North American Journal of Aquaculture 73:49–52, 2011

ISSN: 1522-2055 print / 1548-8454 online
DOI: 10.1080/15222055.2011.544942

COMMUNICATION

Inheritance of Long Fins in Ornamental Koi Carp

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Abstract

Inheritance of long fins in ornamental koi carp *Cyprinus carpio* was studied. Fish segregations with regard to the presence or absence of long fins in two progenies were recorded and analyzed. In progeny 1, produced by crossing a long-fin koi female with a short-fin (wild-type) koi male, the observed segregation of long-fin fish : short-fin fish did not differ significantly from the 1:1 Mendelian ratio. In progeny 2, produced by crossing the same long-fin female with a long-fin male, the observed segregation of long-fin fish : short-fin fish did not differ significantly from the 3:1 Mendelian ratio. Based on these data, it was concluded that the appearance of long fins in koi is under the control of a dominant mutation of one gene (*Lf/lf*). Fish with genotypes *LfLf* and *Lflf* have long fins, while fish with genotype *lflf* do not have this trait. Since the appearance of long fins in koi is controlled by a dominant mutation, the development of a true-bred, long-fin line could be achieved only by identifying heterozygotes *Lflf* by means of test crosses and removing them from the stock.

The Japanese ornamental koi carp *Cyprinus carpio* is one of the most popular decorative fish in many countries all over the world, including the United States. Koi were developed approximately two centuries ago in Japan (Kuroki 1981; Davies 1989). The long-fin variety of koi, also called butterfly koi, is a relatively new morph that has been developed in the last several decades. In the United States, long-fin koi have been developed at Blue Ridge Fish Hatchery (North Carolina) from the middle 1980s by crossing of normal short-fin koi with the long-fin common carp of Asian origin (LeFever 1991, 2010). This long-fin carp apparently originated from Indonesia, where a local long-fin strain of common carp (also called "kumpay") has been described (Kirpichnikov 1981; Sumantadinata 1995; Emmawati et al. 2005). Long-fin common carp has also been found in the southwestern part of China (Wang and Li 2004). There is information (Anonymous 1988) that the long-fin morph of koi was obtained in Japan in the early 1980s by crossing koi with Indonesian long-fin carp. In Japan, long-fin koi are not allowed to be demonstrated at koi competitive shows (Anonymous 1988; Christensen 1999). Therefore, their popularity in Japan and some other countries is relatively low. However, long-fin koi are very popular in the United States, and many fish farms cultivate them for sale.

Publications on the origin and characteristics of long-fin koi (LeFever 1991, 2010) do not contain any information on the inheritance of this trait, and no data on this subject are available. The present study reveals the mode of inheritance of long fins in koi.

METHODS

The experiments were conducted at the Aquaculture Research Center, Kentucky State University (KSU), Frankfort. Two progenies were produced, and fish segregations with regards to presence or absence of long fins in these progenies were recorded and analyzed.

Progeny 1 was produced by crossing a long-fin, white-red koi female with a short-fin (wild-type), white-red koi male. Progeny 2 was produced by crossing of the same long-fin, white-red female with a long-fin, white-red-black male. Long-fin and short-fin fish parents used in crosses were chosen from broodstock without any previous knowledge of their genotypes because no preliminary crosses were performed. To induce final oocyte maturation in female and spermiation in males, fish parents were injected with carp pituitary extract (Sigma Chemical, St Louis, Missouri) at 3 mg/kg of body weight. Eggs were artificially inseminated in plastic bowls and were treated with a water–cow milk mixture (volumetric ratio = 8:1) to remove adhesiveness. Embryos were incubated in McDonald's jars. Approximately 3,000 swim-up larvae from each progeny group (quantities were evaluated by volumetric method) were stocked into two separate 20-m^3 outdoor tanks for rearing. Tanks were supplied with water from a 0.2-ha reservoir. During 5.5 months of rearing, fish were fed an artificial diet; fish also consumed zooplankton and benthic organisms that were developed in tanks and flowed in with the reservoir water. Two months after stocking, several hundred

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Received April 14, 2010; accepted June 16, 2010
Published online February 2, 2011

