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Jack Frankel, *Howard University*



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# Inheritance of Trunk Banding in the Tetra (*Gymnocorymbus ternetzi* Characidae)

J. S. FRANKEL

From the Department of Biology, Howard University, Washington, DC 20059.

Address correspondence to Jack S. Frankel at the address above, or e-mail: jfrankel@howard.edu.

The tetra (*Gymnocorymbus ternetzi*) exhibits two phenotypes associated with trunk banding. Fish possess either a smoky-gray coloration with two prominent black vertical bands located directly behind the operculum (black tetra) or a lighter coloration and lack these bands (white skirt tetra). Segregation patterns observed from the progenies of 11 different crosses suggest that the inheritance of these phenotypes is controlled by two autosomal loci acting in a complementary fashion, with dominance at both loci required for the expression of the darker, banded phenotype.

The teleost suborder Characoidei consists of seven closely related families, with some 200 African species and about 1000 species in South, Central, and southern North America (Mills and Vevers 1982). The true characins, family Characidae, are found in Africa and more abundantly in South and Central America. Most species are relatively small (3–6 cm in length) with an abbreviated dorsal fin and a deeply cleft caudal fin. The tetra [*Gymnocorymbus ternetzi* Boulenger (Characidae)] is particularly popular with hobbyists, since it is attractive in appearance, undemanding in maintenance, and easily bred. It has a large distribution in Paraguay and the Rio Guapote basin, but is also found in Bolivia and Argentina (Tavares 1997). Juveniles of a darkly pigmented variety, called the black tetra, exhibit black flanks which become smoky-gray with increasing age. Adults typically exhibit a smoky-gray epaxial region and a whitish belly with a silvery sheen. Also characteristic of this variety are two prominent vertical black bands that are located directly behind the operculum, along with darkly colored dorsal, anal, and adipose fins (Mills and Vevers 1982).

An alternate variety of this tetra, called the white skirt tetra, is lighter in color and lacks the vertical banding pattern. The inheritance of this banding pattern is of particular interest since it most probably serves a role in protecting the fish from predation. As a result of my interest in the inheritance of disruptive banding and spotting patterns in tropical cyprinid and characid fishes (Frankel 1985, 1991, 1998, 2001, 2002),

the present study was undertaken to ascertain the mode of inheritance of trunk banding in *G. ternetzi*.

## Materials and Methods

Adult specimens of *G. ternetzi* were obtained from a local wholesale distributor in Maryland and maintained in separate 76 L holding tanks at 24°C. Male and female fish exhibiting the darker banded or the lighter nonbanded phenotype were selected at random from stock specimens, placed in separate 76 L tanks at 24°C, and allowed to develop at until sexually mature. Optimal water conditions were provided for all fish (i.e., water hardness 5 or less, pH 6.5, and temperature 24°C) (Axelrod and Vorderwinkler 1995; Mills and Vevers 1982). All progeny for this study were obtained from artificial fertilizations as previously described (Hart and Messina 1972). Parentals exhibiting either the banded (B) or non-banded (N) phenotype, as well as F<sub>1</sub> progeny (F), were used in a series of 28 crosses (Table 1). Embryos from all crosses were incubated at 24°C in 250 ml fingerbowls containing tank water. Dead or developmentally arrested embryos were removed daily. Fry hatched 20–24 h after fertilization and were free-swimming 48–72 h after hatching.

Progeny groups were placed in separate 76 L rearing tanks, fed initially on rotifers, and were allowed to develop until their phenotype could be visually determined. The caudal region of the fish, along with the dorsal fin and anal fin, is jet black in juveniles but turns to smoky-gray as the fish matures. Since banding is also more defined in mature individuals, determination of banding was only scored for mature individuals. Phenotypic data of all progeny were recorded and subjected to chi-square analysis. Pooled and heterogeneity chi-square tests were also performed, treating the progenies from reciprocal N × F<sub>1</sub> crosses and F<sub>1</sub> × F<sub>1</sub> crosses as single large progenies in an analysis of overall goodness-of-fit.

## Results and Discussion

Table 1 presents data for the proposed genotypes of parentals, observed phenotypic numbers, expected ratios,

**Table 1.** Proposed genotypes (PG), observed phenotypic numbers, expected ratios, degrees of freedom (df), chi-square values ( $\chi^2$ ), and probability of fit ( $P$ ) for crosses among banded and nonbanded *G. ternetzi*

