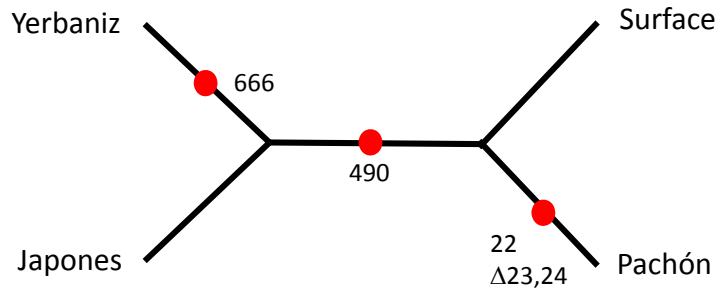


Mutation mapping in *A. mexicanus* nuclear gene most parsimonious unrooted trees

Mc1r (complete coding sequence, 972 bp)



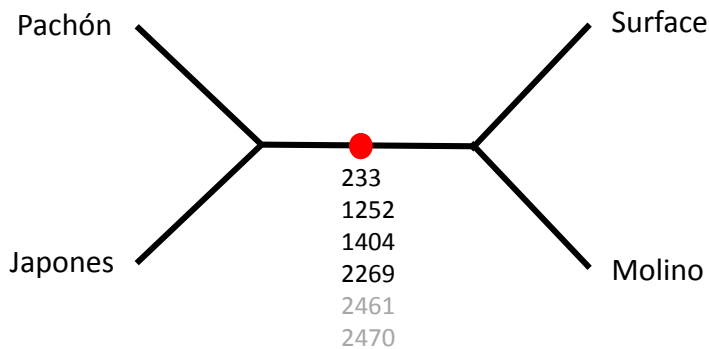
Positions of the mutations

22: C/T non synonymous
 Δ23,24: 2 bp deletion
 490: C/T non synonymous
 666: G/A synonymous

Note: 'Pachon' haplotype is found also in Yerbaniz and Japones

Accession numbers: FJ665983, FJ665984, FJ665985, FJ665986

Oca2 (complete coding sequence, 2499 bp)



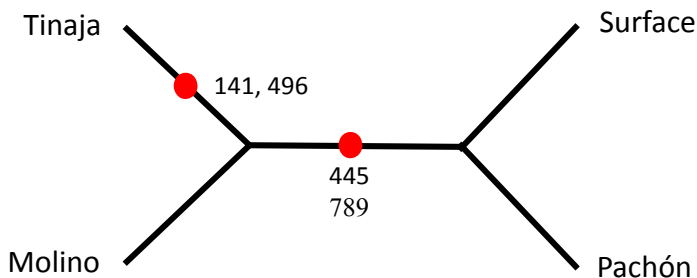
Positions of the mutations

233: G/A non synonymous
 1252: G/A non synonymous
 1404: C/T synonymous
 2269: C/T non synonymous
 2461: C/G non synonymous
 2470: G/A non synonymous

Note: exon 24 containing position 2461 and 2470 is deleted in Pachon sequence.

Accession numbers: no accession numbers, based on Supplementary Table 2 in Protas ME *et al.*: Genetic analysis of cavefish reveals molecular convergence in the evolution of albinism. Nat Genet 2006, 38(1):107-111.

Mc4r (complete coding sequence, 1008 bp)

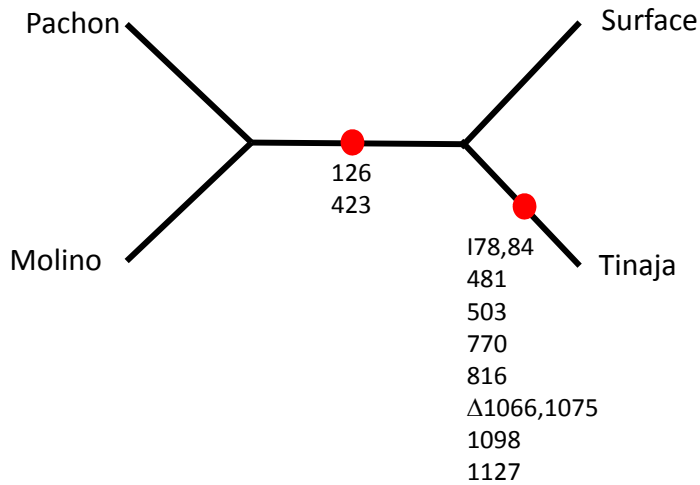


Positions of the mutations

141: C/T synonymous
 445: G/A non synonymous
 496: G/A non synonymous
 789: G/T non synonymous

Accession numbers: no accession numbers, sequences found a Supporting Information File of Aspiras AC *et al.*: Melanocortin 4 receptor mutations contribute to the adaptation of cavefish to nutrient-poor conditions. Proceedings of the National Academy of Sciences 2015, 112(31):9668-9673.

