

Supplementary figures

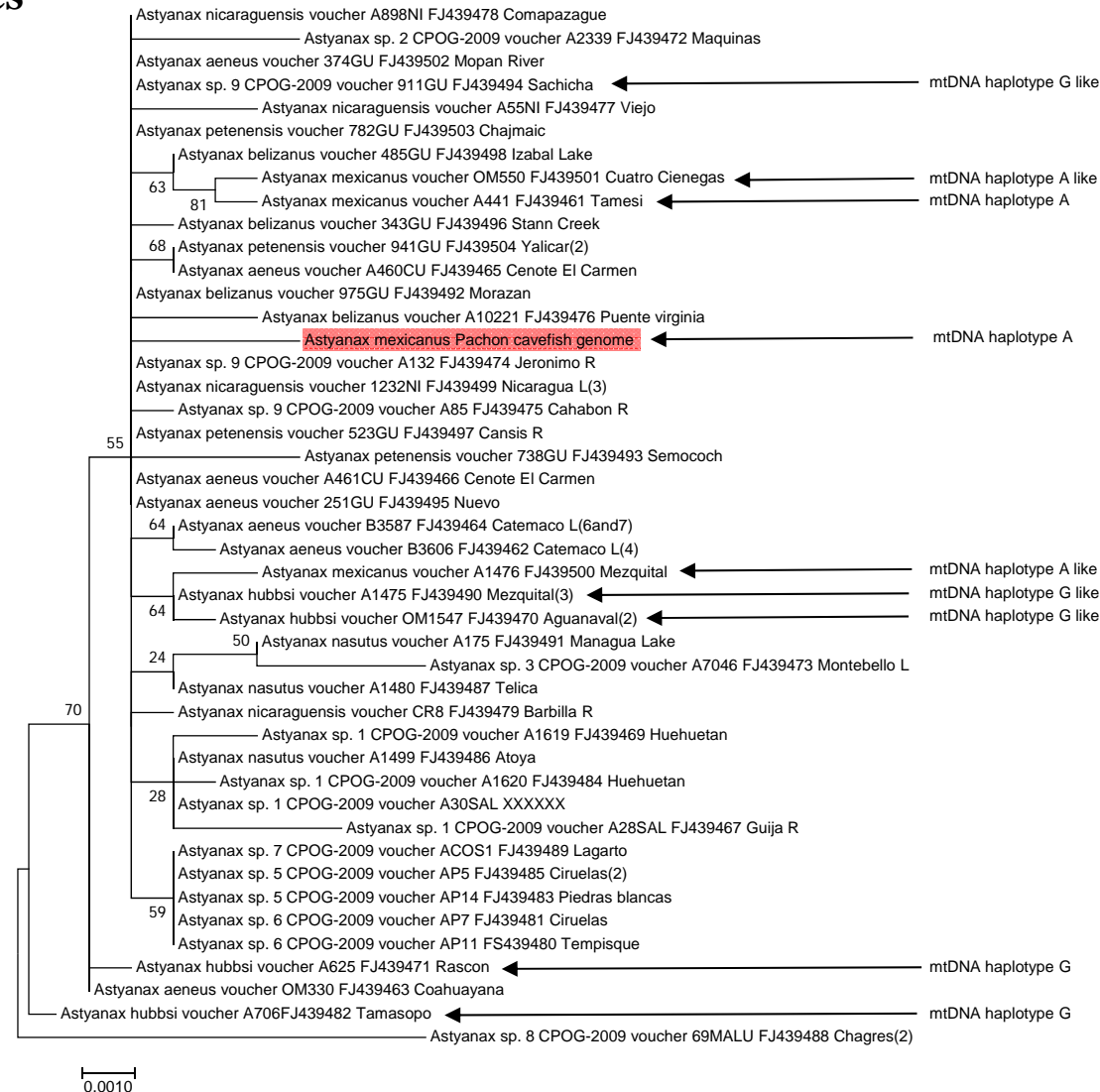


Figure S1: Rag1 phylogeny. The evolutionary tree was inferred by using the Maximum Likelihood method based on the Tamura-Nei model. The analysis involved 45 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1251 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1]. All sequences belong to surface fish, excepted one Pachón cavefish sequence from the genome project and highlighted in red. Individuals with mtDNA belonging to A or G haplogroups are indicated as well as those with mtDNA haplotypes closely related to these haplogroups.

[1] Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution* (10):2731-9.

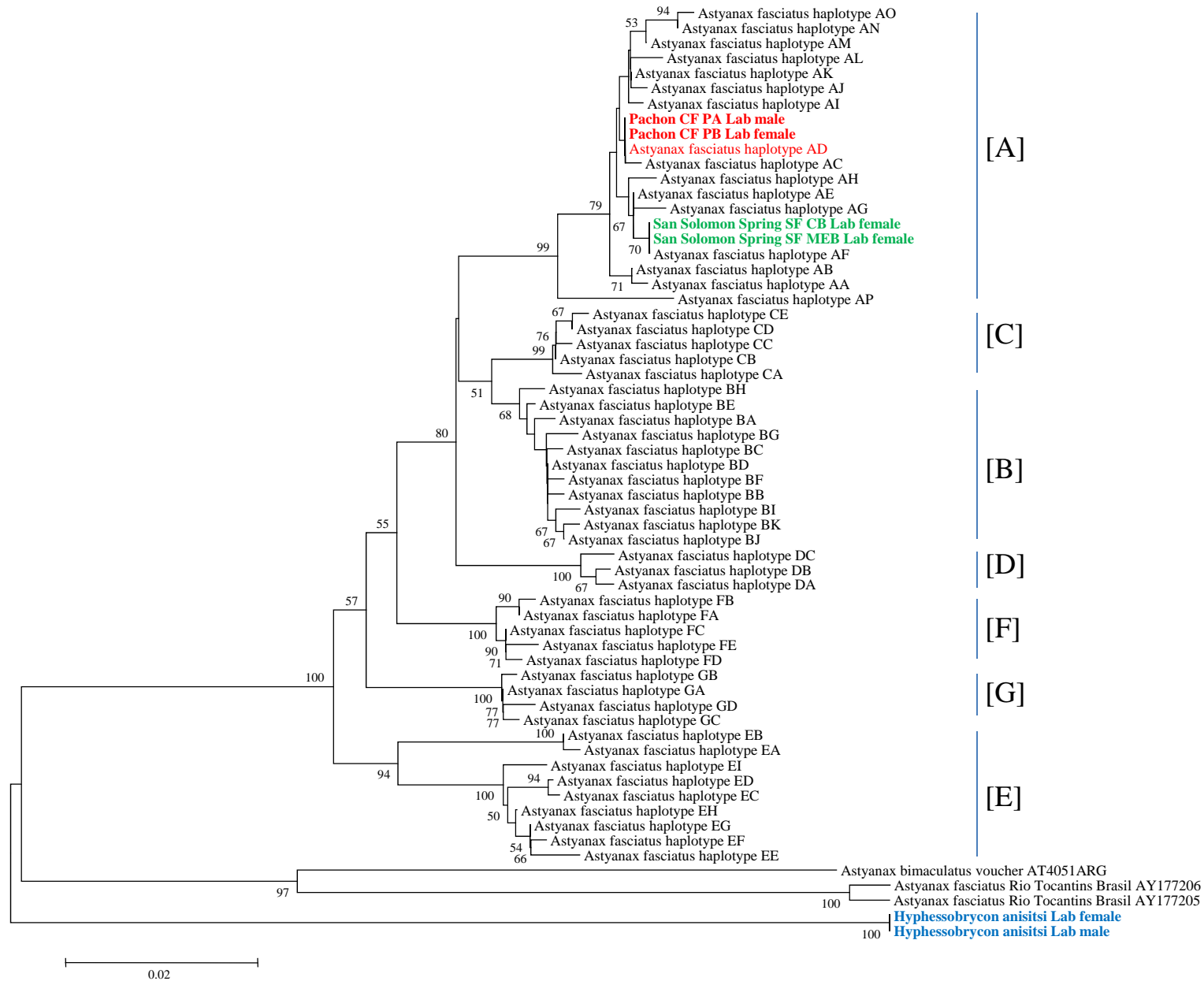


Figure S2: Neighbor joining phylogeny of *Astyanax mexicanus* cytb haplotypes (see Stecker et al. 2004 for more details). Seven haplogroups were identified [A] to [G]. Cavefish haplotypes belong to haplogroup [A] and [G]. In the Pachón cave, only the haplotype AD was found (red). The two San Solomon Spring surface fish are in green, the two *Hyphessobrycon anisitsi* fish are in blue. The names of the lab fish we sequenced are in bold.

