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SELECTIVE BREEDING PROGRAMME OF COMMON CARP (CYPRINUS CARPIO L.) IN SERBIA-PRELIMINARY RESULTS

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Abstract: The aim of this study was to estimate heritability and genetic correlations between weight, length and height of common carp in Serbia (Cyprinus carpio L.) during 3-year growth period. The 50 families of common carp were produced in 2007 and used for the estimation of genetic parameters. The fish were measured at tagging for weight, length and height (W0, L0, H0), then during the first autumn (W1, L1, H1) and during the second autumn (W2, L2, H2). Based on univariate models heritability estimates were high for all traits (0.39, 0.34 and 0.45 for W1, L1 and H1, respectively) and also for the second production year (0.49, 0.47) and 0.44 for W2, L2 and H2, respectively). The genetic correlations were estimated using multivariate models and they were high between W1 and L1 and H1 $(0.81 \pm 0.06 \text{ and } 0.91 \pm 0.03 \text{ for L1} \text{ and H1, respectively)}$, while between H1 and L1 were moderately correlated (0.54 \pm 0.12). In the second production year genetic correlations were also high, between W2 and L2 and H2 (0.64 ± 0.09 and 0.74 ± 0.06 , respectively), while between length and height they were lower (0.24 \pm 0.15). Based on the current results improving growth rate of common carp through genetic selection is expected to be effective.

Key words: carp, selective breeding, heritability, genetic correlation.

Introduction

Common carp (*Cyprinus carpio* L.) is one of the most widely cultured fish in the world, especially in Asia and Central and Eastern Europe. The early beginnings of fish stocking for human consumption are related to this species and according to some authors this practice started more than 2500 years ago in China. Ancestors of

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today's carp are native to tributaries of the Black, Aral and Caspian Sea where the species spreads eastward into Siberia and China, and westward to the basin of the Danube (Balon, 1995). Today, this species is represented by the two subspecies: the East Asian subspecies of Cyprinus carpio haematopterus (Amur River basin and rivers and lakes of Southeast China) and Eastern European subspecies of Cyprinus carpio carpio, which is located in the Caucasus region, Central Asia and across Europe. According to some researchers there is the third subspecies named Cyprinus carpio viridiviolaceus, which inhabits the waterways of Vietnam, Laos, Burma and Southern parts of China, but according to other scientists this subspecies is questionable and it is most likely one variety of the subspecies of Cc haematopterus. The domestication of carp, which led to five clearly defined races (Galician, Bohemian, Franconian, Lausitz and Ayschgrund) and to a great number of local landraces, started in the 16th century and lasted until the 19th century (Kirpichnikov, 1999). Although, common carp production is on the top of the world aquaculture most of this production comes from non-selected strains of carp (Hulata, 1995). Selective breeding for fast growing common carp in the past has been unsuccessful; however, the selection for traits such as resistance to some disease or shape of common carp gave the results. Estimates of heritability and other genetic parameters that could be found in the older literature were mainly compromised by environmental effects. On the other hand, some articles on population genetics and testing genetic differences between different strains of carp show that the selection is possible for characteristics such as the pace of growth as well (Vandeputte, 2003). This primarily depends on the variability of the population that is selected, if the population shows satisfactory properties by selecting the variability can be achieved in the selection process, in this respect, synthetic population, resulting from a combination of different populations from open water and cultivated populations, provide the most opportunities (Vandeputte et al., 2004). The aim of the present study was to estimate genetic parameters for growth-related traits in the established base population. The growth traits were assessed during the three production years to document the potential for genetic improvement of common carp in Serbia through family based selective breeding program.