Mc3r (complete coding sequence, 1158 bp)

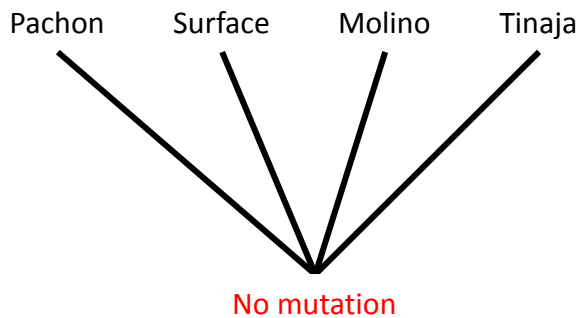


Positions of the mutations

- 178,84: 6 bp insertion
- 126: G/A synonymous
- 423: T/C synonymous
- 481: G/A non synonymous
- 503: T/C non synonymous
- 770: G/C non synonymous
- 816: T/C synonymous
- Δ1066,1075: 12 pb deletion
- 1098: G/A synonymous
- 1127: G/A non synonymous

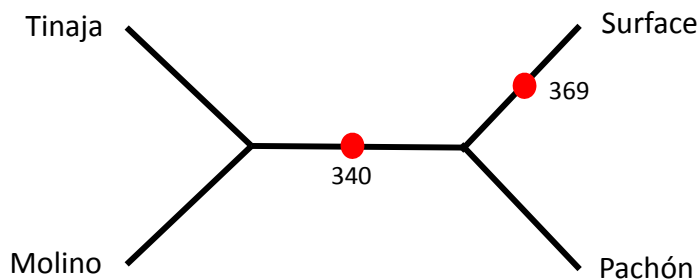
Accession numbers: no accession numbers, sequenes found a Supporting Information File of Aspiras AC *et al.*: Melanocortin 4 receptor mutations contribute to the adaptation of cavefish to nutrient-poor conditions. Proceedings of the National Academy of Sciences 2015, 112(31):9668-9673.

Leptin b (Lepb) (complete coding sequence, 483 bp)



Accession numbers: no accession numbers, sequenes found a Supporting Information File of Aspiras AC *et al.*: Melanocortin 4 receptor mutations contribute to the adaptation of cavefish to nutrient-poor conditions. Proceedings of the National Academy of Sciences 2015, 112(31):9668-9673.

Pomcb (complete coding sequence, 522 bp)

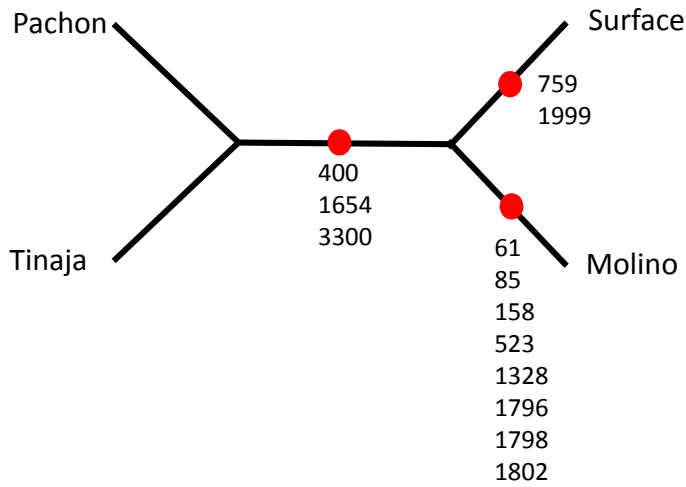


Positions of the mutations

- 340: G/A non synonymous
- 369: C/A synonymous

Accession numbers: no accession numbers, sequenes found a Supporting Information File of Aspiras AC *et al.*: Melanocortin 4 receptor mutations contribute to the adaptation of cavefish to nutrient-poor conditions. Proceedings of the National Academy of Sciences 2015, 112(31):9668-9673.

