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MASS SELECTION FOR INCREASED BODY WEIGHT AT HARVEST OVER FIVE GENERATIONS IN THAI SILVER BARB (Puntius gonionotus)

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INTRODUCTION

Silver barb (*Puntius gonionotus* Bleeker 1850) is an Asian carp that is popular as a food fish. It is distributed throughout Thailand in rivers, canals, reservoirs and swamps. It is also cultured in ponds and paddy fields. Its production from aquaculture in 2003 was estimated at 49,066 metric tons (14 per cent of the total fish production), and valued at 34.6 millions US dollars (Dept. of Fisheries, 2005), ranking third among freshwater fishes cultured in Thailand.

However, the performance of many hatchery populations of silver barb is low, mainly due to a lack of improved stocks. Preliminary results indicate that relative to local available stocks, a Silver barb strain in the Chao Phraya (CP) River has a higher growth potential, and that there is substantial additive genetic variation in body traits (reviewed by Pongthana, 2005), suggesting that performance of this species may be improved by selective breeding. In view of this situation, a selection program for increased growth rate in CP Silver barb strain was started in 1998. In this paper we describe the program and present the results on the achieved response to selection.

MATERIAL AND METHODS

Experimental location and genetic material. The breeding program was conducted at the Pathumthani Fisheries Test and Research Center, Aquatic Animal Genetics Research and Development Institute, Department of Fisheries, Pathumthani province, Thailand (latitude 14≤N, longitude 100≤E, 20 km north of Bangkok). The base population from which the selection and control lines were developed was obtained from the CP River in Nakhonsawan Province. One hundred brooders (50 males and 50 females) were collected from the river and used as parents to produce the first generation offspring.

Production of families and selection procedures. The first generation of silver barb was produced in June 1998 from the Chao Phraya River strain. To generate the full sib progeny groups, single pair matings were performed by the hypophysation technique using carp pituitary extracts. A total of 50 full sib families were generated. Two-day old hatched fry were kept in separate hapas (VVI m³) installed in one 70 m³ concrete tank with a water depth of 70 cm at a stocking density of 10000 fry per hapa, and one hapa per family. Fry were fed with rotifers and Moina sp. ad libitum. After nursing for one week, 240 fry from each of the 50 families were randomly selected and transferred to nurse together in a 600 m³ earthen pond at a stocking density of 20 fish per m3, or 12000 fish per pond. Fry were fed with commercial powder feeds ad libitum. After nursing for one month, 1200 randomly selected fingerlings were allocated to one 600 m³ earthen pond to be reared as generation 1 (G1) stock at a stocking density of 2 fish per m³. Fish were fed three times a day with commercial pellets at 3% body weight. Monthly growth performance was observed in a random sample of 100 fish, measuring body weight, total length, body depth and body width. After 6 months grow-out in earthen pond, body weight was recorded in all surviving fish. Male and female G1 brooders were selected from among 10% G1 stock with the greatest body weights. Control G1 brooders

were selected from male and female fish of the G1 stock with average body weights. Progeny from the G1 selected parents were sampled, with 1200 fingerlings assigned to each of two 600 m³ earthen ponds. One pond provided the stock for the ensuing selection cycles, whereas a second one provided the stock for the genetic gain trial (see section 'Estimation of genetic gain' below). The same procedures for family production and selection were carried out throughout the experimental period of five generations (Table 1). Note that a separate control line was not established, instead, the 'control' fish were re-created by selecting average individuals from within each generation.

Table 1. Information on the breeding program from generations 1 to 5

Generation	Brooders	Brooders	Stock	Stocking	Stocking	Harvest
		(pairs)		number	Dates	Dates
1	Chao Phraya	50	Gi	1200	Jul'98	Mar'99
2	Selected G1	50	G2	1200	Jul'99	Jan'00
3	Selected G2	50	G3	1200	Jun'00	Dec'00
4	Selected G3	60	G4	1200	Aug'01	Mar'02
5	Selected G4	60	G5	1200	Jul'02	Jan'03

Estimation of genetic gain. Genetic gain was estimated from performance evaluations of the offspring of the selected and control brooders following a grow-out period of 6 months (Table 2). Offspring of the control group were produced by 30 single mating pairs of the control in each generation. Grow-out testing of the control fish was carried out in three 100 m³ earthen ponds (2 fish per m³). Fingerlings of the selected line from the second 600 m³ pond were also stocked in three separate 100 m³ earthen ponds at the same density and conditions as the control, except in G5 where selected and control fish were communally reared. Other procedures of fry and fingerling rearing, culture management, harvesting and measurement of the fish were practiced in the same manner as described above.

