	Pima	32.32778	-111.2175	4,069,032	15,278

Table S2: Measures of genetic variation among populations of *Phrynosoma cornutum* based on SNP data. Between population values are presented on the upper diagonal in Nei's genetic distances. The lower diagonal values represent pairwise population differentiation (F_{st}), 95% confidence intervals are indicated in parentheses. Within population variation is presented in Nei's genetic distances.

Between-Populations					Within-Populations	
	Southern	**Plains**	**Desert**		**Southern**	0.113
Southern	-	0.047	0.191		**Plains**	0.094
Plains	0.096 (0.094-0.097)	-	0.195		**Desert**	0.052
Desert	0.402 (0.399-0.405)	0.494 (0.491-0.496)	-			

Table S3. Estimates of effective population sizes from multispecies coalescent (MSC) analyses in BPP. The 'Estimate' and 'Calibrated Estimate' columns indicate mean values obtained by combining two independent runs per data set. All raw parameter values are *1000. Absolute effective population sizes (N_e) were obtained by assuming a per year mutation rate of $8 * 10^{-10}$ (Perry et al., 2018) and a generation time of two years (Jezkova et al., 2016). OG = outgroup; IG = ingroup; DST = Desert (pop 1); STH = Southern (pop 2); PLN = Plains (pop 3). NoAdmix = runs excluding sample KK104 (from DST); Admix = runs including this individual. Estimates in bold italics indicate substantial differences between data sets. * = two peaks in the posterior.

Run	Parameter	Estimate	95% HPD lower	95% HPD upper		Calibrated Estimate	95% HPD lower	95% HPD upper
NoAdmix	θ_{OG}	1.301	0.596	2.128		203,281	93,125	332,500
NoAdmix	$\boldsymbol{\theta_{DST}}$	***1.495***	***1.279***	***1.701***		***233,593***	***199,843***	***265,781***
NoAdmix	θ_{STH}	3.686	2.186	5.231		575,937	341,562	817,343
NoAdmix	θ_{PLN}	1.007	0.618	1.42		157,343	96,562	221,875
NoAdmix	$\boldsymbol{\theta_{Root}}$	***23.55***	***15***	***33***		***3,679,687***	***2,343,750***	***5,156,250***
NoAdmix	$\boldsymbol{\theta_{IG}}$	***4.005***	***3.428***	***4.586***		***625,781***	***535,625***	***716,562***
NoAdmix	$\theta_{\mathrm{STH+PLN}}$	5.956	4.86	7.064		930,625	759,375	1,103,750
Admix	θ_{OG}	1.231	0.511	2.112		192,343	79,843	330,000
Admix	$\boldsymbol{\theta_{DST}}$	***2.228***	***1.936***	***2.532***		***348,125***	***302,500***	***395,625***
Admix	θ_{STH}	3.521	2.093	5.005		550,156	327,031	782,031
Admix	θ_{PLN}	1.036	0.621	1.467		161,875	97,031	229,218
*Admix	$\boldsymbol{\theta_{Root}}$	***16.46***	***0.499***	***26***		***2,571,875***	***77,968***	***4,062,500***
Admix	$\boldsymbol{\theta_{IG}}$	***4.947***	***4.393***	***5.489***		***772,968***	***686,406***	***857,656***
Admix	$\theta_{\mathrm{STH+PLN}}$	6.051	4.672	7.474		945,468	730,000	1,167,812

Table S4. Parameter estimates from the lowest AIC run for each demographic model considered (see Supplementary Fig. S8) for each data set (upper panel: NoAdmix; lower panel: Admix) in the program MOMENTS; standard deviations for each parameter are in parentheses. Models with the lowest AIC are considered the best supported. Parameters are represented by population size (nu; N_{ref} = theta/4μ where μ is mutation rate), migration rate (m; $M_{ij} = 2N_{ref}m_{ij}$), and divergence time (T; T = $2N_{ref}$); the parameters presented here are unscaled. For example, nu1 represents the population size of populations 1 (DST), m12 represents the migration from population 1 into population 2 (e.g., DST into STH), and T1 represents the time interval from divergence to time T2; see Fig. 5 for a visualization. For models with symmetric migration, we report the parameter estimate twice (see split_sym_mig_all).