Materials and Methods

Broodstock and mating design

The mating of broodstock and producing of families were carried out at the Centre for fishery and applied hydrobiology, CFAH, Faculty of Agriculture, University of Belgrade in Serbia. Broodstock was obtained from commercial fish farm and the rest of fish was captured from the river Tisa. There have been no previous records about these broodfish or about their production qualities, but it is sure that these fish farms do not use fish from rivers as the replenishment for the breeding candidates. Altogether, there were 70 broodfish collected and kept

together in 0.40 ha earthen breeding pond until time of mating. A partly factorial mating design was used to produce 48 full-sib families (Table 1). Within these families, there were 14 paternal half-sib groups and 24 maternal half-sib groups (Spasić at al., 2009).

Table 1. Mating scheme of broodstock.

Sex 1										3											
2	52	54	56	59	60	61	63	64	65	66	67	68	69	70	71	72	73	76	77	78	79
1	X																	X			
3							X					X									
3 5 7						X			X												
7								X										X			
8 9				X												X					
					X											X					
10					X	X															
12										X					X						
13														X					X		
14															X	X					
16										X						X					
17	X	X	X																		
20													X				X				
22						X										X					
23							X					X									
24 25															X		X				
25															X						X
27							X				X										
28																			X	X	
30						X											X				
33					X																X
34															X	X					
35							X					X									
36															X		X				

Spawning and hatching

Mature broodfish were selected in May 2007 and were stored at a hatchery in two 6 m³ tanks, where females and males were kept separate. Water flow rate in these tanks was 0.15 l s⁻¹, temperature 19-23°C and 6.6-7.4 mg l⁻¹ of O₂. The age of broodfish was between 3 and 5 years, and they were considered healthy and in good condition. The spawning of broodfish was induced by intramuscular injections of a solution of dried carp pituitary (FAO, 1985). Twenty-four dams were injected twice with dried carp pituitary (0.3 and 3.5 mg kg⁻¹, 36 and 12 h before stripping, respectively) at 21°C. Twenty-one sires were injected with a solution of carp pituitary 12 h before stripping. Both females and males were anesthetised before injection procedure by use of phenoxyethanol (conc. 1:5 000).

All breeders were pictured and measured for weight, length and height. Samples of scales were also taken and used for age determination (Spasić at al., 2009). Artificial insemination was done by the Woynarovich method (Woynarovich and Woynarovich, 1980). After fertilisation, eggs were put in 20 l plastic jars with plastic nets, marked with family combination. Range of water temperature during incubation period was 20-22°C, pH value 7.92-8.07 and oxygen concentration was 6.56-7.04 mg l⁻¹. After 3 days of incubation unfertilised eggs and eggshells were removed and after two weeks hatched larvae were put into 70 l Plexiglas tanks. Feeding of larvae started on the 3rd day after hatching using live *Artemia nauplii*, every 2 h for the first month. After 2 weeks there were about 100 individuals left per tank (family) and body weight/biomass per tank was measured. From this point onwards, a uniform feeding schedule was employed. The amount of feed was 4% of biomass, given every 3 hours. During the next month live feed was combined with powder complete feed for carp fry (48% of proteins and 10% fat). From the 3rd month of hatching, a fry was fed solely by complete carp extruded feed (38% protein + 12% fat).

Tagging

In October 2007, 1,812 fingerlings were randomly sampled and individually tagged with Passive Integrated Transponder (PIT) tags (11 x 2.1 mm), implanted into the abdominal cavity. An average number of tagged fingerlings per family were 38 and mean body weight was 13 g.

Rearing of experimental fish

After tagging, fingerlings were stocked into two 870 m² nursery earthen ponds at a stocking density of ~10 000 fingerlings/ha. Fish were additionally fed on a commercial carp diet SF 32/10 and SF 38/12 according to the estimated quantity of zooplankton and bottom fauna. This stocking density was something lower than usual. Used feeding ratios are typical for carp production in Serbia (Marković and Mitrović-Tutundžić, 2003; Dulić, 2006).

Recorded traits

Individual body weight, length and height of the fish were recorded three times, first at 5 months of age (at tagging in October 2007) at 18 months of age (in November 2008) and the third time at 28 months of age (in September 2009). Fish were weighed with precision of \pm 0.01 g and for the height and length (from the tip of the nose to the end of the caudal peduncle) to the nearest millimetre.