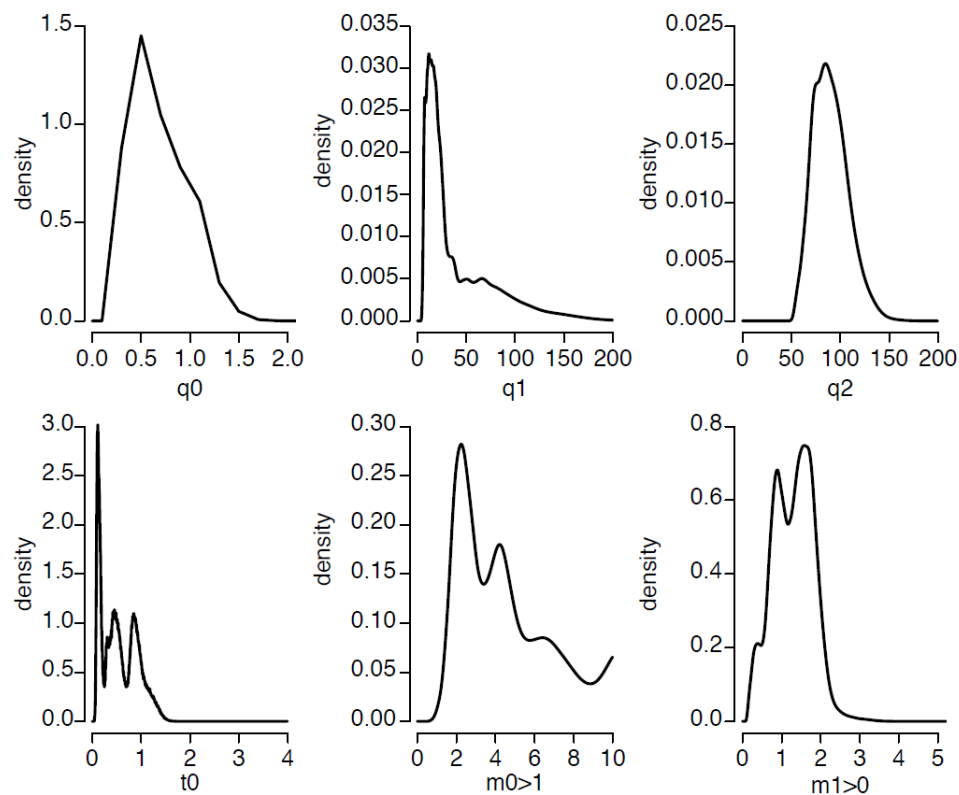
Chica - Surface O8 – S3

Sample size : 22 loci; 60 alleles/locus/population

Command line:

`./IMa2 -iinfileO8S3_n60.u -ooutput_O8S3_n60_m10.out -b200000 -l100000 -d100 -m10 -q200 -t4 -c1 -p23567 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3`

Estimation of demographic parameters with IMa2



	HiPt	HPD 95%
q0 (4N_eu Chica)	0.500	0.300 – 2.500
q1 (4N_eu Surface)	11.700	3.900 – 120.7
q2 (4N_eu Ancestral)	84.900	57.500 – 125.300
t0 (tu)	0.114	0.005- 1.186
m0>1 (m_{0->1}/u)	2.245	1.275 – 9.995
m1>0 (m_{1->0}/u)	1.585	0.275 – 2.145
N_e Chica	250	150 – 1,250
N_e Surface	5,850	1,950 – 60,350
N_e Ancestral	42,450	28,750 – 62,650
t	798	30 – 8,302
m_{s->c}	11.2 x 10 ⁻⁴	6.4 – 50.0 x 10 ⁻⁴
m_{c->s}	7.93 x 10 ⁻⁴	1.3 – 10.7 x 10 ⁻⁴

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 3.5 years (2 years for surface fish and 5 years for cavefish). HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Chica = q0 / 4u ; N_e surface = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{s->c} (migration rate from surface to Chica) = m0>1 x u ; m_{c->s} (migration rate from Chica to surface) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{s->c} and m_{c->s} are migration rate forward in time.

Figure S3:

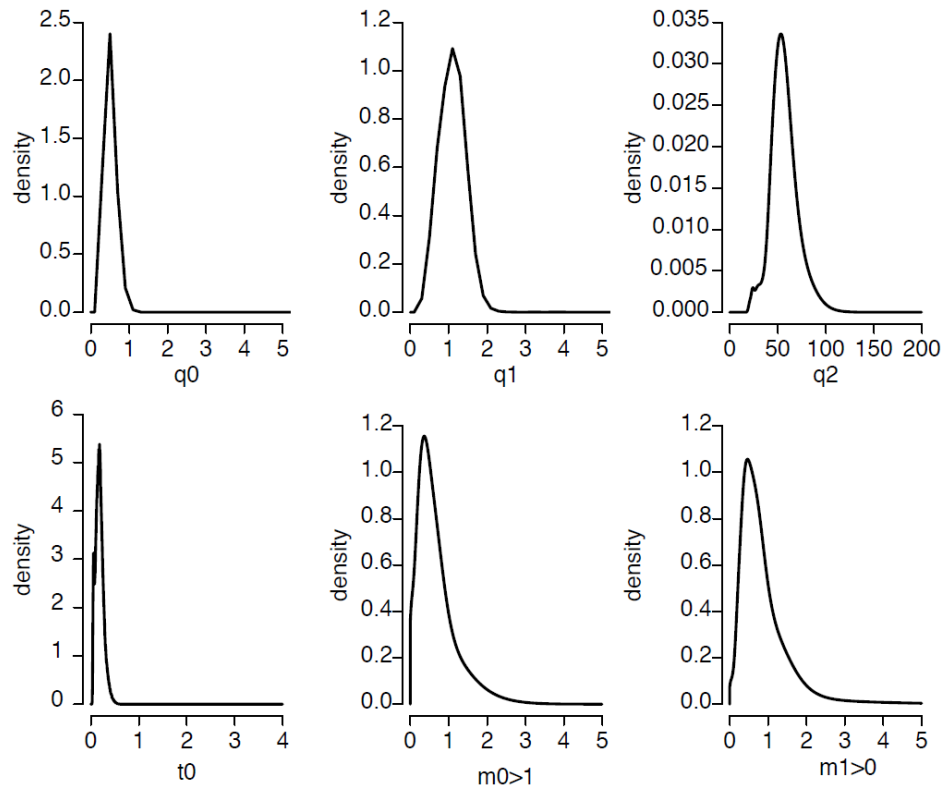
Pachón - Chica

O1 – O8

Sample size : 22 loci; 60 alleles/locus/population

Command line:

`./IMa2 -iinfileO1O8_n60.u -ooutputO1O8_n60_long.out -b10000 -l1100000 -d100 -m5 -q200 -t4 -p2367 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3`



Estimation of demographic parameters with IMA2

	HiPt	HPD 95%
q0 (4N_eu Pachón)	0.500	0.300 – 2.300
q1 (4N_eu Chica)	1.100	0.300 – 3.100
q2 (4N_eu Ancestral)	53.300	28.300 – 88.300
t0 (tu)	0.182	0.038 – 0.346
m0>1 (m_{0->1}/u)	0.686	0.000 – 1.748
m1>0 (m_{1->0}/u)	0.866	0.000 – 2.027
N_e Pachón	250	150 – 1150
N_e Chica	550	150 – 1,550
N_e Ancestral	26,650	14,150 – 44,150
t	1,274	266 – 2,422
m_{C->P}	3.4×10^{-4}	0.0 – 8.7×10^{-4}
m_{P->C}	4.3×10^{-4}	0.0 – 10.1×10^{-4}

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 5 years for cavefish. HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Pachón = q0 / 4u ; N_e Chica = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{C->P} (migration rate from Chica to Pachón) = m0>1 x u ; m_{P->S} (migration rate from Pachón to Chica) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{S->P} and m_{P->S} are migration rate forward in time.