NoAdmix Data set

Model	**log.likelihood**	**AIC**	**chi.squared**	**theta**	**nu1**	**nuA**	**nu2**	**nu3**	**m12**	**m13**	**m21**	**m23**	**m32**	**T1**	**T1a**	**T1b**	**T2**	**T3**
refugia_adj_2	-249.14	514.28	226.15	36.63	1.86 (3.9e-3)	2.60 (8e-4)	2.59 (4.7e-3)	2.01 (3.9e-3)	0.03 (1e-4)		0.03 (1e-4)	0.37 (7e-4)	0.37 (7e-4)	5.02 (1.1e-2)			0.31 (1e-4)	
refugia_asymmig_adjacent	-248.95	517.90	198.72	113.36	0.56 (3e-4)	0.83 (5e-4)	1.62 (4.1e-3)	0.81 (2e-4)	0.22 (1e-4)		0.05(3e-4)	0.31 (2.7e-3)	0.03 (2e-4)	0.91 (8e-4)			0.24 (5e-4)	
refugia_barrier	-252.24	518.48	247.08	103.30	0.55 (1e-4)	1.58 (1.1e-3)	1.03 (2e-4)	0.95 (3e-4)				0.47 (3e-4)	0.47 (3e-4)	0.54 (4e-4)			0.49 (1e-4)	
split_nomig	-253.69	519.38	174.65	160.43	0.41 (2e-4)	0.57 (4e-4)	0.76 (1e-4)	0.46 (1e-4)						0.43 (3e-4)			0.16 (1e-4)	
refugia_adj_1	-255.77	529.54	270.55	84.00	0.70 (4e-4)	20.48 (5.1e-2)	1.50 (1e-3)	0.68 (3e-4)	0.03 (1e-4)		0.03 (1e-4)	0.92 (3e-4)	0.92 (3e-4)	0.28 (1.5e-3)			0.22 (1e-4)	1.25 (6e-4)
refugia_adj_3	-266.52	553.04	332.80	140.36	0.29 (1e-4)	0.34 (2e-4)	0.93 (6e-4)	0.54 (2e-4)	0.08 (4e-4)		0.08 (4e-4)	1.13 (5e-4)	1.13 (5e-4)		0.91 (5e-4)	4.03 (4e-4)	0.94 (5e-4)	
split_asymmig_adjacent	-267.63	559.26	231.18	75.11	0.63 (6e-4)	2.84 (5e-4)	2.01 (7.2e-3)	0.50 (7e-4)	0.07 (2e-4)		0.03(3e-4)	0.42 (6.1e-3)	2.63 (4.6e-3)	0.05 (1e-4)			2.32 (7.5e-3)	
split_sym_mig_all	-290.35	600.70	264.19	171.67	0.30 (2.2e-3)	0.12 (1.3e-4)	2.52 (5e-4)	0.26 (3e-4)	0.04 (2.4e-3)	0.28 (1e-4)	0.04 (2.4e-3)	2.54 (1.2e-2)	2.54 (1.2e-2)	0.22 (1.7e-2)			0.49 (7.3e-3)	
split_symmig_adjacent	-303.33	624.66	246.37	190.95	0.23 (1e-4)	0.45 (1e-4)	0.36 (1e-4)	0.28 (1e-4)	0.18 (2e-4)		0.18 (2e-4)	4.84 (3.2e-3)	4.84 (3.2e-3)	0.14 (1.4e-3)			0.45 (1.7e-3)	
refugia_symmig_all	-305.99	629.98	330.80	56.04	0.07 (2e-4)	5.28 (1e-4)	1.18 (1e-4)	0.03 (3e-4)	0.94 (2e-4)	0.04 (1e-4)	0.94 (2e-4)	1.22 (5e-4)	1.22 (5e-4)	0.56 (6e-4)			3.15 (1.1e-3)	

Admix Data set

Model	**log.likelihood**	**AIC**	**chi.squared**	**theta**	**nu1**	**nuA**	**nu2**	**nu3**	**m12**	**m13**	**m21**	**m23**	**m32**	**T1**	**T1a**	**T1b**	**T2**	**T3**
refugia_barrier	-362.19	738.38	277.12	324.17	0.54 (3e-4)	0.38 (1.6e-3)	1.57 (8e-4)	0.62 (2e-4)				1.20 (8e-4)	1.20 (8e-4)	0.49 (2e-4)			0.20 (7e-4)	
refugia_adj_2	-367.39	750.78	257.94	236.86	0.77 (1.9e-3)	1.18 (5.3e-3)	1.57 (2.3e-3)	1.09 (1.9e-3)	0.15 (1e-4)		0.15 (1e-4)	0.31 (2.4e-3)	0.31 (2.4e-3)	1.08 (5.1e-3)			0.38 (4e-4)	
refugia_adj_1	-380.41	778.82	371.24	160.46	1.19 (6e-3)	1.34 (2e-2)	2.13 (9.4e-3)	1.74 (1e-2)	0.05 (1e-4)		0.05 (1e-4)	0.40 (2.1e-3)	0.40 (2.1e-3)	0.84 (1.3e-2)			0.61 (1.3e-3)	0.65 (5e-4)
refugia_adj_3	-379.66	779.32	301.82	139.00	1.54 (1.9e-3)	1.15 (1.1e-3)	2.43 (2.4e-3)	1.11 (9e-4)	0.06 (1e-4)		0.06 (1e-4)	0.71 (6e-4)	0.71 (6e-4)		0.02 (1e-4)	0.66 (3e-4)	2.39 (2.6e-3)	
split_asymmig_adjacent	-387.52	799.04	298.65	415.02	0.39 (1e-4)	0.36 (8e-4)	0.46 (1e-4)	0.68 (9e-4)	0.04 (2e-4)		0.06 (2e-4)	3.36 (1.3e-3)	0.01(2e-4)	1.74 (2.4e-3)			0.53 (4e-4)	
split_nomig	-414.18	840.36	428.95	310.29	0.66 (1.3e-3)	0.94 (2.2e-3)	13.1 (3.2e-3)	0.49 (3e-4)						0.66 (1.6e-3)			0.66 (1.6e-3)	
split_sym_mig_all	-425.44	870.88	323.88	1026.73	0.13 (1e-4)	0.13 (1e-4)	0.36 (1e-4)	0.32 (1e-4)	0.34 (2e-4)	0.05 (3e-4)	0.34 (2e-4)	0.26 (1e-4)	0.26 (1e-4)	1.21 (5e-4)			0.11 (2e-4)	

refugia_asymmig_adjacent	-432.25	884.50	412.79	141.37	0.89 (1e-3)	14.08 (1.9e-2)	1.25 (1e-4)	1.26 (3e-4)	0.10 (3e-4)		0.14 (2e-4)	2.08 (1e-4)	0.59(5e-4)	2.14 (3e-4)		0.90 (8.9e-3)
split_symmig_adjacent	-487.17	992.34	591.38	193.82	0.52 (6e-4)	10.94 (7.1e-3)	0.89(5e-4)	0.82(7e-4)	0.06(2e-4)		0.06(2e-4)	0.45(4e-4)	0.45(4e-4)	1.26(4.6e-3)		0.32 (5e-4)
refugia_symmig_all	-604.40	1226.80	664.22	1335.13	0.07 (1e-4)	5.28 (1.3e-1)	1.18(1e-4)	0.03(1e-4)	0.94(1e-4)	1.40(2e-4)	0.94(1e-4)	21.89(1e-4)	21.89(1e-4)	1.56(1.4e-2)		13.02(2e-4)