Cross no.	Parents <sup>a</sup> (PG) ♀ × (PG) ♂	Phenotypic numbers		Expected ratio	df	$\chi^2$	$P^b$
		Banded	Nonbanded				
1–5	B-I, -II, -III, -IV ( <i>AABB</i> ) × B-1, -2, -3, -4 ( <i>AABB</i> )	127	0	1:0	—	—	—
6–11	N-I, -II, -III, -IV ( <i>aabb</i> ) × N-1, -2, -3, -4 ( <i>aabb</i> )	0	140	0:1	—	—	—
12	B-I ( <i>AABB</i> ) × N-1 ( <i>aabb</i> )	32 (F-I and F-1)	0	1:0	—	—	—
13	B-II ( <i>AABB</i> ) × N-2 ( <i>aabb</i> )	28 (F-II and F-2)	0	1:0	—	—	—
14	N-II ( <i>aabb</i> ) × B-1 ( <i>AABB</i> )	15 (F-III and F-3)	0	1:0	—	—	—
15	N-III ( <i>aabb</i> ) × B-2 ( <i>AABB</i> )	14 (F-IV and F-4)	0	1:0	—	—	—
16	B-III ( <i>AABB</i> ) × N-3 ( <i>aabb</i> )	22 (F-V and F-5)	0	1:0	—	—	—
17	B-IV ( <i>AABB</i> ) × N-4 ( <i>aabb</i> )	19 (F-VI and F-6)	0	1:0	—	—	—
	Pooled	130	0	1:0	—	—	—
18	N-II ( <i>aabb</i> ) × F-2 ( <i>AaBb</i> )	6	14	1:3	1	0.267	.6053
19	N-III ( <i>aabb</i> ) × F-3 ( <i>AaBb</i> )	8	13	1:3	1	1.921	.1657
20	F-I ( <i>AaBb</i> ) × N-2 ( <i>aabb</i> )	10	26	1:3	1	0.148	.7004
21	F-IV ( <i>AaBb</i> ) × N-1 ( <i>aabb</i> )	12	29	1:3	1	0.398	.5281
22	F-V ( <i>AaBb</i> ) × N-4 ( <i>aabb</i> )	11	27	1:3	1	0.316	.5740
23	N-IV ( <i>aabb</i> ) × F-6 ( <i>AaBb</i> )	8	27	1:3	1	0.086	.7693
	Total				6	3.136	.7915
	Pooled	55	136	1:3	1	1.468	.2256
	Heterogeneity				5	1.668	.8929
24	F-II ( <i>AaBb</i> ) × F-1 ( <i>AaBb</i> )	15	14	9:7	1	0.241	.6234
25	F-III ( <i>AaBb</i> ) × F-4 ( <i>AaBb</i> )	20	15	9:7	1	0.011	.9164
26	F-IV ( <i>AaBb</i> ) × F-3 ( <i>AaBb</i> )	19	19	9:7	1	0.603	.4374
27	F-V ( <i>AaBb</i> ) × F-6 ( <i>AaBb</i> )	12	11	9:7	1	0.155	.6938
28	F-VI ( <i>AaBb</i> ) × F-5 ( <i>AaBb</i> )	20	16	9:7	1	0.007	.9333
	Total				5	1.017	.9611
	Pooled	86	75	9:7	1	0.525	.4687
	Heterogeneity				4	0.492	.9742

<sup>a</sup> B designates banded parentals; N designates nonbanded parentals; F designates F<sub>1</sub> offspring resulting from banded × nonbanded crosses.

<sup>b</sup> The probability for all chi-square tests is greater than .05, thus observed results for all crosses fit the expected frequencies according to Mendelian inheritance.

and the probability of fit for *G. ternetzi* analyzed for the mode of inheritance of trunk banding. Parental fish and progeny from all crosses displayed either the banded or nonbanded phenotype. Banded females B-I, B-II, B-III, and B-IV and males B-1, B-2, B-3, and B-4 were scored as homozygous dominants, as crosses involving these individuals always resulted in banded progeny (crosses 1–5, 12–17). Nonbanded parentals (N-I, N-II, N-III, and N-IV females and N-1, N-2, N-3, and N-4 males) were scored as homozygous recessives, as crosses between these individuals consistently bred true (crosses 6–11). Further, reciprocal crosses between banded and nonbanded parentals always resulted in banded fry (crosses 12–17). When F<sub>1</sub> fishes (F-I, F-IV, F-V, F-2, F-3, and F-6) were crossed with nonbanded parentals (N-II, N-III, N-IV, N-1, N-2, and N-4), both banded and nonbanded progeny resulted and fit the expected 1:3 phenotypic ratio (crosses 18–23). In addition, crosses among F<sub>1</sub> fish always resulted in a satisfactory fit to a 9:7 phenotypic ratio of F<sub>2</sub> progeny (crosses 24–28), commensurate with a modified 9:3:3:1 ratio resulting from dominant complementary gene action (*A\_B\_* is required for the banded phenotype).

The results of this study support the hypothesis that trunk banding in *G. ternetzi* is controlled by two loci acting in

a complementary fashion, with dominance at both loci required for the expression of the banded phenotype. Segregation patterns for the banded and nonbanded phenotypes of *G. ternetzi* clearly fit an autosomal pattern of inheritance, as chi-square tests for individual and pooled progenies do not deviate significantly from expectations. Results of heterogeneity tests also support the acceptance of the null hypothesis for this data. Further, the data also suggest that these loci do not act in an additive fashion, since there is no perceptible difference in the appearance of nonbanded parental fish (*aabb*) with the nonbanded F<sub>2</sub> progeny, some of which would be heterozygous at either the *A* or *B* loci (i.e., *Aabb* or *aaBb*). A similar mode of inheritance has been reported for trunk banding in the Sumatran tiger barb (*Barbus tetrazona*) (Frankel 1985) and for trunk coloration in the three-spot gourami (*Trichogaster trichopterus*) and the lyretail toothcarp (*Aphyosemion australe*) (Frankel 1992, 1997). In these species, banding or color variation is also controlled by a pair of autosomal loci exhibiting dominant complementary gene action. In *G. ternetzi*, the prominent dark bands most probably serve as a disruptive concealment pattern and therefore would give a selective advantage to fish by providing them with an interspecific pattern to evade predation.

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