Figure S4:

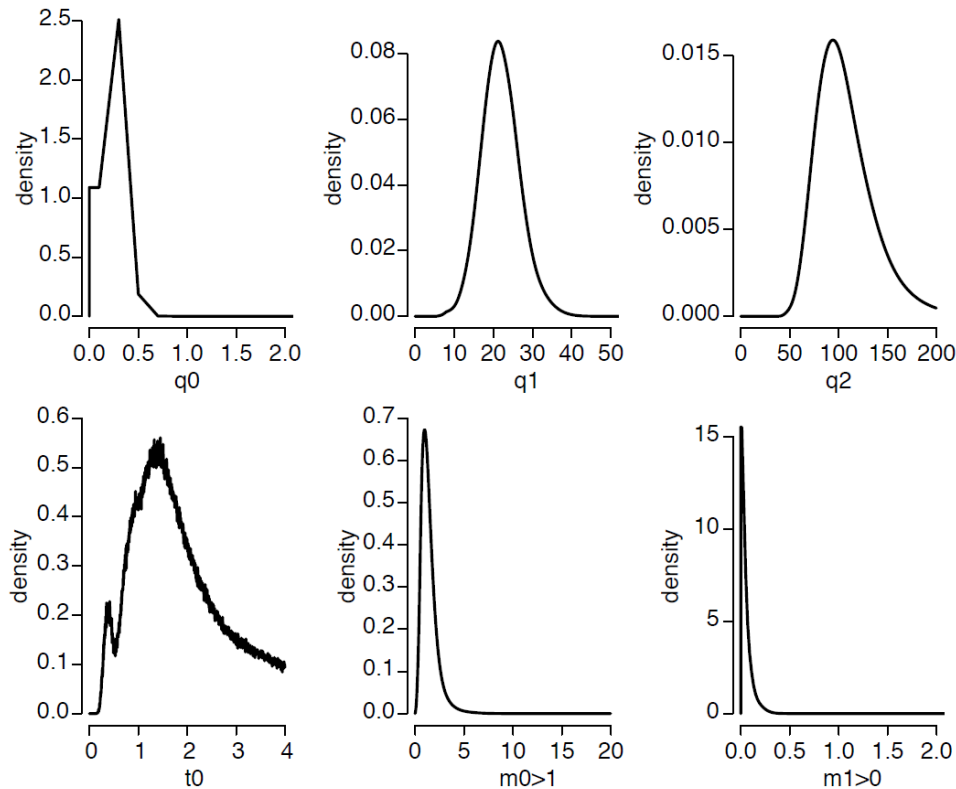
Molino - Surface

N1 – S1

Sample size : 14 loci; 40 alleles/locus/population

Command line:

`./IMa2 -iinfileN1S1_n40.u -ooutput_N1S1_n40_longrun.out -b200000 -l100000 -d100 -m20 -q200 -t4 -c1 -p23567 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3`



Estimation of demographic parameters with IMa2

	HiPt	HPD 95%
q0 (4N_eu Molino)	0.300	0.000 – 1.900
q1 (4N_eu Surface)	21.100	12.100 – 31.900
q2 (4N_eu Ancestral)	94.100	57.900 – 163.100
t0 (tu)	1.450	0.286 – 3.570
m0>1 (m_{0>1}/u)	0.970	0.190 – 3.030
m1>0 (m_{1>0}/u)	0.010	0.000 – 0.250
N_e Molino	150	0 – 950
N_e Surface	10,550	6,050 – 15,950
N_e Ancestral	47,050	28,950 – 81,550
t	10,150	2,002 – 24,990
m_{S->M}	4.9 x 10 ⁻⁴	1.0 – 15.2 x 10 ⁻⁴
m_{M->S}	5.0 x 10 ⁻⁶	0.0 – 1.3 x 10 ⁻⁴

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 3.5 years (2 years for surface fish and 5 years for cavefish). HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Molino = q0 / 4u ; N_e surface = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{S->M} (migration rate from surface to Molino) = m0>1 x u ; m_{M->S} (migration rate from Molino to surface) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{S->M} and m_{M->S} are migration rate forward in time.

Figure S5:

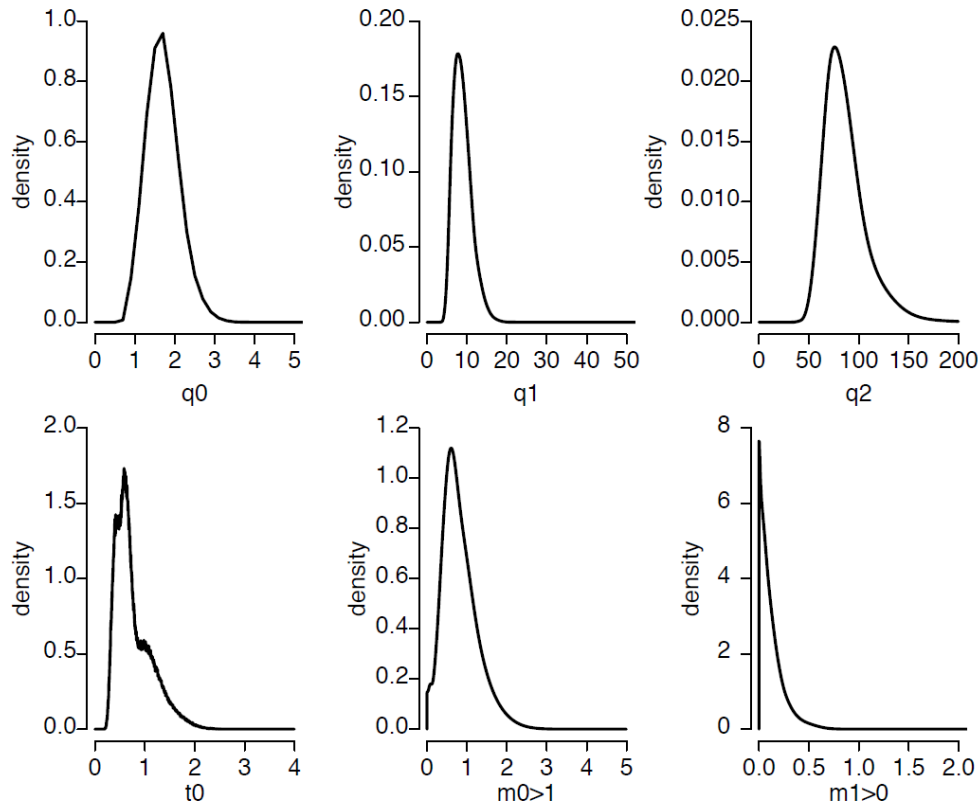
Caballo Moro - Surface

N2 – S2

Sample size : 18 loci; 40 alleles/locus/population

Command line:

/IMa2 -iinfileN2S2_n40.u -ooutput_N2S2_n40_m5_longrun.out -b200000 -l100000 -d100 -m5 -q200 -t4 -c1 -p23567 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3



Estimation of demographic parameters with IMa2

	HiPt	HPD 95%
q0 (4N_eu Caballo M.)	1.700	0.700 – 3.700
q1 (4N_eu Surface)	7.700	4.300 – 13.900
q2 (4N_eu Ancestral)	75.900	50.500- 130.700
t0 (tu)	0.582	0.262 – 1.518
m0>1 (m_{0>1}/u)	0.603	0.008 – 1.657
m1>0 (m_{1>0}/u)	0.003	0.000 – 0.363
N_e Caballo Moro	850	350 – 1,850
N_e Surface	3,850	2,150 – 6,950
N_e Ancestral	37,950	25,250 – 65,350
t	4,074	1,834 – 10,626
m_{s->c}	3.0 x 10 ⁻⁴	0.0 – 8.3 x 10 ⁻⁴
m_{c->s}	1.5 x 10 ⁻⁶	0.0 – 1.8 x 10 ⁻⁴

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 3.5 years (2 years for surface fish and 5 years for cavefish). HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Caballo Moro = q0 / 4u ; N_e surface = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{s->c} (migration rate from surface to Caballo Moro) = m0>1 x u ; m_{c->s} (migration rate from Caballo Moro to surface) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{s->c} and m_{c->s} are migration rate forward in time.

Figure S6:

Subterráneo - Surface

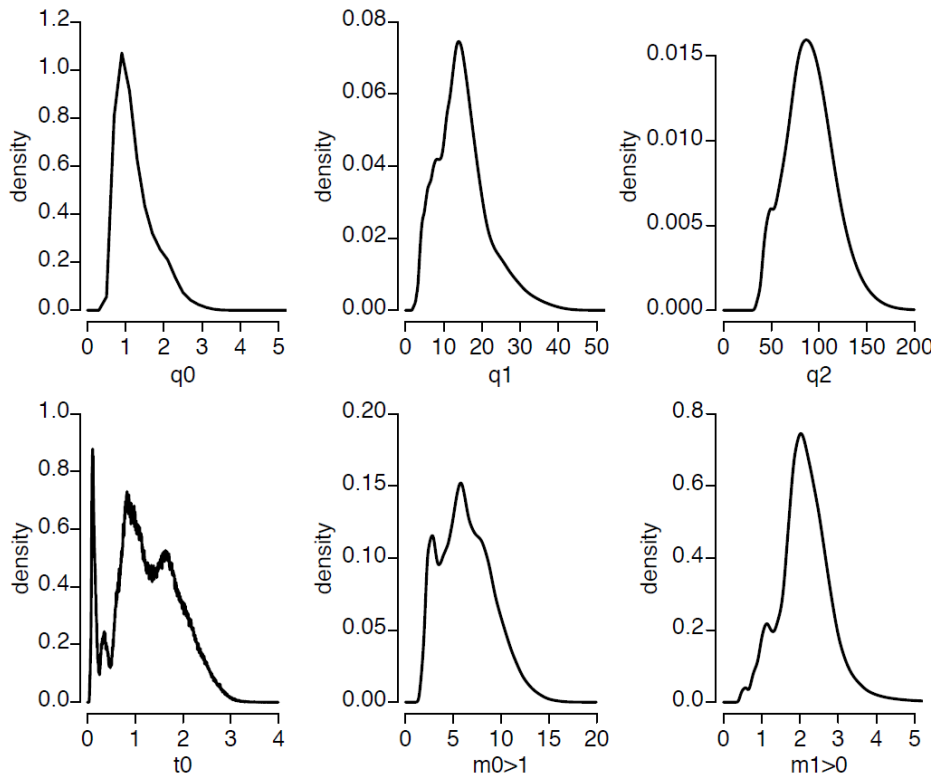
N3 – S4

Sample size : 21 loci; 40 alleles/locus/population

Command line:

/IMa2 -iinfileN3S4_n40.u -output_N3S4_n40_m20_longrun.out -b200000 -l100000 -d100 -m20 -q200 -t4 -c1 -p23567 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3

Estimation of demographic parameters with IMA2



	HiPt	HPD 95%
q0 (4N_eu Subterráneo)	0.900	0.500 – 3.300
q1 (4N_eu Surface)	13.900	3.100 – 28.700
q2 (4N_eu Ancestral)	86.700	40.700 – 138.300
t0 (tu)	0.110	0.058 – 2.462
m0>1 (m_{0->1}/u)	5.790	1.790 – 11.430
m1>0 (m_{1->0}/u)	2.030	0.750 – 3.430
N_e Subterráneo	450	250 – 1,650
N_e Surface	6,950	1,550 – 14,350
N_e ancestral	43,350	20,350 – 69,150
t	770	406 – 17,234
m_{s->c}	29.0 x 10 ⁻⁴	9.0 – 57.2 x 10 ⁻⁴
m_{c->s}	10.2 x 10 ⁻⁴	3.8 – 17.2 x 10 ⁻⁴

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 3.5 years (2 years for surface fish and 5 years for cavefish). HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Subterráneo = q0 / 4u ; N_e surface = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{s->c} (migration rate from surface to Subterráneo) = m0>1 x u ; m_{c->s} (migration rate from Subterráneo to surface) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{s->c} and m_{c->s} are migration rate forward in time.

Figure S7:

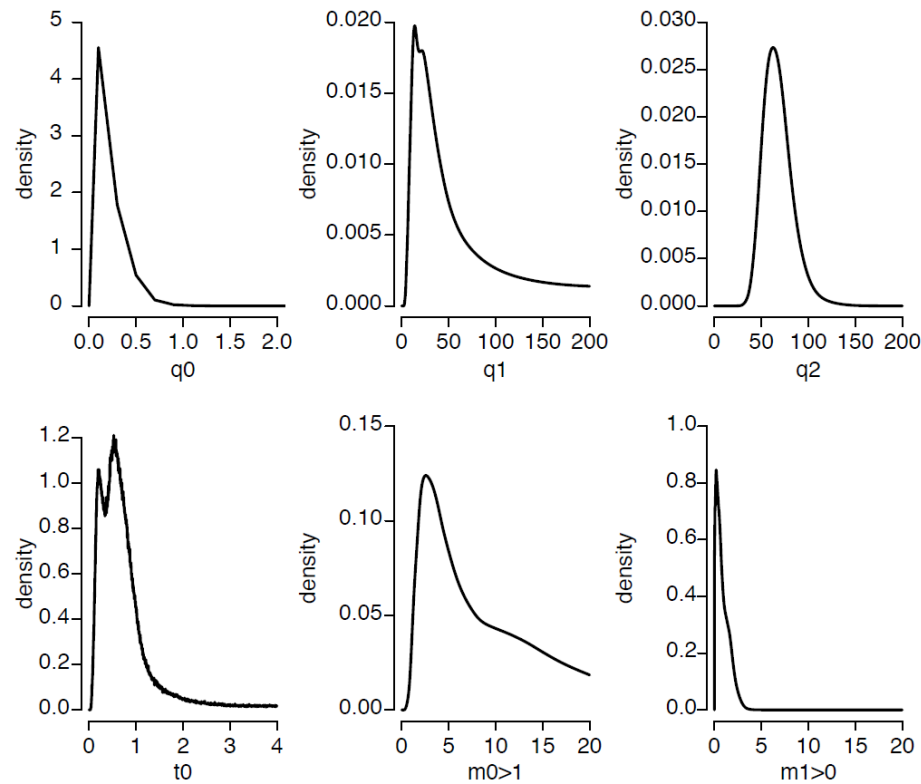
Curva - Surface

O6 – S3

Sample size : 14 loci; 20 alleles/locus/population

Command line:

/IMa2 --infileO6S3_1.u -ooutput_06S3_1_m20_longrun.out -b200000 -l100000 -d100 -m20 -q200 -t4 -c1 -p23567 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3



Estimation of demographic parameters with IMA2

	HiPt	HPD 95%
q0 (4N_eu Curva)	0.100	0.000 – 1.900
q1 (4N_eu Surface)	13.900	4.300 – 166.300
q2 (4N_eu Ancestral)	62.500	39.700 – 99.300
t0 (tu)	0,526	0.050 – 1.982
m0>1 (m_{0>1}/u)	2.570	0.930 – 17.790
m1>0 (m_{1>0}/u)	0.190	0.000 – 2.230
N_e Curva	50	0 – 950
N_e Surface	6,950	2,150 – 83,150
N_e ancestral	31,250	19,850 – 49,650
t	3,682	350 – 13,874
m_{s->c}	12.8 x 10 ⁻⁴	4.7 – 89.0 x 10 ⁻⁴
m_{c->s}	1.0 x 10 ⁻⁴	0.0 – 11.2 x 10 ⁻⁴

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 3.5 years (2 years for surface fish and 5 years for cavefish). HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Curva = q0 / 4u ; N_e surface = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{s->c} (migration rate from surface to Curva) = m0>1 x u ; m_{c->s} (migration rate from Curva to surface) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{s->c} and m_{c->s} are migration rate forward in time.

Figure S8:

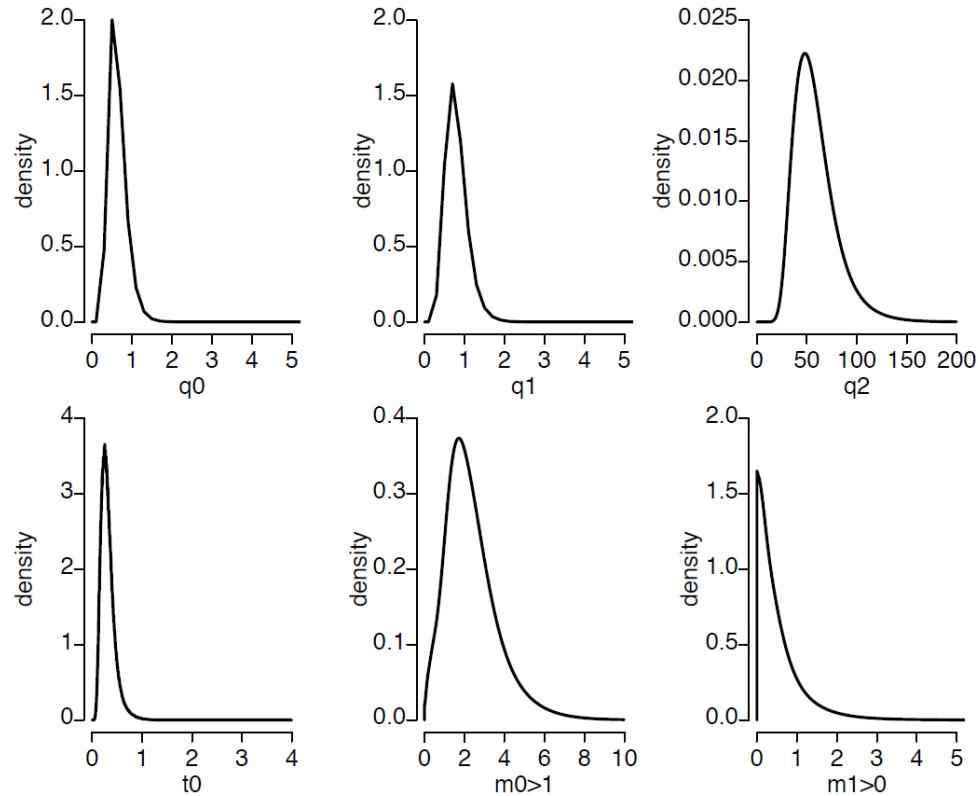
Pachón - Curva

O1 - O6

Sample size : 14 loci; 20 alleles/locus/population

Command line:

/IMa2 -iinfileO1O6_0.u -ooutput_O1O6_0_m10_longrun.out -b200000 -l100000 -d100 -m10 -q200 -t4 -c1 -p23567 -r25 -u1 -hfg -hn50 -ha0.999 -hb0.3



Estimation of demographic parameters with IMA2

	HiPt	HPD 95%
q0 (4N_eu Pachón)	0.500	0.300 – 2.500
q1 (4N_eu Curva)	0.700	0.300 – 2.700
q2 (4N_eu Ancestral)	48.100	23.900 – 101.500
t0 (tu)	0.254	0.086 – 0.598
m0>1 (m_{0>1}/u)	1.715	0.105 – 4.905
m1>0 (m_{1>0}/u)	0.005	0.000 – 1.705
N_e Pachón	250	150 – 1,250
N_e Curva	350	150 – 1,350
N_e ancestral	24,050	11,950 – 50,750
t	2,540	860 – 5,980
m_{C->P}	8.58×10^{-4}	$0.53 - 24,52 \times 10^{-4}$
m_{P->C}	2.50×10^{-6}	$0.00 - 8.53 \times 10^{-4}$

We assumed a mutation rate (u) of 0.0005 and a mean generation time (g) of 5 years. HiPt: the highest value in the histogram of the posterior marginal density. HPD 95%: the lower and upper bound of the estimated 95% highest posterior density (HPD) interval. Effective population size (N_e) Pachón = q0 / 4u ; N_e Curva = q1 / 4u ; N_e ancestral = q2 / 4u ; t (divergence time in years) = t0 x g / u ; m_{C->P} (migration rate from Curva to Pachón) = m0>1 x u ; m_{P->C} (migration rate from Pachón to Curva) = m1>0 x u. m0>1 and m1>0 are migration rate backward in time, whereas m_{C->P} and m_{P->C} are migration rate forward in time.

Figure S9:

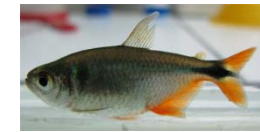
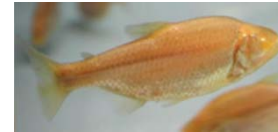
Lab populations collected in the wild in 2000

Purchased in 2012

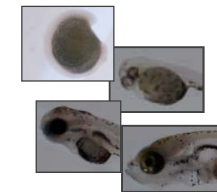
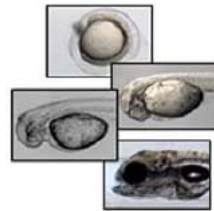
A. mexicanus Texas surface fish

A. mexicanus Pachón cavefish

H. anisitsi



Fifty to 200 embryos/larvae from several independent spawn events and several developmental stages (6 hpf to 15 dpf) were pooled.



Number of RNA sequences:

Sanger
454
Illumina

$1 \cdot 10^5$
 $1 \cdot 10^6$
 $250 \cdot 10^6$

$1 \cdot 10^5$
 $1 \cdot 10^6$
 $250 \cdot 10^6$

$250 \cdot 10^6$

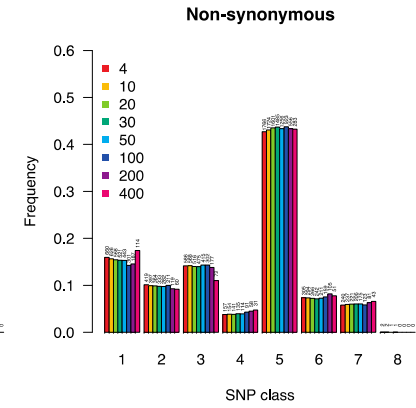
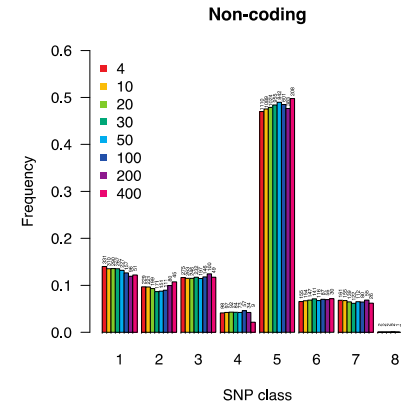
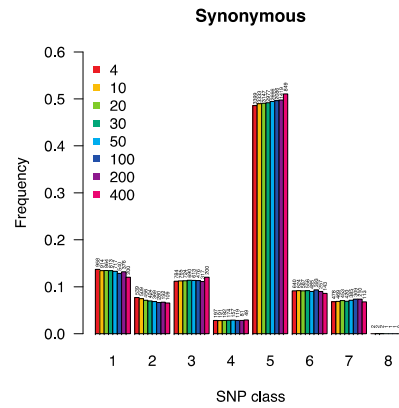
Figure S10: Population sampling and RNA sequencing

Effect of “sequencing depth” threshold, *i.e.* the minimal number of reads in each population.

Blast e-value = 10^{-5}

Minor allele frequency : 0.05

Window : 50

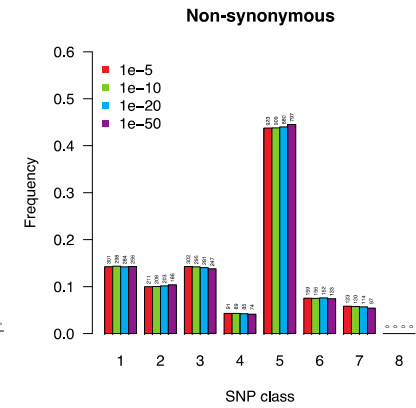
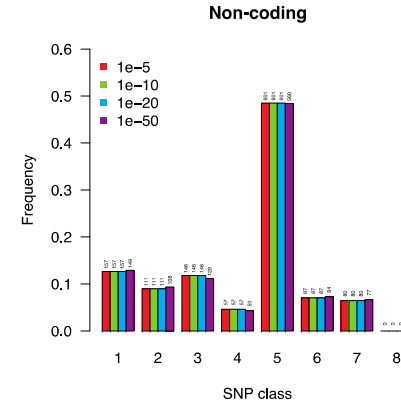
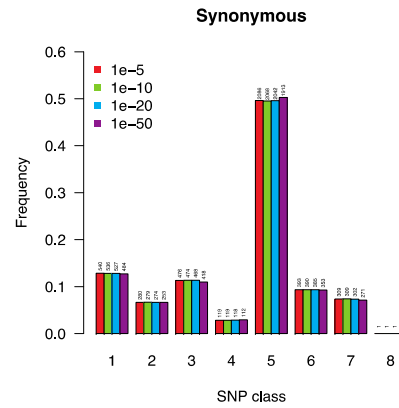


Effect of “sequence conservation” threshold, *i.e.* the blast best hit e-value between the contig and the zebrafish sequence.

Sequencing depth = 100

Minor allele frequency : 0.05

Window : 50



Effect of “SNP isolation” threshold, *i.e.* no other SNP in a window of a given size

Blast e-value = 10^{-5}

Sequencing depth = 100

Minor allele frequency : 0.05

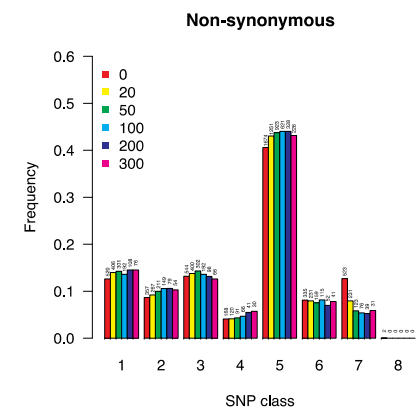
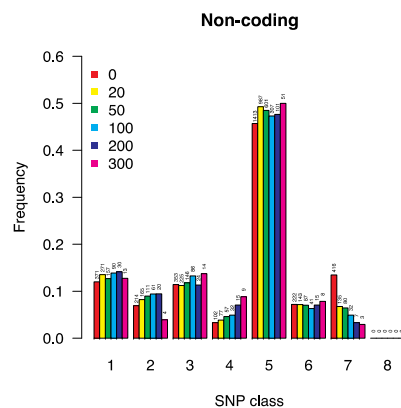
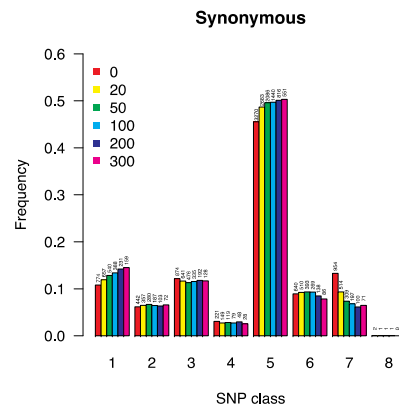


