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Genetic analysis of common carp (*Cyprinus carpio*) strains
I: Genetic parameters and heterosis for growth traits and survival

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ABSTRACT

The aim of this study was to estimate genetic parameters and heterosis for weight, length and survival traits for common carp measured at different time periods at commercial farm conditions. A diallel cross between two land race strains (Duna and Amur), and two farmed strains (Tata and Szarvas 15) was used. Five females and 10 males per strain were used to produce six families for each of the 16 cross combinations resulting in 96 families each with 20 fish. The fish were weighed at tagging (W0), and also their length were measured at first autumn (W1, L1), second spring (W2, L2), and second autumn (W3, L3). Survival was defined as survival from second spring (W2) to second autumn (W3). Heritabilities for weight and length traits were estimated using univariate models, whereas genetic correlations and heritabilities for survival were estimated using multivariate models. The difference between the strains with respect to survival was clearly significant with Duna having the highest expected survival rate (81%), followed by Amur (69%), Tata (53%) and Szarvas 15 (51%). The level of heterosis (cross vs. purebred) varied from −14 to 29% for weight traits, from 1.7 to 8.3% for length traits, and from 8–37% for pond survival. Heritabilities were low for early weight and length traits (W0, W1, W2, L1, and L2, 0.11–0.16) but high for W3 and L3 (0.49, 0.50). For survival the heritability on the underlying scale was 0.34 ± 0.09 corresponding to a heritability of ~0.2 on the observable scale. High genetic correlations (0.81–0.98) were estimated between weight and length measured at the same time (W2/L2, and W3/ L3) and between weight measured in the first autumn (W1) and second spring (W2). Genetic correlations between weight and survival were low and non-significant for W2 (0.06 ± 0.35), but high and significant for W3 (0.65 ± 0.15). The high levels of heritabilities for length and weight at harvest (W3) and the moderate heritability for survival indicate that selective breeding for these traits could be successful in common carp.

1. Introduction

The common carp is one of the most important farmed freshwater fish species in the world (FAO, 2008). However, unlike other aquacultural species, selective breeding programs for common carp are not frequently implemented. Breeding programs in common carp are in general characterised by developing different strains, which are used for crossbreeding. High level of heterosis exists for traits related to growth (e.g. Hulata, 1995; Linhart et al., 2002; Vandeputte, 2003), which may explain why crossbreeding has received much attention in this species. However, some pure strains appear to perform about as well as the best crosses (Wohlfarth et al., 1975). One of the problems related to crossbreeding in common carp is that a large part of the observed heterosis most likely is caused by the fact that the parental strains are highly inbred. However, this may be a problem since inbreeding usually implies reduced performance for both fitness traits (e.g. survival, resistance to diseases and reproduction) and production traits (e.g. growth rate) thus adding extra cost for maintaining the strains. In addition, crossbreeding itself gives no accumulated progress in the long run and therefore should be looked upon as a supplement to pure breeding, i.e., selection for additive genetic effects within the parental strains (e.g. Bowman, 1959; and discussion in Gjerde, 1988).

Selective breeding programs to exploit additive genetic variation has not been widely implemented in common carp, maybe due to the early results of no response to within-spawn selection for increased growth rate in ponds over five generations (Moav and Wohlfarth, 1976). However, Brody et al. (1980) found large differences in growth between half sib families of common carp, and Brody et al. (1981) estimated the heritability of growth in common carp at 0.47 from parent offspring regression. More recently, Vandeputte et al. (2008) reported a heritability of 0.44 for harvest body weight in common

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carp using records from three generations. Nevertheless, the majority of worldwide common carp production has so far been based on non-improved genetic stocks (Vandeputte, 2003). The development of genetically improved strains of common carp has thus a large potential for a more efficient production.

Genetic improvement programs for common carp should be tailored to improve traits related to production as well as fitness such as survival and resistance to the koi herpes virus which has become a problem in European common carp production (Hedrick et al., 2000; Haenen et al., 2004). This involves selection for additive genetic effects and strategies for capitalizing also on non-additive genetic effects [e.g. by creating a synthetic population (Skjervold, 1982)] if such effects are found to be of importance. Introducing selective breeding programs in European common carp would provide potential for increased productivity and production efficiency in the industry.

