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Genetic parameters estimation of growth in *Salmo trutta caspius* as a function of body weight and Length

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Abstract

There is no available adequate information on the biology and genetics of the Caspian salmon (*salmo truta Caspiu)* living in the Caspian Sea with other species such as common carp families, sturgeons and etc., therefore we are interested in knowing whether selection for rapid growth rate in *salmo trutta Caspius* will potentially lead to correlated genetic response in body weight and length. The potential for correlated responses was evaluated by the heritability estimation, estimating heritabilities of body weight and length. The genetic parameter estimations were obtained for different stages of growth from 5400 fish consisting 27 unrelated families that reached maturity at 36 months of age. The parent which used to produce separate family groups had been caught from the Caspian Sea and spawned during the autumn season. The estimated heritability of body weight and length was 0.42±0.13 and 0.49±0.01, respectively based on differential and selection response between parent pairs and their offsprings. Several factors may have affected the creation of this high level of estimation, dominant effect, inherited from different breeders to offspring.

Keywords*: Salmo trutta caspius*, Genetic parameters, Heritability, Caspian Sea

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Introduction

The genetic management of breeding stocks is very important in order to ensure proper and long-term harvesting of the breeders. Increasing the production and growth rate are usually the main traits to be improved by individual selection of breeders, without having any information of genetic basses of fish which usually the farmers have special interest in, since it is simple and cheaper to set up in practical condition while family selection seems to be more effective (Gjedrem 1983; Hershberger et al., 1990).

The *Salmo trutta Caspius* is a very important fish in the Caspian Sea and due to its high market price and as an alternative of rainbow trout, it is of interest to be propagate and rearing. The *Salmo trutta Caspius* is a very slow fish at early development. We designed a program to enhance individual selection. Growth rate is the main breeding goal of fish breeders, but individual selection has often shown poor responses in fish species. The technique introduced by Chevassus and his teamwork in 2004, was developed to overcome possible factors that may contribute to this low success using a high number of breeders and repeated growth challenge. This technique was used by some modification to establish the lines as gene bank for managing a cross breeding design for restocking the fish in the Caspian Sea. Yet, there are not any references on the genetic analysis of developmental stage of this fish.

There are several technical studies in genetic analysis of Salmonids. In a study done by Ferguson et al., 1985 the effect on hatching time rainbow trout was found. Also, Smoker in 1986 observed a small maternal effect and a significant sire and dam effect in this fish. In brown trout, the heritability of early survival is about zero (Kanis et al., 1976). No such data for *Salmo trutta caspius* are reported in literature at this time. In the present study, in order to better define a set up of the response to selection of *Salmo trouta Caspius*, an experiment was designed to determine the genetic parameters of growth-related traits at different stages of development.

Materials and methods

The prepared fish for the present study were reared in fresh water during the whole experiment at Propagation and Culture Station S.B. Kelardasht, Iran. In December 2006, 27 mature 3-6 year old female fish were artificially striped and mated with 27 males with the same ages, in which three males were mated with one female. A total of 27 unrelated families were produced as the base population of gene bank. Fertilized eggs were incubated separately for 30 days, after which, they were transferred into indoor 150-L tanks (2000 larvae in each tank). The order of egg tray and larval tanks were randomized in incubation and rearing facilities. In spring 2007, in each family tank, family

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size was standardized to 200 individuals. During rearing in tanks, the fish were fed with commercial dry pelted feed (Chine product, Tehran, Iran), composed of 45% protein, 21% fat, 1% fiber and 7% ash. Water oxygen concentration was maintained above 95% over the duration of the experiments daily. The temperature of the experimental station was not constant from 2°C in winter to 15°C in summer. Therefore the amount of feed was adjusted for temperature and fish biomass in the tanks and in the pond. Further, the condition of the fish was monitored at least twice. The fish were weighted and measured at different stages of growing. The hierarchic complex was employed. The first experiments with hierarchical complexes were performed by Nenashev (1966, 1969) with the common carp.The external fertilization of eggs in this fish and the high fertility of females facilitate the simultaneous conduct of a large number of crosses. In the hierarchical complex one female from several different males are half sibs with respect to each other, while the individuals within each given offspring represent full sibs. An analysis, of the variation of different groups of offspring makes it possible to calculate the heritability of the trait under study. In the treatment of lengths or weight measurements for a limited number of individuals originated from each cross the first task involves calculation of the sum total of square deviations from the mean (SS) separately for females. For males it crossed with one and the same female within different broods and for all the fishes measured. The calculations are made using the following formulae:

