Electronic Supplementary Appendix

Selection analysis on the rapid evolution of a secondary sexual trait

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Appendix S1. Common-garden methods:

In March 2009, we collected a subset of juvenile guppies from both introduction sites and the source Guanapo high predation site. They and their descendents were reared for two generations under common garden conditions. In summary, once the collected females reached maturity, they were randomly mated to a mature male from their population to form the first generation line. Offspring from these parings were then randomly selected from each female line, then mated randomly in a new tank to an unrelated male. Second generation offspring from those matings were removed, then analyzed for genetic divergence in colouration between ancestral and derived populations once they became adults. The final sample contained 18 males from Guanapo HP, 47 from Lower La Laja and 37 from Upper La Laja.

Two generations of common garden rearing limits maternal and environmental effects experienced by the wild-caught juveniles before capture. Any differences between the ancestral and derived populations are likely to have a genetic basis and represent evolution of male colouration in our introduction populations. Note that in order to be comparable, common garden comparisons on different populations ought to be performed simultaneously. Doing so carries the assumption that there has been no evolution of male colouration in the Guanapo HP site since the introduction so they do indeed represent the ancestral state. The assessment of evolution in the context of the mark-recapture study carries no such assumption since the founders are included in the analyses.

Appendix S2. Pedigree reconstruction methods and allele diversity

The pedigree was reconstructed by genotyping all individuals at 12 mictosatellite loci that had an average of 20 alleles each at the beginning of the introduction (Table S1). Pedigrees were reconstructed with the program COLONY [1]. After one year, the mother and father of each individual could be assigned with greater than a 90 percent level of confidence. Pedigree data indicated that the introduced individuals showed an average level of heterozygosity of 0.77 for the genotyped loci. This is very close to the average heterozygosity for these loci in multiple wild populations [2]. The loss of heterozygosity was minimal for the subsequent cohorts in the introduced population (0.75 and 0.76 in the two rivers; Table S1). This suggests that the level of neutral genetic variation in the introduced populations was representative of natural conditions and therefore founder effects and genetic drift should be weak.

Table S1. Details of the microsatellite loci used for pedigree reconstruction

Accession No.	Locus	Source	DOI	Fstat Gene Diversity	# alleles	Fstat Allelic richness
AY83094	Pret9	Paterson et al. 2005	10.1111/j.1471-8286.2005.00895.x	0.839	19	18.988
AY830942	Pret13	Paterson et al. 2005	10.1111/j.1471-8286.2005.00895.x	0.867	21	20.91
AY830943	Pret15	Paterson et al. 2005	10.1111/j.1471-8286.2005.00895.x	0.934	26	25.992
AY830946	Pret26	Paterson et al. 2005	10.1111/j.1471-8286.2005.00895.x	0.824	21	20.758
AB100321	Pret27	Watanabe et al. 2003	10.1046/j.1471-8286.2003.00490.x	0.856	19	18.919
AB100322	Pret28	Watanabe et al. 2003	10.1046/j.1471-8286.2003.00490.x	0.876	20	19.839
AB100328	Pret38	Watanabe et al. 2003	10.1046/j.1471-8286.2003.00490.x	0.643	22	21.255
AB100334	Pret46	Watanabe et al. 2003	10.1046/j.1471-8286.2003.00490.x	0.47	15	14.636
AB100354	Pret80	Watanabe et al. 2003	10.1046/j.1471-8286.2003.00490.x	0.589	15	14.989
DQ855573	Pret43	Shen et al. 2007	10.1111/j.1471-8286.2006.01589.x	0.839	39	39
DQ855588	Pret145	Shen et al. 2007	10.1111/j.1471-8286.2006.01589.x	0.651	7	6.915
DQ855605	Pret289	Shen et al. 2007	10.1111/j.1471-8286.2006.01589.x	0.749	16	16

Diversity and richness was calculated with Fstat v2.9.3.2 (2002) following Goudet [3]

Table S2. Maximum likelihood estimates of male monthly capture probabilities (mean+se)

	Lower La Laja	Upper La Laja
April	0.90±0.06	0.96±0.04
May	1.00±0.00	0.84±0.10
June	0.94±0.06	0.86±0.09
July	1.00±0.00	0.87±0.09
August	0.89±0.05	0.72±0.09
September	0.86±0.06	0.88±0.08
October	0.85±0.05	0.87±0.08
November	0.89±0.04	0.75±0.08
December	0.81±0.05	0.77±0.09
January	0.79±0.05	0.81±0.08
February	0.67±0.06	0.57±0.08
March	0.90±0.04	0.80±0.06

References

1. Wang J, Santure AW. 2009 Parentage and sibship inference from multilocus genotype data under polygamy. *Genetics* **181**, 1579–1594.

2. Paterson IG, Crispo E, Kinnison MT, Hendry AP, Bentzen P. 2005 Characterization of tetranucleotide microsatellite markers in guppy (*Poecilia reticulata*). *Mol. Ecol. Notes* **5**, 269-271.

3. Goudet J. 1995 FSTAT (Version 1.2): A computer program to calculate F-statistics. *Jour. of Heredity*, **86**, 485-486.