Leptin receptor (Lepr) (complete coding sequence, 3354 bp)



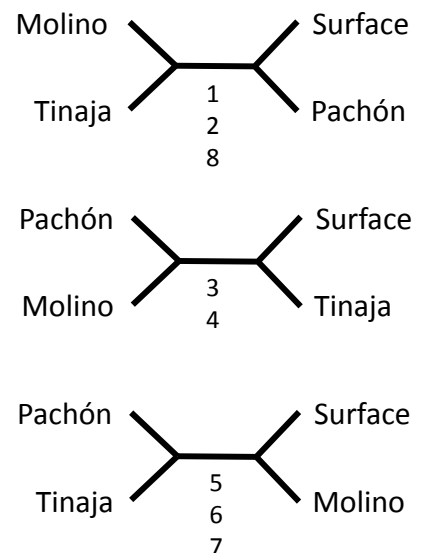
Positions of the mutations

- 61: G/T non synonymous
- 85: C/T non synonymous
- 158: G/C non synonymous
- 400: G/A non synonymous
- 523: G/A non synonymous
- 759: G/T synonymous
- 1328: C/T non synonymous
- 1654: G/A non synonymous
- 1796: G/C non synonymous
- 1798: G/A non synonymous
- 1802: C/T non synonymous
- 1999: G/T non synonymous
- 3300: G/T synonymous

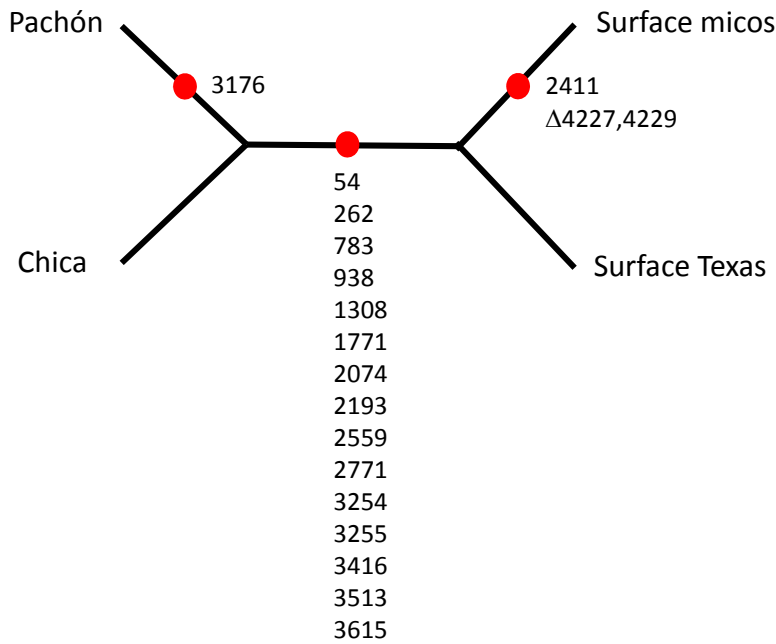
Accession numbers: no accession numbers, sequences found a Supporting Information File of Aspiras AC *et al.*: Melanocortin 4 receptor mutations contribute to the adaptation of cavefish to nutrient-poor conditions. Proceedings of the National Academy of Sciences 2015, 112(31):9668-9673.

Informative sites in Mc4r, Mc3r, Lepr and Pomcb

	Genes							
	Mc4r		Mc3r		Lepr			Pomcb
	1	2	3	4	5	6	7	8
Surface	G	G	G	C	G	A	G	G
Pachón	G	G	A	T	A	G	T	G
Tinaja	A	T	G	C	A	G	T	A
Molino	A	T	A	T	G	A	G	A



Per1 (complete coding sequence, 4296 bp)

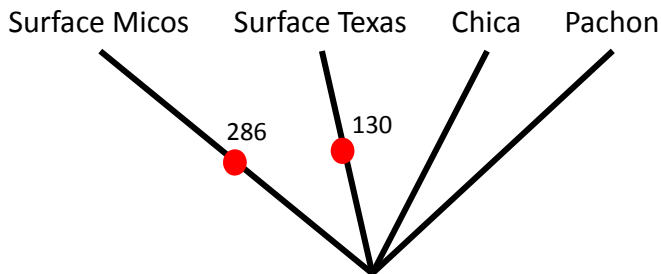


Positions of the mutations

- 54: C/T synonymous
- 262: T/A non synonymous
- 783: G/A synonymous
- 938: T/A non synonymous
- 947: G/A non synonymous
- 1308: G/C non synonymous
- 1771: G/A non synonymous
- 2074: G/C non synonymous
- 2193: G/C synonymous
- 2411: T/C non synonymous
- 2559: G/A synonymous
- 2771: G/A non synonymous
- 3176: C/T non synonymous
- 3254: C/A non synonymous
- 3255: C/T synonymous
- 3416: G/A non synonymous
- 3513: G/T non synonymous
- 3615: G/A synonymous
- Δ4227,4229 : 3 bp deletion