Figure S11: The effect of different thresholds on the estimation of SNP class frequencies

Supplementary tables

Table S1

number of alleles genotyped / locus / locality

			A13e5	Hc5	Vf9	Ra8	Xa3	Ib1	A13f8	A14d12	A19c8	A14d8	M_f4	Vf3	A7c5
surface	Guatemala	S1	56	64	56	70	70	72	40	72	60	72	44	82	80
surface	Guatemala	S2	32	54	24	62	68	52	64	74	36	48	24	74	60
surface	El Abra	S3	142	166	126	170	180	176	108	212	154	178	102	228	210
surface	Micos	S4	44	52	28	44	34	58	34	58	40	42	24	56	56
cave	Pachón	O1	68	82	0	74	86	66	88	88	30	78	38	84	80
cave	Yerbaniz	O2	16	20	4	22	22	16	22	22	16	20	18	24	20
cave	Japones	O3	16	18	4	14	16	14	18	20	14	20	18	18	20
cave	Arroyo	O4	14	22	0	14	20	16	22	24	8	16	10	22	22
cave	Tinaja	O5	8	8	0	8	8	4	8	8	4	4	4	8	8
cave	Curva	O6	8	20	0	14	22	6	26	26	0	16	26	18	18
cave	Toro	O7	4	6	0	4	6	6	6	6	4	4	4	6	6
cave	Chica	O8	206	210	206	220	206	180	228	162	196	198	142	218	220
cave	Molino	N1	34	42	26	32	42	36	44	44	38	32	34	44	44
cave	Caballo Moro	N2	32	44	34	44	44	26	48	52	46	42	42	50	50
cave	Subterráneo	N3	78	122	106	124	124	52	140	138	54	136	0	134	144
			A5f9	A2a7	a4g11	a6f1	wd11	a12f10	Lb9	wc12	a6h6	wf6	A10b5	vc10	a8g5
surface	Guatemala	S1	84	82	70	68	80	78	82	78	82	74	70	28	58
surface	Guatemala	S2	66	76	68	58	60	56	56	58	46	54	30	32	42
surface	El Abra	S3	224	226	202	158	198	208	188	210	194	202	184	66	128
surface	Micos	S4	58	58	44	54	52	54	48	54	44	56	40	32	40
cave	Pachón	O1	86	84	86	80	70	82	74	80	54	84	76	74	84
cave	Yerbaniz	O2	22	22	22	22	22	16	16	16	16	20	22	16	16
cave	Japones	O3	18	20	10	12	12	16	16	16	16	16	10	14	18
cave	Arroyo	O4	24	24	16	18	18	20	22	20	22	18	14	22	24
cave	Tinaja	O5	8	8	8	8	8	6	8	8	8	8	8	8	8
cave	Curva	O6	26	26	26	22	26	22	26	22	26	18	18	8	14
cave	Toro	O7	6	6	6	6	6	6	6	6	6	4	2	0	2
cave	Chica	O8	234	216	212	216	208	196	216	184	216	232	234	224	232
cave	Molino	N1	44	44	22	30	36	38	42	42	42	44	44	42	42
cave	Caballo Moro	N2	44	50	40	38	44	50	52	52	52	50	50	52	52
cave	Subterráneo	N3	138	142	130	128	108	140	136	140	136	140	128	130	140

Table S2a:

Classification of polymorphisms in *Astyanax mexicanus* Texas surface vs the Pachón cave populations

	Class	Synonymous		Non-coding		Non-synonymous	
		n	%	n	%	n	%
Ancestral fixed SF, derived fixed CF	(1)	612	14.6	180	14.6	343	16.3
Ancestral fixed CF, derived fixed SF	(2)	351	8.4	144	11.7	246	11.7
Polymorphism CF, ancestral fixed SF	(3)	434	10.3	130	10.6	274	13.0
Polymorphism CF, derived fixed SF	(4)	110	2.6	49	4.0	81	3.8
Polymorphism SF, ancestral fixed CF	(5)	2,062	49.1	588	47.8	911	43.3
Polymorphism SF, derived fixed CF	(6)	391	9.3	84	6.4	155	7.4
Shared polymorphism	(7)	240	5.7	55	4.5	96	4.6
Divergent	(8)	0	0.0	0	0.0	0	0.0
Total		4,200	100.0	1,230	100.0	2,106	100.0
Polymorphism SF	(5+6+7)	2,693		727		1,162	
Polymorphism CF	(3+4+7)	784		234		451	
Ratio SF/CF		3.43		3.11		2.58	
Derived and fixed SF	(2+4)	461		193		327	
Derived and fixed CF	(1+6)	1,003		264		498	
Ratio CF/SF		2.18		1.37		1.52	

Thresholds: 100; MAF > 10%; Score Blast < 10⁻⁵; interval > 50bp (see materials and methods for threshold definitions.)

CF: Cavefish; SF: Surface fish; numbers in brackets are class identifiers described in fig. 4.

Table S2b:

Classification of polymorphisms in *Astyanax mexicanus* Texas surface vs Pachón cave populations

	Class	Synonymous		Non-coding		Non-synonymous	
		n	%	n	%	n	%
Ancestral fixed SF, derived fixed CF	(1)	462	11.0	123	9.9	247	11.6
Ancestral fixed CF, derived fixed SF	(2)	207	4.9	83	6.7	173	8.1
Polymorphism CF, ancestral fixed SF	(3)	495	11.8	154	12.4	317	14.9
Polymorphism CF, derived fixed SF	(4)	123	2.9	57	4.6	94	4.4
Polymorphism SF, ancestral fixed CF	(5)	2,105	50.0	609	49.0	935	43.8
Polymorphism SF, derived fixed CF	(6)	414	9.8	100	8.0	177	8.3
Shared polymorphism	(7)	400	9.5	117	9.4	187	8.8
Divergent	(8)	2	0.0	1	0.1	4	0.2
Total		5,387	100.0	1,244	100.0	2,134	100.0
Polymorphism SF	(5+6+7)	2,919		826		1,299	
Polymorphism CF	(3+4+7)	1,018		328		598	
Ratio SF/CF		2.87		2.52		2.17	
Derived and fixed SF	(2+4)	330		140		267	
Derived and fixed CF	(1+6)	876		223		424	
Ratio CF/SF		2.65		1.59		1.59	

Thresholds: 100; MAF > 1%; Score Blast < 10⁻⁵; interval > 50bp (see materials and methods for threshold definitions).

CF: Cavefish; SF: Surface fish; numbers in brackets are class identifiers described in fig. 4.

Table S3a:

Best score and age of the cavefish population with different sets of demographic parameters.