Supplementary Figures

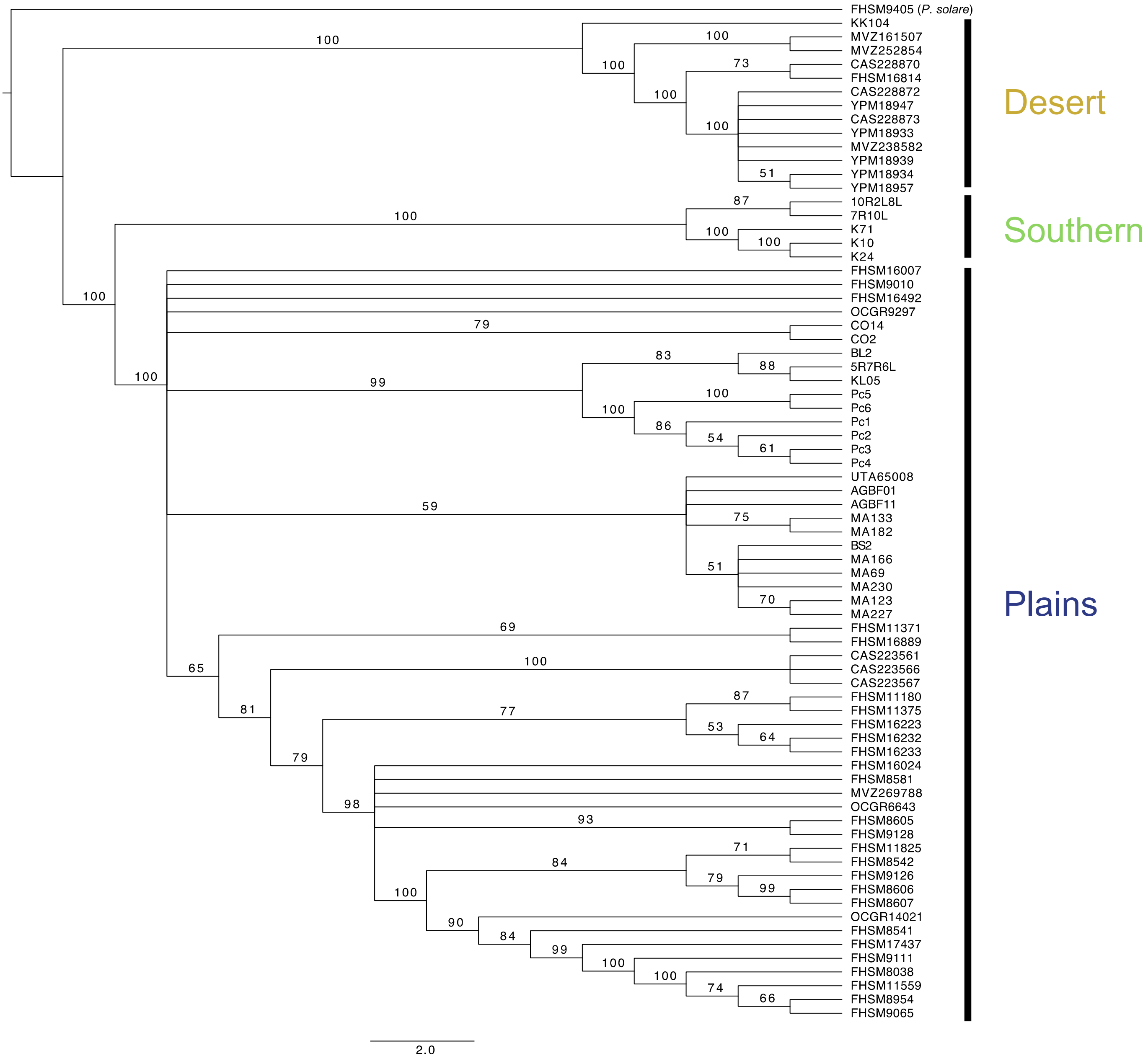


Fig. S1. Majority-rule bootstrap consensus tree from coalescent analysis in SVDquartets. Tree was inferred using an unlinked SNP matrix (54,634 SNPs). Branch values represent nonparametric bootstrap support (100 replicates).