Table 2. Performance testing of the selected and control progeny

Group	No. of selected Brooder	No. of control brooder	Stocking Selected and Control fish	No. of pond	Pond size (m³)	Stocking number (fish/pond)	Stocking Dates	Harvest Dates
G2	50	30	Separate	12	100	200	Jul'99	Jan'00
G3	50	30	Separate	6	100	200	Jun'00	Dec'00
G4	60	30	Separate	6	100	200	Aug'01	Feb'02
_G5	60	30	Communal	3	600	1200	Jul'02	Jan'03

Statistical analyses. Data were collected over five years (1999 to 2003) on 7699 individuals from the genetic gain trial. Preliminary analyses using a general linear model tested significance of all possible effects associated with body weight, length, depth and width. The final mixed model included the random effect of testing ponds and the fixed effects of sex (male and female), group (selection and control), generations (4 classes) (all P<0.001) and two-way interaction between group and generation (P<0.05). All analyses were carried out using SAS (SAS/STAT software, 1997).

RESULTS AND DISCUSSION

Figure 1 shows the direct response in body weight and the correlated responses in body length, depth and width at harvest. Over five generations, the differences in body weight between the selection and control fish were all statistically significant (P<0.001). The responses in body weight for generations 2 to 5 were 35.3, 56.9, 30.1 and 14.5%, respectively, expressed as a

percentage of the control. The average genetic gain of 34% was high and could be biased upwards. The reason(s) is not known but unintended differences between the grow-out ponds of the two lines are suspected. Generally responses have been more conservative (e.g. Ponzoni et al., 2005). Note that in the fifth generation both lines were communally grown out, and the response was smaller and of the order reported in the literature.

Although selection was for body weight only, correlated responses achieved for body length, depth and width were all in a positive direction and following a pattern similar to that for growth rate. This resulted from the high and positive correlations between body weight and length, depth or width. The estimates of the residual correlations among the traits using the MANOVA procedure in SAS (SAS/STAT software, 1997) ranged from 0.55 to 0.83 (P<0.001). However, the extent of the pleiotropic gene effects on these traits for this species needs to be verified by future estimation of genetic correlations.

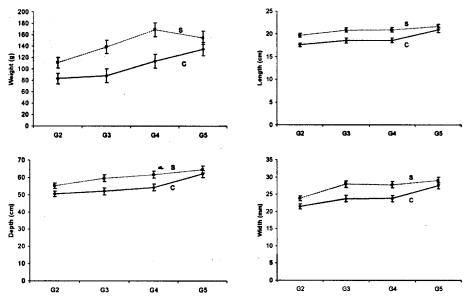


Figure 1. Selection (S) line and Control (C) group least squares means for body weight, body length, depth and width at harvest in generations 2 to 5

CONCLUSION

The selection line had significantly greater body weight than the control. However, there could be a bias in the estimate of the response in generations 2 to 4 due to the growing out of control and selected fish in different ponds. In generation 5, when a decision was made to communally rear control and selected fish, the response was smaller than in earlier generations. Although the number of pairs mated each generation would appear to be sufficient to maintain inbreeding at a satisfactory level (Bentsen and Olesen, 2002), the relatively intense selection (10%) could have resulted in a reduction of the effective population size. Hence, the breeding program is currently being reinvigorated by crossing with other stock, maintaining a full pedigree, and fitting an individual animal model to estimate genetic merit and select replacements. This will enable a more rigorous conduct of the genetic improvement program and the monitoring of the genetic trends from the average breeding values in different generations.

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