

# Inheritance of Shoulder Spotting in the Tetra, *Hyphessobrycon bentosi* Characidae

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**Abstract:** The tetra (*Hyphessobrycon bentosi*) exhibits two phenotypes associated with shoulder spotting. Fish possess either a prominent black vertical spot located directly behind the operculum (*H. b. bentosi*, bentosi white tip tetra) or lack this spot (*H. b. rosaceus*, rosy tetra). Segregation patterns observed from the progenies of ten 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 spotted phenotype.

## INTRODUCTION

Fishes in the teleost suborder Characoidei exhibit a wide variety of body markings and coloration patterns [1-3]. The Characoidei consists of seven closely related families, with some 200 African species and about 1,000 species in South, Central, and southern North American [2]. The true characins, family Characidae, are found in Africa and more abundantly in South and Central America. Most species are relatively small (i.e. 3-6 cm in length) with an abbreviated dorsal fin and a deeply cleft caudal. The tetra, *Hyphessobrycon bentosi* Durbin, is particularly popular with hobbyists, since it is attractive in appearance, undemanding in maintenance, and easily bred. It has a large distribution throughout Guyana and the lower Amazon (i.e. Rio Guapore basin) [3]. Juveniles and adults of a strikingly red-pigmented variety (*H. b. bentosi*), offered to the aquarist as the bentosi white tip tetra or the ornate tetra, typically exhibit white coloration on the distal portions of the dorsal, anal, and pelvic fins with varying degrees of black pigmentation along the fin margins. Of particular note in this variety is a prominent vertical black spot or patch located directly behind the operculum [3]. An alternate variety of this tetra, the rosy tetra (*H. b. rosaceus*), is typically, but not exclusively, more pinkish in body color. However, a distinct difference between these two varieties is that the latter lacks the vertical shoulder spot. The inheritance of this spotting pattern is of particular interest, since it most probably serves some role in protecting the fish from predation. As a result of our interest in the inheritance of disruptive banding and spotting patterns in tropical cyprinid and characid fishes [4-9], the present study was undertaken to ascertain the mode of inheritance of shoulder spotting in *H. bentosi*.

## MATERIALS AND METHODOLOGY

Adult specimens of *H. bentosi* were obtained from a wholesale distributor in Maryland, U.S.A., and maintained in

separate 76 liter holding tanks at 26° C. Male and female fish exhibiting the spotted “*bentosi*” phenotype or the non-spotted “*rosaceus*” phenotype, were selected at random from stock specimens, placed in separate 76 liter tanks, and allowed to develop at 26° C until sexually mature. Optimal water conditions were provided for all fish (i.e. low water hardness of 5° dGH, pH 6.5, and temperature 26°C) [3]. All progeny for this study were obtained from artificial fertilizations as previously described [10]. Parental fishes, exhibiting either the spotted (S) or unspotted (U) phenotype, along with F<sub>1</sub> progeny (F), were used in a series of 23 crosses (Table 1). Embryos from all crosses were incubated at 26° C in 250ml fingerbowls containing tank water. Dead or developmentally arrested embryos were removed daily. Fry hatched 24-36 hours post-fertilization and were free-swimming 96-120 hours post-hatching. Progeny groups were placed in separate 36 liter rearing tanks, fed initially on rotifers and allowed to develop until their phenotype could be visually determined. Since spotting is more defined in mature individuals, determination of spotting 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 U x F<sub>1</sub> crosses and F<sub>1</sub> x 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 parental fishes, observed phenotypic numbers, expected ratios, and probability of Fit for *H. bentosi* analyzed for the mode of inheritance of shoulder spotting. Parental fishes and progeny from all crosses clearly displayed either the spotted or unspotted phenotype. Spotted females SI, SII, and SIII and males S1, S2, and S3 were scored as homozygous dominants, as crosses involving these individuals always resulted in spotted progeny (crosses 1-4, 10-13). Parental fishes lacking shoulder spots (UI, UII, UIII, UIV females and U1, U2, U3, U4 males) were scored as homozygous recessives, as crosses amongst these individuals consistently bred true (crosses 5-9). Further, reciprocal crosses between spotted and unspotted parental fishes always resulted in spotted

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progeny (crosses 10-13). When these F<sub>1</sub> fishes (FII, FIV, F1, F2, and F3) were mated with parental fishes lacking the shoulder spotting (UI, UII, UIII, U3, and U4), both spotted and unspotted fry resulted and, based on Chi-square analyses, conformed to the expected 1:3 phenotypic ratio (crosses 14-18). In addition, crosses amongst F<sub>1</sub> fish always resulted in a satisfactory fit to a 9:7 genotypic ratio of F<sub>2</sub> progeny (crosses 19-23), commensurate with a modified 9:3:3:1 ratio resulting from dominant complementary gene action (A-B- is required for the spotted phenotype).