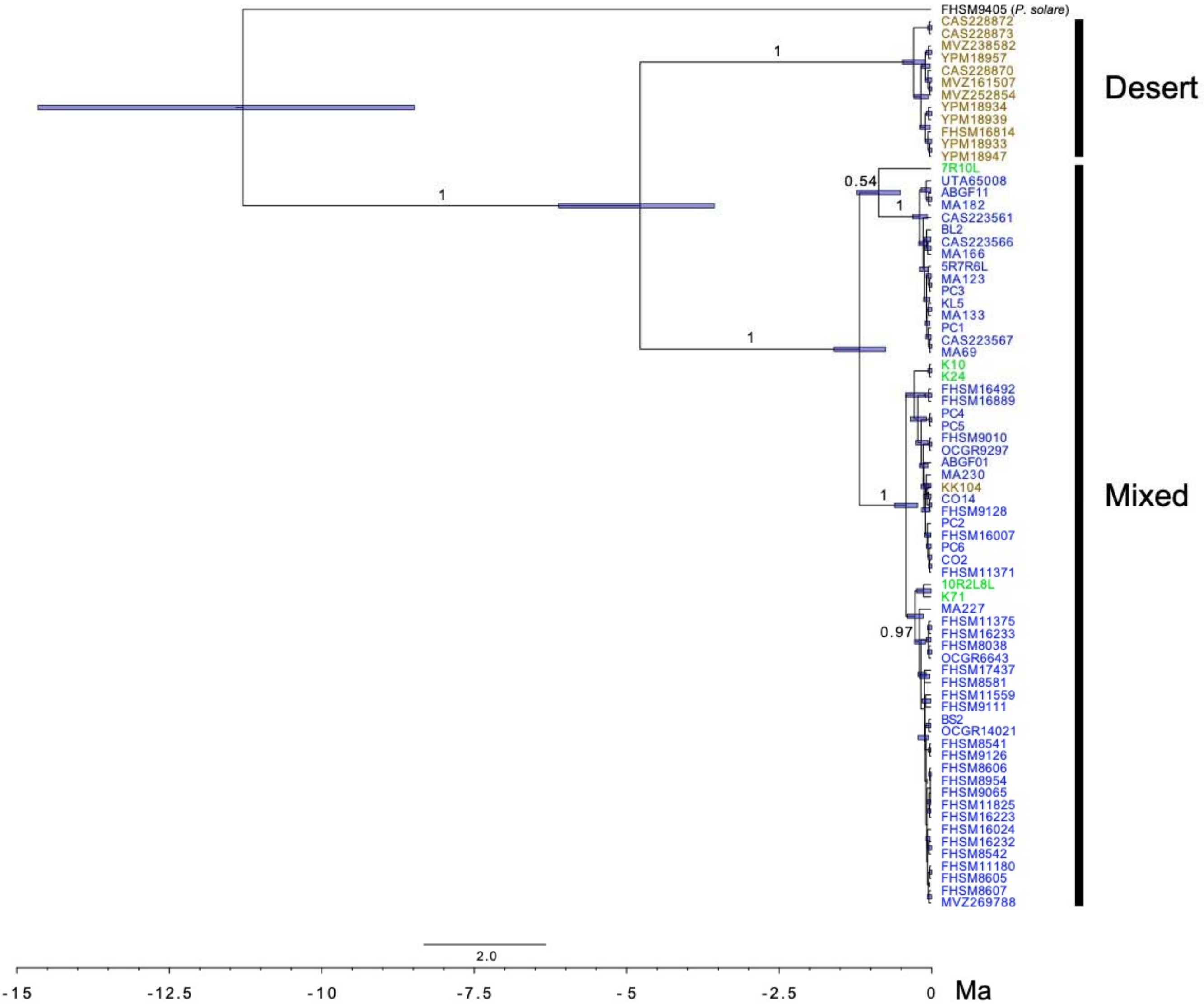


Fig. S2. Bayesian maximum clade credibility (MCC) tree from BEAST based on ND1, tRNA leucine, tRNA isoleucine, tRNA glutamine, and portions of 16S and tRNA methionine. Sample tips are color coded to match those in Fig. 2. Values at nodes represent posterior probability values. Node bars indicate 95% HPD for mean node heights. The horizontal scale bar represents time in millions of years (Ma).

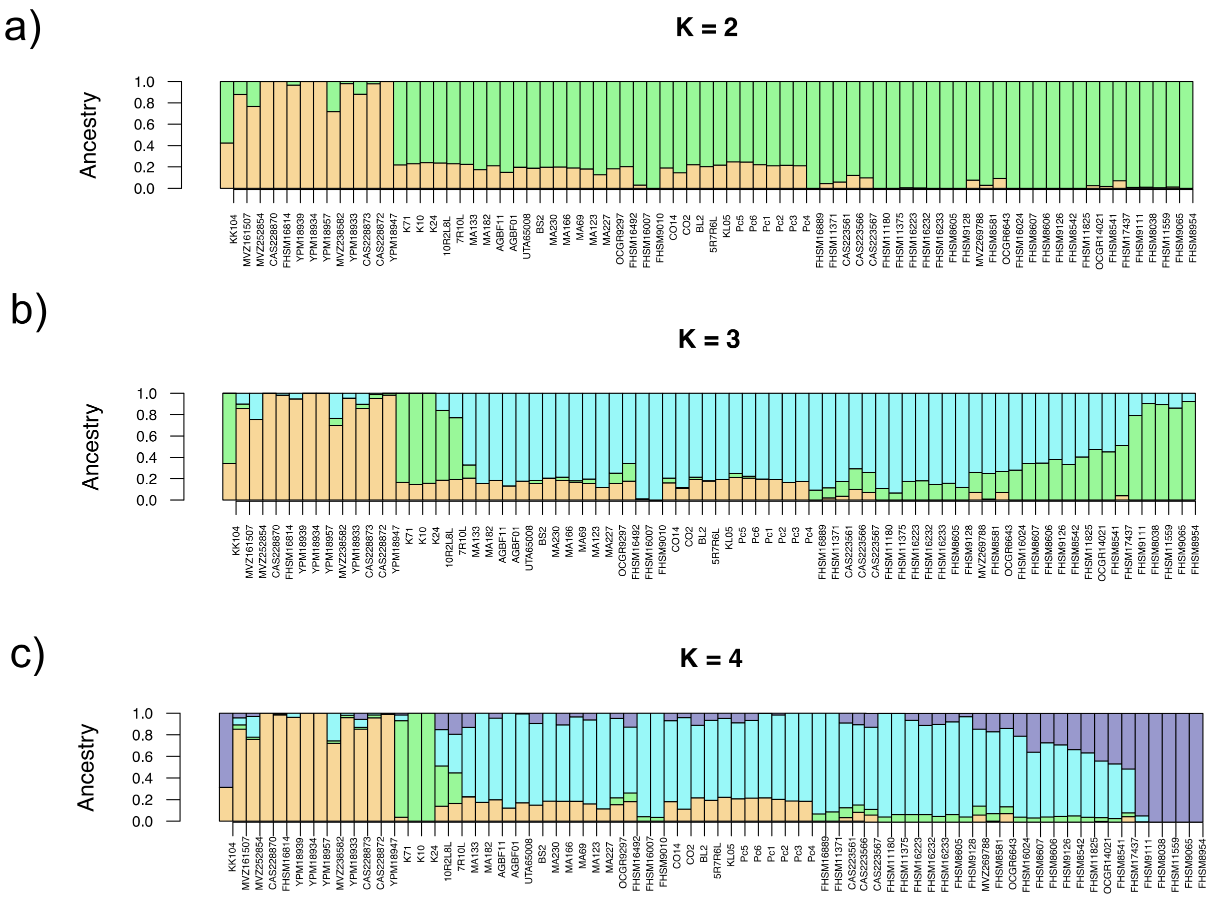


Fig. S3. sNMF admixture results for varying values of *K*. Each bar represents a sampled individual, with colors indicating the proportion of ancestry assigned to a particular ancestral population. Note that the outgroup (*P. solare*) was removed prior to analysis.