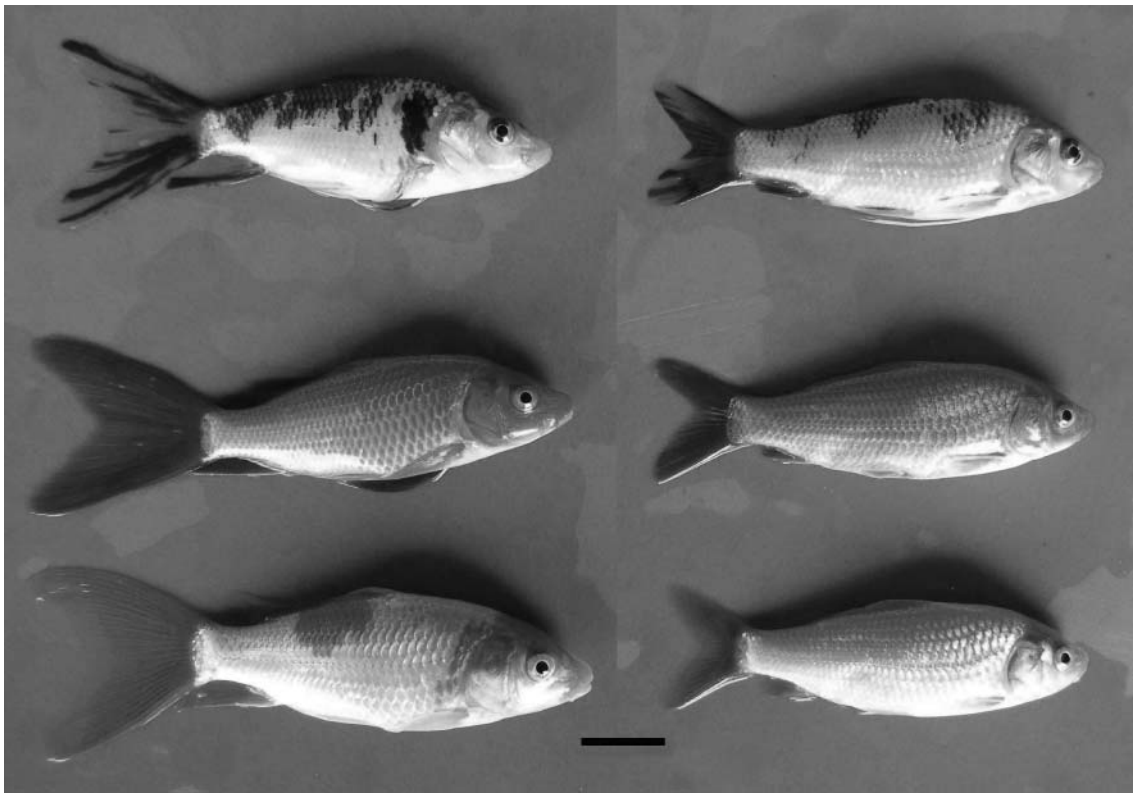

FIGURE 1. Long-fin (left) and short-fin (right) fish from progeny 2; bar = 2 cm.

fry were randomly removed from each tank to decrease fish density and provide better growth conditions for the remaining fish.

After 5.5 months of rearing, tanks were drained and all fish were collected and analyzed. Fin type (long-fin or short-fin) and color of each collected fish were recorded. Samples of long-fin and short-fin fish from progenies were taken for individual measuring; fish total length (TL) and standard length (SL) were measured. Based on length measurements, the percentage index "relative tail length" (RTL) was calculated for each fish in samples (according to the formula [TL—SL] × 100/SL). The typical numbers of fish in samples taken for measurements were 21 or 24. However, 100 long-fin fish from progeny 2 were measured since the distribution of fish in this category with regard to RTL was obtained and analyzed.

Segregations of fish in progenies with regard to both fin and color types were compared using a chi-square test (Zar 1999). Differences in mean RTL values between different groups of fish were evaluated by a Student's *t*-test (Zar 1999). Distribution of long-fin fish from progeny 2 with regard to the RTL index was compared with normal distribution by means of a Kolmogorov–Smirnov goodness-of-fit test (Zar 1999).

RESULTS

Numbers of fish analyzed and segregations of long-fin fish : short-fin fish in progenies 1 and 2 are given in Table 1. As an illustration, a photograph of several fish from progeny 2 is presented in Figure 1. In progeny 1, the observed segregation of long-fin fish : short-fin fish did not differ significantly ($P > 0.05$) from the 1:1 Mendelian ratio. In progeny 2, the observed segregation of long-fin fish : short-fin fish did not differ significantly from the 3:1 Mendelian ratio ($P > 0.05$).

In progeny 1, the mean ± SD SL and TL of short-fin fish were 5.65 ± 0.88 cm and 6.87 ± 1.03 cm ($n = 21$), respectively, while those of long-fin fish were 5.79 ± 0.68 cm and 8.18 ± 0.97 cm ($n = 24$), respectively. In progeny 2, the mean ± SD SL and TL of short-fin fish were 7.83 ± 1.36 cm and 9.48 ± 1.63 cm ($n = 24$), respectively, while those of long-fin fish were 6.92 ± 1.17 cm and 9.93 ± 1.55 cm ($n = 100$), respectively. The mean ± SD RTL indices were 21.73 ± 2.61% and 40.98 ± 3.42% for short-fin and long-fin fish and 21.23 ± 2.27% and 43.91 ± 4.30% in progenies 1 and 2, respectively. In both progenies, the differences in mean RTL indices between short-fin and long-fin fish were statistically significant ($P < 0.001$). Long-fin fish had a 1.89 and 2.07 times larger mean RTL index than short-fin fish in progenies 1 and 2, respectively. Distribution of long-fin fish in progeny 2 with regard to the RTL index is given in

TABLE 1. Characteristics of progenies and segregation of fish with regard to fin length.