Results of this study support the hypothesis that shoulder spotting in *H. bentosi* is controlled by two loci acting in a complementary fashion, with dominance at both loci required for the expression of the spotted phenotype. Segregation patterns for the spotted and unspotted phenotypes of *H. bentosi* clearly fit an autosomal pattern of inheritance, as Chi-square tests do not deviate significantly from expectations. Results of heterogeneity tests also support the acceptance of the null hypothesis for this data. Further, observations of the extent of spotting in parental, F<sub>1</sub>, and F<sub>2</sub> fishes also suggest that these loci do not act in an additive fashion,

**Table 1. Probable Genotypes (PG), Observed Phenotypic Numbers, Expected Ratios, Degrees of Freedom (df), Chi-square Values (X<sup>2</sup>) and Probability of Fit (P) for Crosses Amongst Spotted and Unspotted *Hyphessobrycon bentosi***

Cross No.	Parents*		Phenotypic Numbers		Exp. Ratio	df	X <sup>2</sup>	P <sup>†</sup>
	♀ (PG)	♂ (PG)	Spotted	Unspotted				
1	SI (AABB)	x S1 (AABB)	35	0	1:0			
2	SII (AABB)	x S2 (AABB)	47	0	1:0			
3	SI (AABB)	x S3 (AABB)	48	0	1:0			
4	SIII (AABB)	x S1 (AABB)	56	0	1:0			
			Pooled	186	0	1:0		
5	UI (aabb)	x U1 (aabb)	0	32	0:1			
6	UI (aabb)	x U2 (aabb)	0	38	0:1			
7	UII (aabb)	x U1 (aabb)	0	28	0:1			
8	UIII (aabb)	x U3 (aabb)	0	24	0:1			
9	UIV (aabb)	x U4 (aabb)	0	35	0:1			
			Pooled	0	157	0:1		
10	SI (AABB)	x U1 (aabb)	32 (FI&1)	0	1:0			
11	SIII (AABB)	x U2 (aabb)	33 (FII&2)	0	1:0			
12	UI (aabb)	x S1 (AABB)	27 (FIII&3)	0	1:0			
13	UII (aabb)	x S3 (AABB)	40 (FIV&4)	0	1:0			
			Pooled	132	0	1:0		
14	UI (aabb)	x F1 (AaBb)	9	31	1:3	1	0.133	0.7150
15	UII (aabb)	x F2 (AaBb)	12	29	1:3	1	0.398	0.5281
16	UIII (aabb)	x F3 (AaBb)	8	27	1:3	1	0.086	0.7693
17	FII (AaBb)	x U3 (aabb)	13	37	1:3	1	0.027	0.8703
18	FIV (AaBb)	x U4 (aabb)	11	25	1:3	1	0.593	0.4414
			Heterogeneity			4	1.072	0.8986
19	FI (AaBb)	x F2 (AaBb)	36	30	9:7	1	0.078	0.7801
20	FII (AaBb)	x F1 (AaBb)	28	20	9:7	1	0.085	0.7711
21	FIII (AaBb)	x F4 (AaBb)	20	15	9:7	1	0.011	0.9164
22	FIV (AaBb)	x F3 (AaBb)	20	13	9:7	1	0.254	0.6140
23	FIV (AaBb)	x F4 (AaBb)	24	22	9:7	1	0.311	0.5773
			Heterogeneity			4	0.738	0.9465

\* (S) = spotted parental fishes; (U) = unspotted parental fishes; (F) = F<sub>1</sub> spotted offspring.

† The probability for all X<sup>2</sup> tests is > .05; thus, observed results for all matings fit the expected ratio according to Mendelian inheritance.

since there is no perceptible difference in the appearance of presumptive *aabb* parentals (U) with unspotted F<sub>2</sub> progeny, some of which would be heterozygous at one of the loci involved (i.e. *Aabb* or *aaBb*).

A similar mode of inheritance has been reported for trunk banding in the Sumatran tiger barb (*Barbus tetrazona*) [4] and the black tetra (*Gymnocorymbus ternetzi*) [9], and for trunk coloration in the three-spot gourami (*Trichogaster trichopterus*) [11] and the lyretail toothcarp (*Aphyosemion australe*) [12]. In these species, banding or color variation is also controlled by a pair of autosomal loci exhibiting dominant complementary gene action. In *H. bentosi*, the prominent dark shoulder spot most probably serves as a disruptive coloration pattern or as an “eye-spot” and, therefore, would give a selective advantage to those individuals possessing this feature by providing an interspecific signal to minimize predation.

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