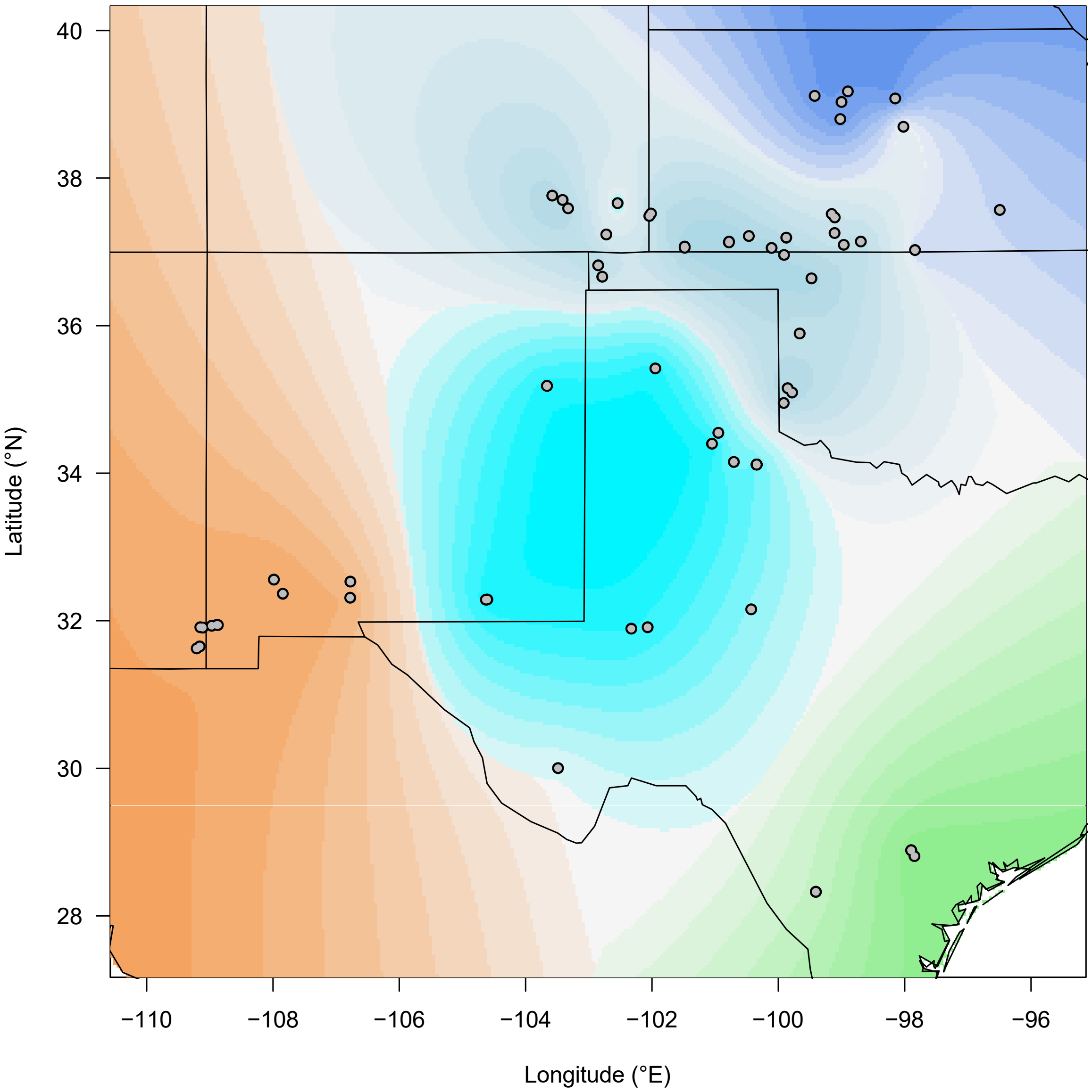


Fig. S4. Geographic distribution of the five ancestral populations of *P. cornutum* as inferred by sNMF. Colors correspond to those in Figs. 2 and S3.