		Ne ancestral = 10,000																	
		5,000				Ne SF 10,000				20,000									
		% of migrant fish																	
		1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%						
75	0.10																		
	0.01																		
	0.001																		
	0.0001																		
	0.0					15.81	1,200			15.81	1,000			19.06	900				
150	0.10	53.19	73,800			51.19	76,300			47.53	14,700								
	0.01	1.63	90,700			1.37	72,100			5.14	82,500								
	0.001	9.47	2,300			13.97	1,900			14.47	54,300								
	0.0001	12.87	2,200			16.47	2,000			15.97	1,900								
	0.0	13.03	2,000			16.77	2,300			16.94	2,200								
313	0.10	94.76	63,600			102.20	39,300			93.05	47,300								
	0.01	4.30	90,400			4.48	50,100			7.63	48,000								
	0.001	3.95	13,900			8.10	37,500			4.95	83,500								
	0.0001	5.81	4,100			10.64	4,800			13.76	3,800								
	0.0	5.63	5,300			6.92	4,800			12.90	4,700			11.99	3,800				
625	0.10	118.60	89,900			123.54	68,000			110.15	27,400								
	0.01	23.69	49,700			24.18	23,700			13.41	30,200								
	0.001	2.01	11,600			1.06	28,600			3.11	74,800								
	0.0001	1.03	9,300			5.51	10,300			10.21	9,800								
	0.0	1.00	11,200			5.28	10,200			8.81	10,100								
1,250	0.10	123.32	77,600	63.99	80,000	133.67	54,400	54.15	72,600	120.07	20,500	45.95	19,100						
	0.01	55.39	94,600	9.24	17,200	59.80	28,100	1.27	27,100	44.52	24,800	2.03	73,200						
	0.001	11.52	19,700	5.35	17,000	0.68	21,500	1.13	21,100	2.04	51,000	4.80	21,500						
	0.0001	7.60	16,300	6.78	15,700	1.71	20,500	1.47	21,100	3.56	22,300	3.79	18,100						
	0.0	8.14	16,400	7.03	16,100	6.14	13,800	1.06	19,100	1.54	19,000	4.40	19,700	5.12	16,700				
2,500	0.10	128.43	64,900	94.14	91,600	137.76	8,300	76.99	95,000	123.72	25,400	68.34	23,000						
	0.01	98.60	97,300	41.88	18,600	83.03	30,400	13.29	36,700	72.82	17,200	5.65	76,200						
	0.001	46.00	17,600	35.05	21,900	12.06	26,700	8.09	27,900	8.72	51,000	5.35	37,100						
	0.0001	30.18	19,300	31.41	25,000	6.82	32,600	7.22	28,100	5.34	34,200	4.11	31,000						
	0.0					30.10	21,100			8.39	30,800			4.70	34,300				
5,000	0.10	129.69	97,100	111.16	93,900	141.32	96,100	107.74	32,600	127.73	20,900	94.27	24,800						
	0.01	83.72	81,800	35.92	17,500	83.72	49,700	53.69	29,600	90.50	39,900	31.37	65,400						
	0.001	76.51	15,500	67.12	28,700	41.08	40,400	27.74	49,600	23.38	85,100	13.87	65,200						
	0.0001	69.12	22,900	68.84	33,500	27.95	42,100	29.32	54,500	12.24	66,900	13.01	50,000						
	0.0	75.10	12,100	75.07	18,000	29.37	44,700	25.11	37,300	13.13	61,800	13.07	67,900						
10,000	0.10	129.75	99,700	123.88	80,800	96.26	12,300	63.98	20,300	29.21	44,300			12.37	56,900				
	0.01	130.37	87,200	109.00	12,600	99.99	13,500	115.02	20,500	80.04	20,400	61.27	28,200	97.61	13,000	55.67	51,500	29.65	90,800
	0.001	104.11	9,300	98.88	17,600	102.56	13,400	79.82	38,000	53.87	39,200	58.48	48,100	53.97	42,700	34.13	97,200	31.40	94,000
	0.0001	89.72	14,500	94.96	9,600	82.89	14,000	56.97	39,000	58.37	45,700	55.21	29,200	33.37	84,100	31.26	78,100	31.83	96,000
	0.0	95.54	9,300	101.17	9,000	95.74	12,800	57.47	41,000	59.44	43,600	56.06	42,100	28.88	96,900	31.94	61,000	34.15	50,800
	0.0					96.86	12,700			60.38	35,700			31.59	93,100				

For each simulation, the best score (left value) and the age of the cavefish population (right value) are given. score < 3, green background; 3 < score < 15, orange background; score > 15, red background.

When the percentage of migrants is less than one fish at each migration, the model is equivalent to the model without migration and the cell was colored in grey.

Table S3b:

Best score and age of the cavefish population with different sets of demographic parameters.

Ne ancestral = 20,000

		5,000				Ne SF 10,000 % of migrant fish				20,000											
		1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%								
75	0.10																				
	0.01																				
	0.001																				
	0.0001																				
	0.0					20.39	900			20.27	1,000			22.47	1,000						
150	0.10	56.72	78,000			59.03	94,600			61.23	52,200										
	0.01	1.58	89,600			3.18	90,100			5.47	99,500										
	0.001	17.01	2,200			17.28	1,900			14.85	42,700										
	0.0001	15.45	1,900			19.77	1,900			21.53	1,800										
	0.0	15.32	2,100			20.55	1,700			19.52	2,300										
313	0.10	98.33	66,600			110.68	86,300			110.36	28,300										
	0.01	3.16	94,100			6.74	96,400			9.80	51,900										
	0.001	8.16	5,500			10.89	34,600			4.87	97,100										
	0.0001	7.82	4,800			16.63	4,600			17.98	3,700										
	0.0	8.98	4,400			12.78	5,000			17.48	4,300										
625	0.10	116.35	99,300			128.52	93,000			128.01	15,600										
	0.01	29.57	92,000			24.23	70,800			26.98	91,400										
	0.001	3.71	10,100			3.14	27,000			1.50	80,900										
	0.0001	3.23	9,900			6.18	9,000			9.93	8,900										
	0.0	5.72	10,100			7.58	9,500			11.73	8,700										
1,250	0.10	130.78	99,300	87.63	98,200	144.17	98,600	60.04	58,000	140.36	87,700	57.64	70,200								
	0.01	36.89	23,700	44.96	17,900	63.25	98,500	2.54	24,600	53.67	28,900	6.28	54,200								
	0.001	14.01	13,100	11.95	15,300	2.90	25,400	2.11	19,400	0.81	38,600	5.45	19,100								
	0.0001	11.11	14,600	11.50	14,200	1.35	18,900	3.24	20,300	4.39	23,000	5.02	17,200								
	0.0	10.53	13,400	11.89	14,000	1.63	18,900	1.74	17,900	5.31	20,500	4.62	20,000								
2,500	0.10	133.00	94,800	105.77	73,900	157.76	94,700	88.14	80,700	147.32	90,900	86.35	76,500								
	0.01	101.60	81,800	56.16	16,100	95.49	97,900	18.84	37,800	79.54	61,600	4.30	51,200								
	0.001	51.63	16,300	38.42	19,300	24.34	28,600	9.30	29,000	4.99	60,800	1.48	37,600								
	0.0001	42.88	21,100	45.48	20,600	7.23	29,700	6.69	29,900	1.49	38,400	1.61	38,300								
	0.0					39.55	20,600			8.13	29,200			1.73	33,500						
5,000	0.10	136.44	88,200	117.40	99,600	150.63	76,500	119.71	99,700	146.97	93,900	114.89	22,200								
	0.01	424.11	83,400	105.31	13,900	117.80	74,100	57.54	32,500	113.56	66,700	34.72	89,500								
	0.001	101.21	10,600	90.36	22,300	57.12	43,100	31.45	45,100	31.00	59,900	7.93	67,000								
	0.0001	80.47	15,900	87.95	13,700	37.59	34,500	32.99	46,200	9.23	89,200	8.41	56,200								
	0.0	89.50	27,200	92.71	16,300	32.21	45,200	31.99	44,300	7.69	66,800	7.49	62,100								
10,000	0.10	136.69	91,500	130.94	92,300	119.40	13,800			84.13	14,900			6.78	57,000						
	0.01	131.75	94,000	121.94	7,500	122.98	12,800	148.03	90,200	124.50	88,100	68.76	35,100	152.48	20,300	137.31	95,600	26.73	83,600		
	0.001	126.12	9,800	118.82	12,700	119.23	14,600	124.62	96,000	97.47	28,900	73.38	66,000	124.49	62,300	65.85	57,200	29.74	83,200		
	0.0001	122.93	8,400	118.28	13,300	117.15	7,600	93.29	25,900	78.34	59,900	74.66	44,300	69.36	57,900	32.83	76,400	29.89	82,100		
	0.0	120.00	13,800	124.57	10,300	118.15	9,600	73.06	45,400	74.58	81,100	68.74	42,100	33.29	95,100	32.84	96,700	29.91	92,300		
					120.72	12,000			74.51	42,000	72.85	58,400	68.20	61,000	31.85	92,700	27.34	83,200	28.45	89,000	
										74.07	41,700							29.49	86,200		

For each simulation, the best score (left value) and the age of the cavefish population (right value) are given.

score < 3, green background; 3 < score < 15, orange background; score > 15, red background.

When the percentage of migrants is less than one fish at each migration, the model is equivalent to the model without migration and the cell was colored in grey.

Table S3c:

Best score and age of the cavefish population with different sets of demographic parameters.