In several large-scale experiments and selective breeding programs in other fish species, up to 15% genetic change has been obtained per generation (Gjedrem, 2000). In order to design a practical and efficient selective breeding program for common carp there is a need to obtain accurate estimates of genetic parameters; i.e., heritabilities of the traits of interest and genetic correlations among the traits, and to gain a better understanding of the relative performance of different strains and their crosses for traits of importance to the industry. Heritability estimates for weight and length varies from zero to 0.55 (see review by Vandeputte, 2003) but many of these estimates are expected to be biased upwards due the design applied (e.g. difficulties to separate the environmental and non-additive genetic effects common to full-sibs from the additive genetic effects when full-sib families are reared in separate tanks until tagging). Therefore, Vandeputte (2003) concluded that the reliability of most existing heritability estimates in common carp are low. In addition, genetic parameters of fitness traits such as survival and disease resistance (Vandeputte, 2003) are scarce.

This study is part of a large EU project aiming at identifying disease and stress resistant common carp strains, families and individuals (EUROCARP, Project no. 022665). In this paper we report on genetic parameters and heterosis for body weight, length, and survival traits measured at different time periods for fish produced from a complete diallel cross between four strains and farmed in an earthen pond at a commercial farm. The main aim of this study was to estimate the genetic variation within and between the four strains of common carp for growth and survival traits. Secondly, the aim was to establish a broad genetic base to be used for further selective breeding.

2. Material and methods

2.1. Fish material and crossing design

Fish used in the experiment were breed by the Fish Biology Department at the Research Institute of Fisheries, Aquaculture and Irrigation (HAKI), at Szarvas, Hungary and were from four different strains provided from the live gene bank of common carp (Gorda et al., 1995). There were two strains representing “wild” strains (Duna and Amur), which are native in the Danube and Amur rivers but have been kept in the live gene bank by HAKI for at least three generations, and two farmed strains (Tata and Szarvas 15). Tata is presumably an inbred strain that has been selected for rapid growth and round body shape, and Szarvas 15 has been selected for high heterosis in line crosses (Bakos and Gorda, 1995). These four different strains were selected based on known origin and their documented breeding history in order to obtain the widest possible genetic differences between the strains.

A diallel cross design between the four common carp strains was applied (Table 1). Five females and 10 males per strain were used to produce six full-sib families for each of the 16 cross combinations (four purebred strains and their six crossbred strains with reciprocals), resulting in 96 different families in total. The number of fish produced and individually tagged within each of the 96 family was 100. However, for one of these families, 400 fish were produced. Each of the 96 families with 100 fish each (plus the 300 extra fish from one family) was held in separate tanks with a volume of 250 l such that the total number of tanks was 99. The diallel cross design was optimised in order to be able to separate additive genetic effects from tank effects (an effect common to all members of the full-sib family) and heterosis effects. Thus each dam was mated to six sires and each sire was mated to three dams.

Table 1
Schematically presentation of the applied diallel crossing design between the four carp strains Duna, Amur, Tata, and Szarvas 15. Five females and ten males per strain was used to produce six full-sib families for each of the sixteen cross combinations (four purebred strains and 12 crossbred strains including the reciprocals).

Female		Duna					Amur					Tata					Szarvas 15				
Male	N°	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
Duna	1	X							X									X			
	2	X							X									X			
	3		X									X							X		
	4		X									X							X		
	5			X									X								
	6			X									X								
	7						X							X							
	8						X							X							
	9							X									X				
	10							X									X				
Amur	1				X		X														X
	2				X		X														X
	3					X									X		X				
	4					X									X		X				
	5	X														X					
	6	X														X					
	7									X		X									
	8									X		X									
	9										X									X	
	10										X									X	
Tata	1		X							X									X		
	2		X							X									X		
	3			X									X							X	
	4			X									X							X	
	5				X									X							
	6				X									X							
	7							X							X						
	8							X							X						
	9								X									X			
	10								X									X			
Szarvas 15	1					X		X									X				
	2					X		X									X				
	3	X														X		X			
	4	X														X		X			
	5		X																		
	6		X																		
	7										X	X									
	8										X	X									
	9						X						X								X
	10						X						X								X

2.2. General management and recordings

2.2.1. Mating and production of fry

The production of the full-sib families took place at HAKI on May 12, 2006. Males and females were held in separate tanks before artificial reproduction. Males were injected with carp pituitary (CP) with a dose of 2 mg/kg body weight and females received CP in a dose of 0.5 mg/kg body weight. Twelve hours later all males were stripped and the individually collected samples of sperm were stored at 1–3 °C. After collecting the sperm, the females were treated secondary with CP of 4.0 mg/kg of body weight and the genital pores were sutured. In all cases CP was homogenized and dissolved in 0.65% NaCl solution. All