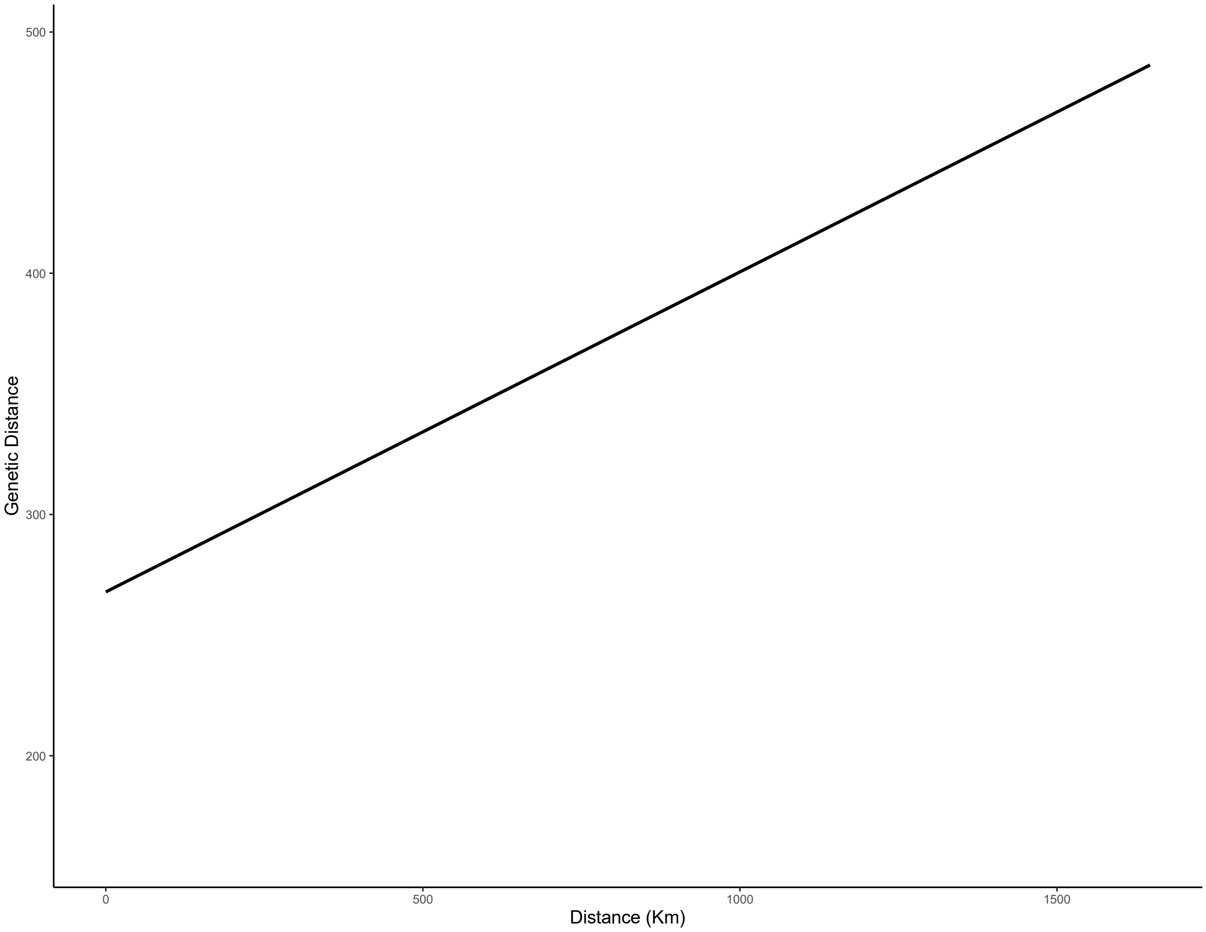


Fig S5. Relationship between genetic and geographic distances for all individuals (grey points). The black solid line is linear model fit, with the grey shaded regions representing the 95% confidence interval.

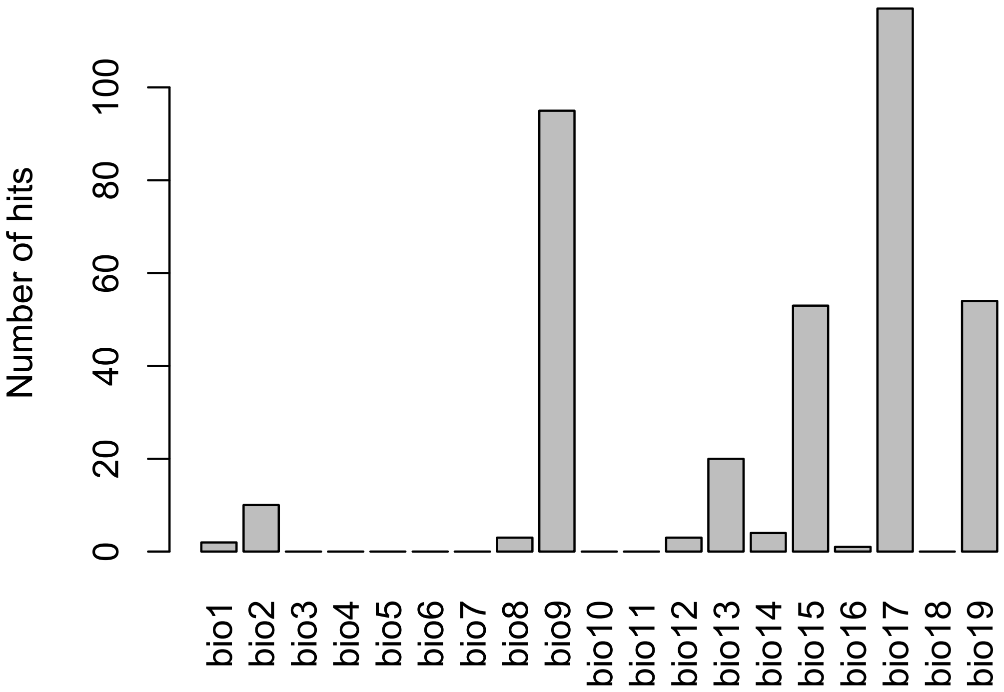


Fig. S6. Number of hits for different bioclimatic variables as inferred using LFMM. The largest number of SNPs were statistically correlated with bio9 (mean temperature of the driest quarter) and bio17 (precipitation of the driest quarter).

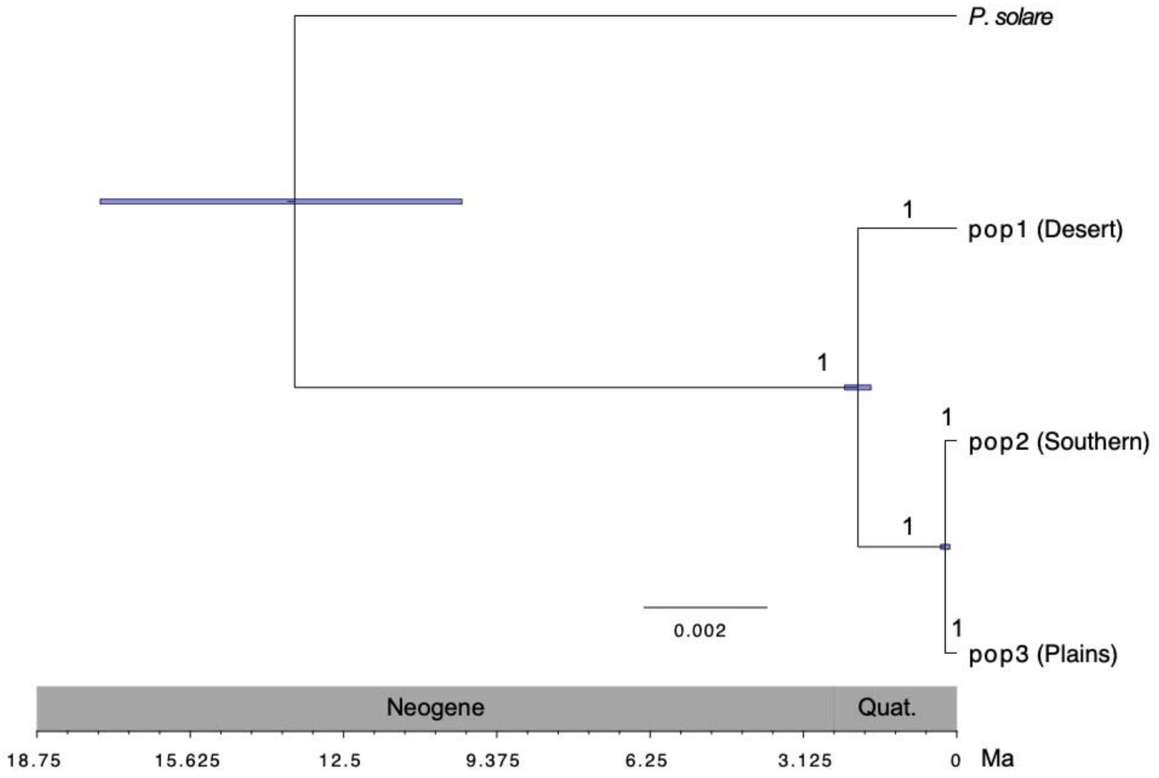
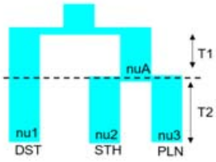
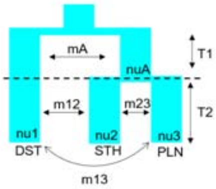