Statistical analysis

Initial univariate analysis of weight, length and height was conducted to test significance of model factors. The final model included fixed effect of pond (2

levels in the first year and 3 levels in the second year) and random additive genetic effects. Random common environmental effect of full-sib family was tested but it was not significant for any of the traits. Variance components, heritabilities and genetic correlations between traits were estimated in a multivariate analysis using the DMU software (Madsen and Jensen, 2007). The model had the following characteristics:

$$Y = \begin{bmatrix} Y \text{ weight} \\ Y \text{ length} \\ Y \text{ height} \end{bmatrix} = Xb + Zu + e$$

where Y is the vector of observations, b is the vector of fixed effects (containing effects of pond and year for each trait), $u = [u]_{weigh} u_{length} u_{heigh} = N(0, G \otimes A)$ is the vector of random additive genetic effects for the three traits, and e e = $[e]_{weigh} e_{length} e_{heigh} = N(0, R \otimes I)$ is the vector of random residual effects. X and Z are known incidence matrices, and G and R are the (co)variance matrices of additive genetic and residual effects, respectively.

Results and Discussion

Phenotypic variation for weight, length and height

The mean, standard deviation and coefficients of variation (CV, %) for weight, length and height of fish during the three production years are presented in Table 2.

Table 2. Mean, standard deviation (SD) and coefficient of variation (CV, %) for body weight (W), total length (L) and height (H) during the three production years.

Traits	No. of fish	Mean	SD	CV (%)
W0	1812	12.73 g	9.91	77.85
L0	1812	79.33 mm	16.24	20.47
Н0	1812	25.32 mm	6.42	25.36
W1	1157	453.34 g	171.09	37.74
L1	1157	28.21 cm	4.15	14.71
H1	1157	8.83 cm	13.49	15.28
W2	929	1002.95 g	386.36	38.52
L2	929	37.77 cm	4.90	12.97
H2	929	11.63 cm	1.95	16.77

W0-weight of 5 months old fish; L0-length of 5 months old fish; H0-height of 5 months old fish; W1-weight of 18 months old fish; L1-length of 18 months old fish; H1-height of18 months old fish; W2-weight of 28 months old fish; L2-length of 28 months old fish; H2-height 28 months old fish. SD-standard deviation; CV-coefficient of variation.

Heritabilities and correlations

Heritabilities and genetic correlations estimated from the multi-trait model are shown in Table 3. Heritability estimates in the first production year were significantly different from zero for all three traits studied, and they varied between 0.34 and 0.45. The genetic correlations between weight and height and between weight and length were very high (0.81 and 0.91, respectively), while a lower genetic correlation was estimated between length and height (0.54). In the second production year heritabilities were also high and they varied between 0.44-0.49, while genetic correlations were lower than in the first year, especially between length and height (0.24). The genetic correlation between weight and length and between weight and height were moderate high (0.64 and 0.74, respectively).

Table 3. Multi-trait animal model heritabilities \pm S.E. (diagonal), genetic correlations \pm S.E. (bold) for growth-related traits in the first and second production year.

Year 2008	W1	L1	H1		
W1	0.39 ± 0.09	0.81 ± 0.06	0.91 ± 0.03		
L1		0.34 ± 0.09	0.54 ± 0.12		
H1			0.450 ± 0.08		
Year 2009	W2	L2	H2		
W2	0.49 ± 0.09	0.64 ± 0.09	0.74 ± 0.06		
L2		0.47 ± 0.08	$\boldsymbol{0.24 \pm 0.15}$		
H2			0.44 ± 0.08		

S.E.-standard error.

The estimated heritabilities for growth-related traits (0.34-0.45, in the first year and 0.44-0.49 in the second year) are in accordance with earlier studies on common carp (Nenashev, 1966; Nagy et al., 1980; Smisek, 1981; Tanck et al., 2001; Vandeputte, 2003; Wang, 2009).