Progeny number	Female phenotype	Male phenotype	Number of fish analyzed	Segregation (%)		Proposed type of cross	Proposed theoretical segregation
				Long fin	Short fin		
1	Long fin	Short fin	377	49.6[a]	50.4[a]	*Lflf* × *lflf*	1:1
2	Long fin	Long fin	222	72.1[b]	27.9[b]	*Lflf* × *Lflf*	3:1

[a]Not significantly different from 1:1 ($P > 0.05$).
[b]Not significantly different from 3:1 ($P > 0.05$).

Figure 2. This distribution did not differ significantly ($P > 0.05$) from normal.

DISCUSSION

Long-fin and short-fin fish segregations in progenies 1 and 2 did not differ significantly from Mendelian ratios of 1:1 and 3:1, respectively. Based on these data, it may be concluded that appearance of long fins in koi is under the control of a dominant mutation of one gene (*Lf/lf*). Fish with genotypes *LfLf* and *Lflf* have long fins, while fish with genotype *lflf* do not have this trait. Proposed genotypes of fish parents used in crosses are shown in Table 1. These are the first reported data on inheritance of long fins in koi. Earlier, Tan and Phang (1994) revealed that elongation of fins in zebrafish *Danio rerio*, which belong to the same Cyprinidae family as koi, is also caused by a dominant mutation of one gene.

Long-fin koi are characterized by elongation of both paired and unpaired fins. In order to characterize the rate of fin elongation quantitatively, we calculated and compared the RTL index. In both progenies, the mean RTL index is approximately two times larger in long-fin fish compared with short-fin fish.

Since the phenotypic ratio of fish with long and short fins in progeny 2 was close to 3:1, the category of long-fin fish should consist of heterozygotes *Lflf* and homozygotes *LfLf* with a ratio of 2:1. Distribution of long-fin fish in progeny with regard to RTL index did not differ significantly from a unimodal normal distribution. This indicates that the *Lf* allele is characterized by complete dominance. If incomplete dominance for this allele occurred, the difference between fish with genotypes *Lflf* and *LfLf* would have resulted in a bimodal distribution of fish with regard to RTL index.

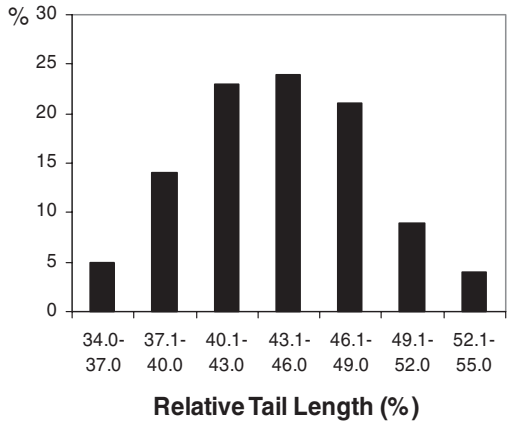

FIGURE 2. Distribution of long-fin fish in progeny 2 with regard to the relative tail length index.

In both analyzed progenies, short-fin and long-fin fish did not differ significantly with regard to color segregations (data not presented). This indicates that mutation causing elongation of fins is not associated with color traits.

The results of the present study should be taken into account by producers of long-fin koi who are interested in developing a true-bred, long-fin line of koi (giving only long-fin fish in consecutive generations). Since appearance of long fins is controlled by a dominant mutation, it would be relatively difficult to develop a true-bred, long-fin line since the crossing of two heterozygotes (*Lflf*) gives the mixed progeny. Development of a true-bred, long-fin line could be achieved only by identifying heterozygotes *Lflf* by means of test crosses and removing them from the stock. For identification of fish genotypes, long-fin fish should be test crossed with short-fin fish (*lflf*): crosses of homozygous fish *LfLf* will produce only long-fin fish (*Lflf*), while crosses of heterozygous fish *Lflf* will result in progenies consisting of long-fin fish and short-fin fish with the 1:1 ratio.

ACKNOWLEDGMENTS

Support for this study was provided by Kentucky's Regional University Trust Fund to the Aquaculture Program as KSU's Program of Distinction. The authors thank Robert Durborow for valuable suggestions and Sid Dasgupta for advice on statistical treatment of the obtained data. Special thanks to Andrei and Lena Bukin for advising on literature sources on the subject in koi literature and providing copies of some articles.

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