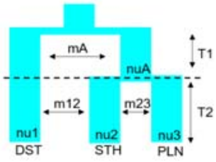
Fig. S7. Divergence time estimates of *Phrynosoma cornutum* populations based on MSC analysis of nGBS data in BPP (500 loci). Parameter estimates were based on data sets that excluded the highly admixed sample KK104. Values at tips represent posterior probability support for species/population. Values adjacent to nodes represent posterior probability support for phylogenetic relationships.



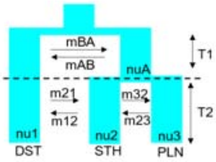
"split_nomig"
Divergence with no
migration



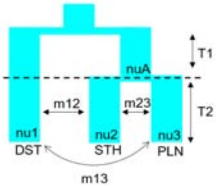
"split_sym_mig_all"
Divergence with continuous
symmetrical migration



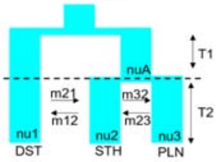
"split_sym_mig_adj"
Divergence with continuous
adjacent symmetrical
migration



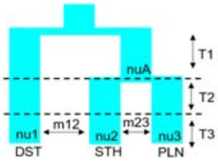
"split_asym_mig_adj"
Divergence with continuous
adjacent asymmetrical
migration



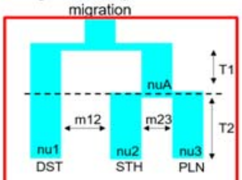
"refugia_sym_mig_all"
Divergence in isolation
secondary contact and
divergence with symmetrical
migration



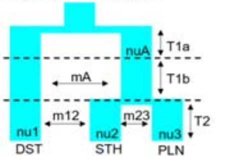
"refugia_asym_mig_adj"
Divergence in isolation
secondary contact and
divergence with adjacent
asymmetrical migration



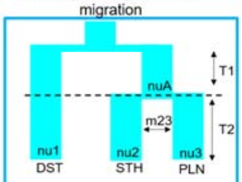
"refugia_adj_1"
Divergence in isolation
followed by divergence in
isolation. Secondary contact
with adjacent symmetrical
migration



"refugia_adj_2"
Divergence in isolation
secondary contact and
divergence with adjacent
symmetrical migration



"refugia_adj_3"
Divergence in isolation
secondary contact with
symmetrical migration.
Divergence with adjacent
symmetrical migration



"refugia_barrier"
Divergence in isolation with
no secondary contact.
Secondary divergence with
symmetrical migration.

Fig. S8. Demographic models explored using the program MOMENTS. Analyses were performed with and without sample KK104 that had substantial mixed ancestry. The data set with KK104 favored the "refugia_barrier" model (blue), whereas the data set without KK104 supported the "refugia_adj_2" model (red).