Ne ancestral = 50,000

		5,000				Ne SF 10,000				20,000									
		% of migrant fish				% of migrant fish				% of migrant fish									
		1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%						
75	0.10																		
	0.01																		
	0.001																		
	0.0001																		
	0.0				20.21	900					23.38	900		21.20	900				
150	0.10	54.47	95,300			73.29	95,000					75.05	2,500						
	0.01	2.33	92,100			8.47	98,400					17.83	78,400						
	0.001	15.27	1,900			19.39	1,900					20.23	2,200						
	0.0001	16.63	2,100			19.06	1,800					21.12	2,200						
	0.0	16.59	2,100			19.71	1,900					21.63	1,900						
313	0.10	193.91	81,400			128.97	96,400					124.06	3,900						
	0.01	5.58	97,100			11.80	82,100					18.27	30,000						
	0.001	11.70	5,600			14.58	29,800					11.74	64,800						
	0.0001	11.93	5,000			17.34	4,100					18.39	4,400						
	0.0	11.58	4,100			13.58	3,000					15.24	4,200						
625	0.10	126.61	99,500			125.84	900					145.80	2,400						
	0.01	29.82	86,600			34.06	80,900					33.71	86,700						
	0.001	8.95	11,500			7.09	17,300					5.95	49,300						
	0.0001	6.58	9,000			10.46	8,900					14.70	9,500						
	0.0	6.39	9,200			9.87	9,700					13.64	8,300						
1,250	0.10	128.07	95,600	78.10	98,300	154.06	98,700	71.01	86,700			155.98	1,900	75.47	82,900				
	0.01	75.38	97,200	20.85	16,700	67.07	90,800	6.71	27,800			70.85	92,800	3.85	49,500				
	0.001	26.42	18,300	16.19	14,000	9.25	28,600	4.46	17,800			3.98	42,400	8.41	21,300				
	0.0001	18.46	15,800	16.02	14,100	4.94	19,800	5.54	17,300			8.12	25,800	7.38	20,600				
	0.0	15.81	15,600	15.94	15,000	4.89	17,600	5.61	19,100			7.24	18,700	8.42	17,600				
2,500	0.10	137.62	88,900	108.57	97,800	161.09	300	110.18	95,300			161.18	1,100	107.18	12,000				
	0.01	111.66	96,900	74.49	16,700	116.81	99,200	26.03	26,800			112.16	30,400	8.14	60,700				
	0.001	69.78	14,500	55.17	20,500	28.29	36,500	13.03	28,300			4.52	52,000	2.45	38,100				
	0.0001	54.78	21,200	51.95	18,600	13.41	31,000	12.52	29,700			2.46	38,500	3.04	36,000				
	0.0					52.71	20,100					12.30	27,700		2.91	37,500			
5,000	0.10	141.77	85,600	131.81	94,500	160.27	92,000	135.08	87,300			164.31	300	140.52	7,100				
	0.01	123.05	97,500	123.23	9,800	138.39	99,600	83.45	29,400			137.45	15,900	47.83	61,400				
	0.001	124.25	9,000	108.76	15,000	74.78	23,800	48.73	40,600			42.52	66,400	12.25	69,000				
	0.0001	107.21	11,700	104.53	16,700	47.84	38,900	42.85	42,000			11.20	62,500	8.92	65,200				
	0.0	109.24	10,500	108.51	11,600	46.24	34,400	46.17	46,200			9.62	65,400	9.83	56,400				
10,000	0.10	138.94	99,000	139.14	98,100	135.90	9,900	105.16	15,100			143.42	37,500		8.05	63,400			
	0.01	143.98	98,500	139.04	9,200	131.51	8,700	165.52	100	149.29	98,000	93.94	27,800	169.33	1,600	152.84	8,400	97.33	80,600
	0.001	140.97	7,000	136.75	6,400	133.83	10,200	126.97	97,400	117.59	16,600	97.00	51,800	151.68	6,500	90.36	45,200	36.62	93,900
	0.0001	136.54	8,300	132.85	7,300	137.88	9,000	121.34	14,800	97.46	28,400	93.32	30,700	85.17	49,500	42.27	74,400	36.78	86,700
	0.0	135.45	8,900	132.46	7,600	137.88	9,600	94.06	32,300	93.52	33,800	94.41	39,700	36.57	89,900	36.80	80,500	35.23	84,800
	0.0					133.05	8,300					97.90	38,400			39.34	91,700		

For each simulation, the best score (left value) and the age of the cavefish population (right value) are given.

score < 3, green background; 3 < score < 15, orange background; score > 15, red background.

When the percentage of migrants is less than one fish at each migration, the model is equivalent to the model without migration and the cell was colored in grey.

Table S3d:

Best score and age of the cavefish population with different sets of demographic parameters.

Ne ancestral = 100,000

		Ne SF															
		5,000				10,000				20,000							
		% of migrant fish															
		1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%	1%	0.1%	0.01%	0%				
75	0.10																
	0.01																
	0.001																
	0.0001																
	0.00001																
	0.0					20.76	900				22.42	900			23.50	900	
150	0.10	59.65	99.700			79.90	1,400						75.38	2,200			
	0.01	8.43	97.100			17.23	95.900						23.03	23,400			
	0.010	13.35	1,900			19.83	2,000						22.00	2,000			
	0.0010	16.58	2,100			19.83	1,800						20.83	2,100			
	0.00010	17.87	2,100			19.95	1,800						21.34	1,800			
	0.0					17.76	1,900				19.76	2,100			21.46	1,800	
313	0.10	102.85	98,400			131.45	2,200						129.33	2,700			
	0.01	7.89	96,900			18.76	95,700						22.03	8,200			
	0.010	12.32	5,500			15.65	5,600						15.96	38,300			
	0.0010	12.28	4,600			16.88	4,700						19.83	4,200			
	0.00010	12.34	4,500			16.96	4,200						17.46	70,300			
	0.0					12.11	4,600				15.30	4,600			20.00	3,900	
625	0.10	125.84	97,300			152.49	1,100						147.10	1,800			
	0.01	29.81	95,300			42.23	82,300						36.50	10,300			
	0.010	8.62	9,500			9.62	32,600						12.46	70,300			
	0.0010	7.66	8,700			11.74	10,400						15.64	8,100			
	0.00010	8.79	9,200			10.66	9,600						15.80	7,600			
	0.0					8.64	8,700				11.42	9,600			14.97	8,900	
1,250	0.10	134.35	95,900	85.30	99,900	161.50	400	79.23	98,600				161.63	700	84.25	11,600	
	0.01	36.15	91,500	25.25	15,700	66.53	10,200	8.57	20,300				66.22	26,300	7.94	32,500	
	0.010	23.26	13,100	19.29	13,200	11.10	23,400	7.17	17,300				6.91	43,100	9.43	19,500	
	0.0010	18.42	14,100	18.49	13,700	7.08	18,300	7.05	17,000				11.42	18,100	10.16	16,300	
	0.00010	18.88	13,700	17.88	14,100	6.97	17,400	6.94	17,100				9.38	17,500	10.30	16,700	
	0.0					18.41	13,600				7.21	18,600			10.32	18,600	
2,500	0.10	140.12	96,600	126.78	99,600	168.91	400	126.30	7,100				163.56	1,100	122.14	7,800	
	0.01	117.38	94,800	75.30	13,600	132.62	8,800	33.71	30,200				120.50	10,400	11.60	47,400	
	0.010	79.15	17,400	61.05	19,500	33.03	31,500	17.41	29,300				9.24	41,700	5.14	38,000	
	0.0010	57.99	17,300	58.02	21,300	16.23	29,500	15.17	29,000				4.61	38,700	5.19	34,600	
	0.00010																
	0.0					59.20	19,200				16.37	27,700			5.02	36,100	
5,000	0.10	146.85	98,100	135.37	95,500	170.44	200	152.61	4,800				167.40	1,600	148.32	6,000	
	0.01	149.59	96,200	127.95	7,100	154.77	8,400	84.58	20,100				146.33	8,200	57.65	46,900	
	0.010	132.81	7,500	115.37	12,500	96.46	32,500	56.52	44,700				45.53	73,400	16.39	63,500	
	0.0010	119.10	9,600	111.55	14,400	53.32	40,000	54.84	40,800				16.23	61,800	13.23	60,800	
	0.00010	116.89	12,900	116.57	15,700	51.84	42,900	51.58	38,600				13.49	57,600	13.16	58,700	
	0.0					114.74	10,600				54.03	42,200			13.21	60,300	
10,000	0.10	149.54	96,200	152.75	93,500	171.25	400	161.04	3,400	109.11	30,400			170.03	0	157.85	5,800
	0.01	150.84	98,700	148.10	7,800	160.53	2,700	128.97	15,300	107.31	29,500			157.54	5,900	101.47	40,300
	0.010	143.42	5,500	142.87	6,700	129.57	21,000	113.11	23,200	105.76	33,300			100.48	40,600	53.09	90,900
	0.0010	123.03	6,600	142.16	8,700	108.38	32,100	109.23	26,300	106.34	31,600			50.80	71,400	47.90	92,000
	0.00010	123.03	6,600	142.16	8,700	107.77	32,100	109.31	31,100	106.74	29,900			47.97	88,100	46.00	79,600
	0.0					143.19	7,800				107.89	39,300			47.26	81,600	

For each simulation, the best score (left value) and the age of the cavefish population (right value) are given.

score < 3, green background; 3 < score < 15, orange background; score > 15, red background.

When the percentage of migrants is less than one fish at each migration, the model is equivalent to the model without migration and the cell was colored in grey.