Accession numbers: KF737843, KF737844, KF737845

Per2 (coding sequence, 481 bp)

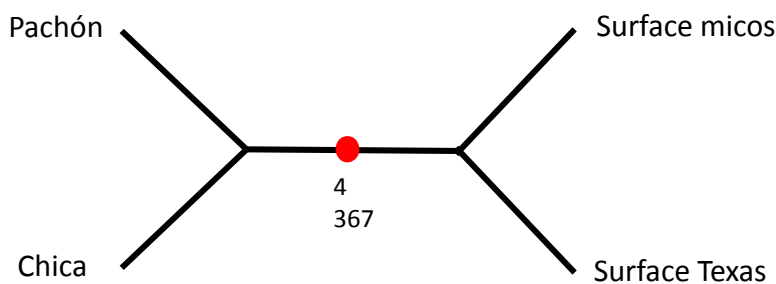


Positions of the mutations

- 130: C/T synonymous
- 286: G/A synonymous

Accession numbers: KF737849, KF737850, KF737851

Tef1 (coding sequence, 396 bp)

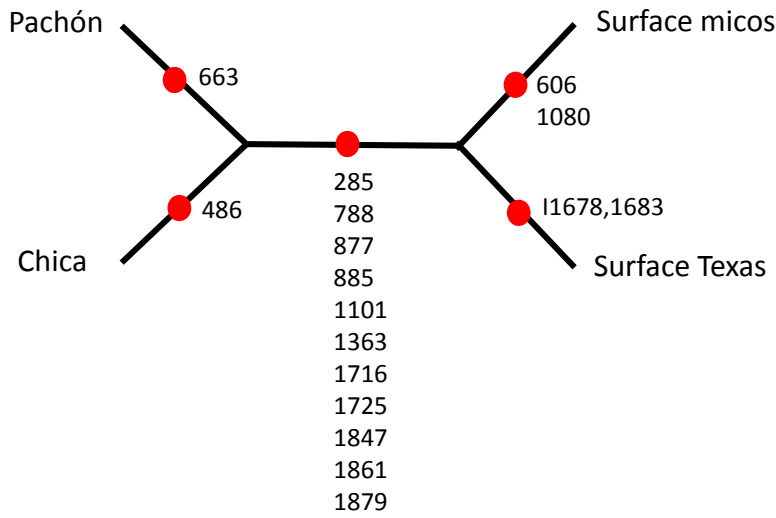


Positions of the mutations

- 4: G/A synonymous
- 367: G/T non synonymous

Accession numbers: KF737852, KF737853, KF737854

Cry1a (complete coding sequence, 1884 bp)

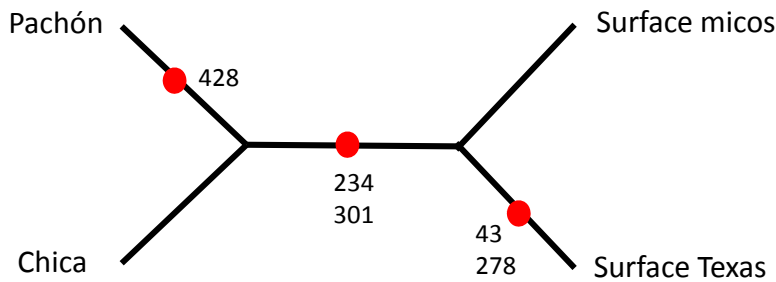


Positions of the mutations

- 285: G/T synonymous
- 486: G/A synonymous
- 606: C/A synonymous
- 663: C/T synonymous
- 788: G/A non synonymous
- 877: C/A non synonymous
- 885: C/T synonymous
- 1080: C/T synonymous
- 1101: G/C synonymous
- 1363: C/A non synonymous
- 11678,1683: 6 pb insertion
- 1716: C/A synonymous
- 1725: C/T synonymous
- 1847: C/T non synonymous
- 1861: G/C non synonymous
- 1879: C/A non synonymous

Accession numbers: KF737846, KF737847, KF737848

Cpd photolyase (complete coding sequence, 890 bp)



Positions of the mutations

- 43: C/Y non synonymous
- 234: T/C/Y synonymous
- 278: C/Y non synonymous
- 301: G/A non synonymous
- 428: C/T non synonymous

Note: Surface Texas population is polymorphic (T,C) at position 43, 234, 278.

Accession numbers: KF737857, KF737858, KF737859