The genetic correlation varied during the two years from 0.24-0.91, but in general they are high. Similar studies (Vandeputte et al., 2004, 2008) showed that these correlations are close to unity and that genetic improvement for weight can be achieved by an indirect selection for length, which might be easier to measure in the field.

Common environmental effects may arise as a result of early common rearing of families, and, if ignored, such effects are likely to inflate heritability estimates. In the final multi-trait analysis common environmental effects were not included. Preliminary multi-trait models including common environmental family effects did not converge. However, the convergence was achieved in single-trait models including both genetic and common environmental family effects, but the latter

type of effects was generally of little significance. The latter may be explained by the fact that the traits were recorded at 18 months of age, and effects of early common rearing are therefore expected to be diluted over time. Similarly, considering mating design in this study, the dam component may be inflated by non-additive (dominance) and maternal effects (e.g. caused by different egg size among the female breeders and possible cytoplasmatic genetic effects). However, such effects are likely to be included in the common environmental family effects, which were generally nonsignificant in this study.

Genotype by environment (G×E) interactions causing re-ranking of genetic groups in different environments (e.g., intensive vs. extensive environment) has been shown in earlier studies of common carp (Wohlfarth et al., 1983; Gross and Wohlfarth, 1994). There have been no significant differences in the mean of the different traits among different ponds in this study, but interactions in more variable environments are still yet to be tested.

Based on the estimated genetic variation one can expect significant genetic improvement in growth traits in common carp through selective breeding. This is in accordance with recently conducted studies (Reddy et al., 2002; Vandeputte et al., 2004, 2008; Nielsen et al., 2010) which showed that genetic improvement of growth and survival of carp can indeed be obtained through selective breeding.

Conclusion

The present study confirms that substantial genetic variation exists within the Serbian carp population, indicating a broad genetic basis of the population. The estimated heritabilities for growth-related traits are in accordance with earlier studies on common carp and the results strongly indicate a potential for genetic improvement through selective breeding. This is a basis for further development of a National breeding programme for common carp in Serbia.

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PROGRAM SELEKTIVNOG UZGOJA ŠARANA (*CYPRINUS CARPIO* L.) U SRBIJI-PRELIMINARNI REZULTATI

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Rezime

Cilj ove studije je bio da se procene heritabilnost i genetičke korelacije telesne mase, dužine i visine šarana u Srbiji u toku trogodišnjeg ciklusa. U toku 2007. godine proizvedeno je 50 familija šarana i ove jedinke iskorišćene su za procenu heritabilnosti i genetičke korelacije. Merenja riba su obavljena za osobine telesna masa, dužina i visina u momentu označavanja (W0, L0, H0), zatim pri starosti riba prva jesen (W1, L1, H1) i pri starosti druga jesen (W2, L2, H2). Na osnovu jednovarijantnih statističkih modela za svaku osobinu procene heritabilnosti su bile visoke (0.39, 0.34 i 0.45 za W2, L2 i H2). Genetičke korelacije su procenjene na osnovu multivarijacionih statističkih modela i bile su visoke između W1 i, L1 i H1 (0.81 \pm 0.06 i 0.91 \pm 0.03 za L1 i H1), dok su između H1 i L1 bile umereno korelisane (0.54 \pm 0.12). U drugoj produkcionoj godini korelacije su takođe bile visoke, između W2 i, L2 i H2 (0.64 \pm 0.09 i 0.74 \pm 0.06), dok su između osobina dužina i visina, L2 i H2, bile niže (0.24 \pm 0.15). Na osnovu navedenih rezultata očekuje se da bi poboljšanje prirasta u navedenoj populaciji šarana u Srbiji, putem selekcije familija, bilo uspešno.

Ključne reči: šaran, selektivni uzgoj, heritabilnost, genetička korelacija.

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