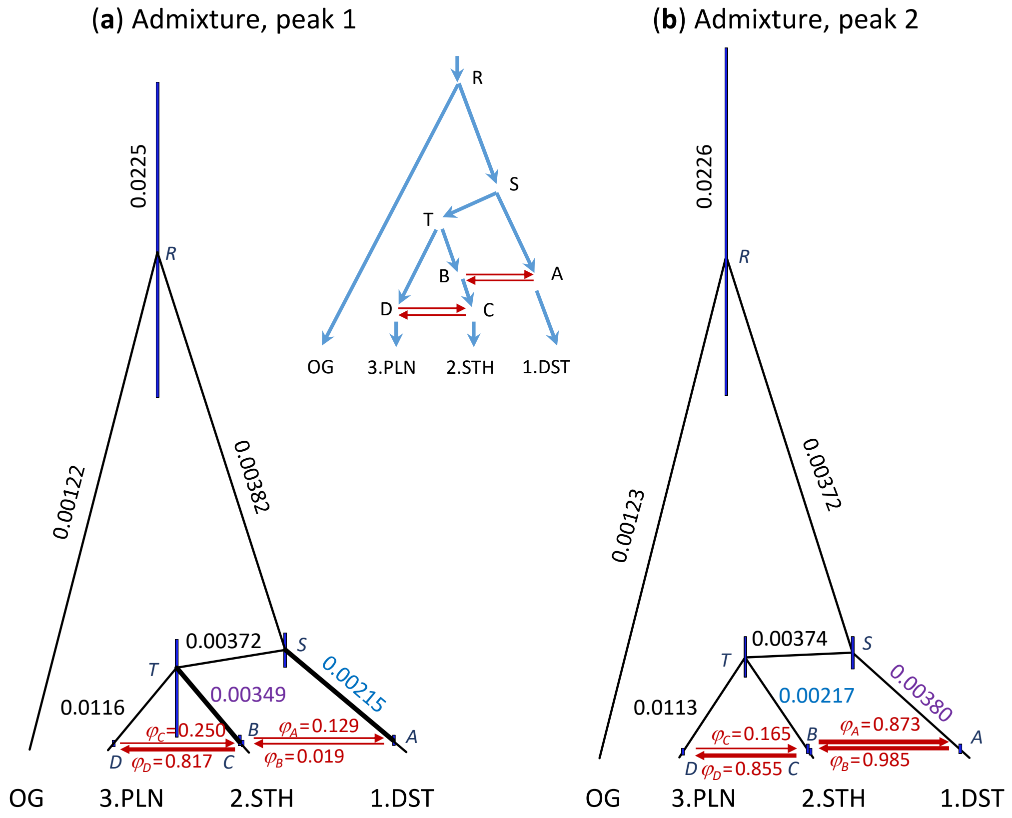
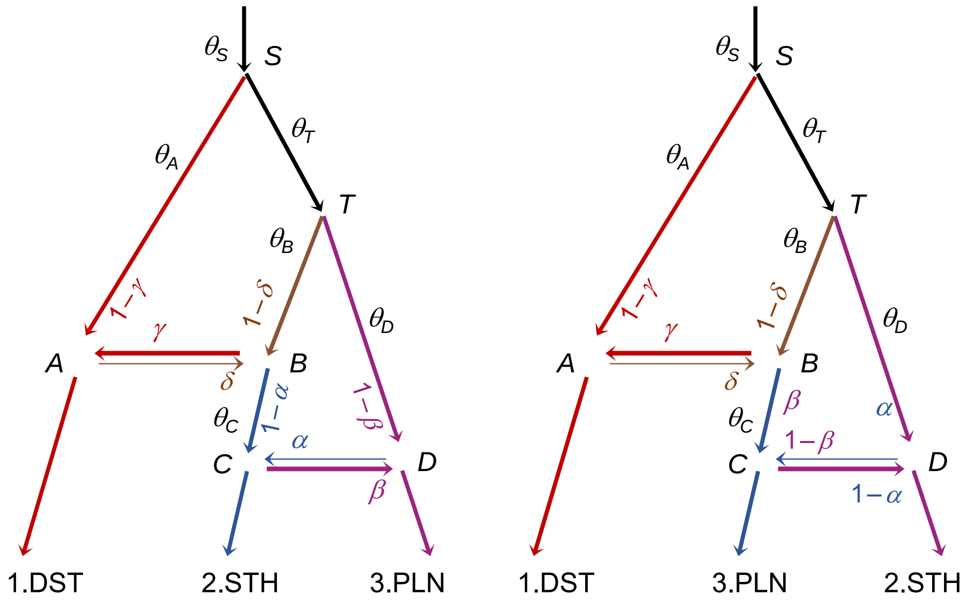


Fig. S9. Two local peaks in the posterior for parameters in the MSci model in the BPP analysis of the admixed data including KK104. See Supplementary Table S6 for the parameter estimates. See legend to Fig. 7 for additional information.

(**a**) Tree S_1 with Θ_1 (**b**) Tree S_2 with Θ_2



(**c**) Tree S_3 with Θ_3 (**d**) Tree S_4 with Θ_4

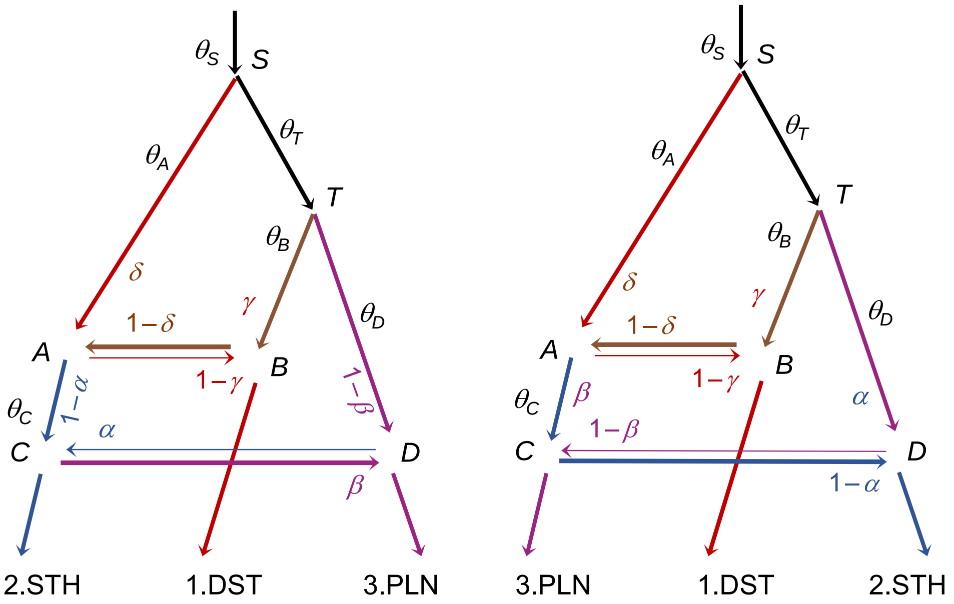


Fig. S10. Four unidentifiable models due to introgression events at nodes *A* and *B* and at *C* and *D*. Thickness of the horizontal (introgression) lines reflect estimates of introgression probabilities for peak 1 using the Non-Admixed dataset from Supplementary Table S6: $\alpha = \varphi_C = 0.065$, $\beta = \varphi_D = 0.935$, $\gamma = \varphi_A = 0.868$, and $\delta = \varphi_B = 0.090$. Tree S_1 is the model of Fig. 7a, while trees S_2, S_3, and S_4 are alternative models that are unidentifiable by genomic sequence data. The outgroup and node *R* of Fig. 7 are omitted for simplicity. One way of seeing the unidentifiability or equivalence of the four models is to confirm that the four models predict the same major genealogical routes when we trace the sampled sequences backwards in time and follow the major parental paths at each hybridization node (indicated by the introgression probabilities). Thus, all four models predict the most recent common ancestor to be node *C* for most of the sequences from populations 2 and 3 or node *B* for populations 1 and 2 (or 3).