SS♀♀ = ab Σ($\overline{X}$ ♀- $\overline{X}$)2;

SS♂♂ = n Σ ($\overline{X}$ w- $\overline{X}$ ♀)2;

SSw =Σ (X- $\overline{X}$ w)2;

SSph=Σ (X- $\overline{X}$)2,

where $\overline{X}$ is a common mean for all fishes, $\overline{X}$ w mean values for different offspring. $\overline{X}$ ♀ mean values for different offspring of one and the same female X is individual measurements, n is the number of individuals in a given offspring. a is the number of females. b= the number of males crossed with one female.

The so-called observed variances (MS or Y) may then be calculated. They are obtained after the division of the sum total of the squared values by the number of degrees of freedom: a-1 for SS♀♀.a (b-1) for SS♂♂. ab(n-1) for SSw and abn-1 for SSph. After this division we obtain:

V♀♀ or VD- the variance of mean values for females (dam component);

V♂♂ or Vs - the variance of mean values for males crossed with one female (sire component);

V random or VW -the variance of differences within separate offspring:

V Ph - the variance for all descendants.

Each of these observed components of 1111: variance is non- uniform and contains a number of components of different origin (Falconer, 1960):

$$V_D = \sigma_W^2 + n\sigma_S^2 + bn\sigma_D^2;$$

$$V_S = \sigma_W^2 + n\sigma_S^2; \qquad V_W = \sigma_W^2$$

Then it is easy to determine the values for σ_s^2 and σ_D^2

$$\sigma_D^2 = \frac{V_D - V_s}{bn}; \qquad \sigma_S^2 = \frac{V_S - V_W}{n}$$

Each of the variances σ_s^2 and σ_D^2 contains. as calculated, one quarter of the additive genetic variation of the patents. Heritability can be obtained from the following formulae:

$$h^2_{\text{♂}} = \frac{4\sigma_S^2}{\sigma_{Ph}^2}; \qquad h^2_{\text{♀}} = \frac{4\sigma_D^2}{\sigma_{Ph}^2}; \qquad h^2_{\text{♂♀}} = \frac{2(\sigma_S^2 + \sigma_D^2)}{\sigma_{Ph}^2}$$

Results

The mean weight and length of offspring, based on family crossing, at different time of sampling are shown in table 1. The average over all fish weights at the four time of sampling were 0.8, 4.5, 21.3 and 98.6 g. Also, the average lengths of fish during four times were 4.2, 7.7, 12.5 and 21.2 cm, respectively.

Table1: Mean and standard deviation of weight and length at different age of growing (n=30 sample number)

Time of sampling	1^{th} spring	1^{th} summer	1^{th} winter	2^{th} spring
	Mean± SD	Mean± SD	Mean± SD	Mean± SD
Weight(g)	0.8±0.4	4.5±1.1	21.3±6.7	98.6±21.8
Range(g)	0.3-1.8	2.4-6.3	7.9-33.8	67.1-150.4
Length(cm)	4.2±0.6	7.7±0.9	12.5±1.6	21.3±3
Range (cm)	3.4-5.6	6.4-10.8	9-16	18.2-33.7
No of offspring	5400	5082	5011	3968

The survival rate was 92% over year rearing out of 5400 fingerlings. Table 1 shows the high variation between weight and length at different families at the first stage of growing. A comparison was done on mean weight of the offspring in different families (Fig. 1). The difference was highly significant (P<0.00) at all sampling stages. It gave the same results for length of fish at different sampling stages. The heritability estimation for growth parameter at four interval periods are presented in table 2. Heritability of growth was quite high in *Salmo trutta Caspius* of the Caspian Sea.

Table2. Heritability estimation and additive genetic correlations

Time of Sampling for length				
1^{th} spring	*0.5021**			
1^{th} summer	0.0229	*0.4909*		
1^{th} winter	0.0498	0.1112	*0.5087*	
2^{th} spring	0.1333	0.0229	0.0642	*0.5070*

Time of Sampling for weight				
1^{th} spring	*0.4421*			
1^{th} summer	0.0715	*0.4674*		
1^{th} winter	0.0025	0.0159	*0.5024*	
2^{th} spring	0.0022	0.0854	0.0551	*0.5043*

*The italic number shows the heritability estimation

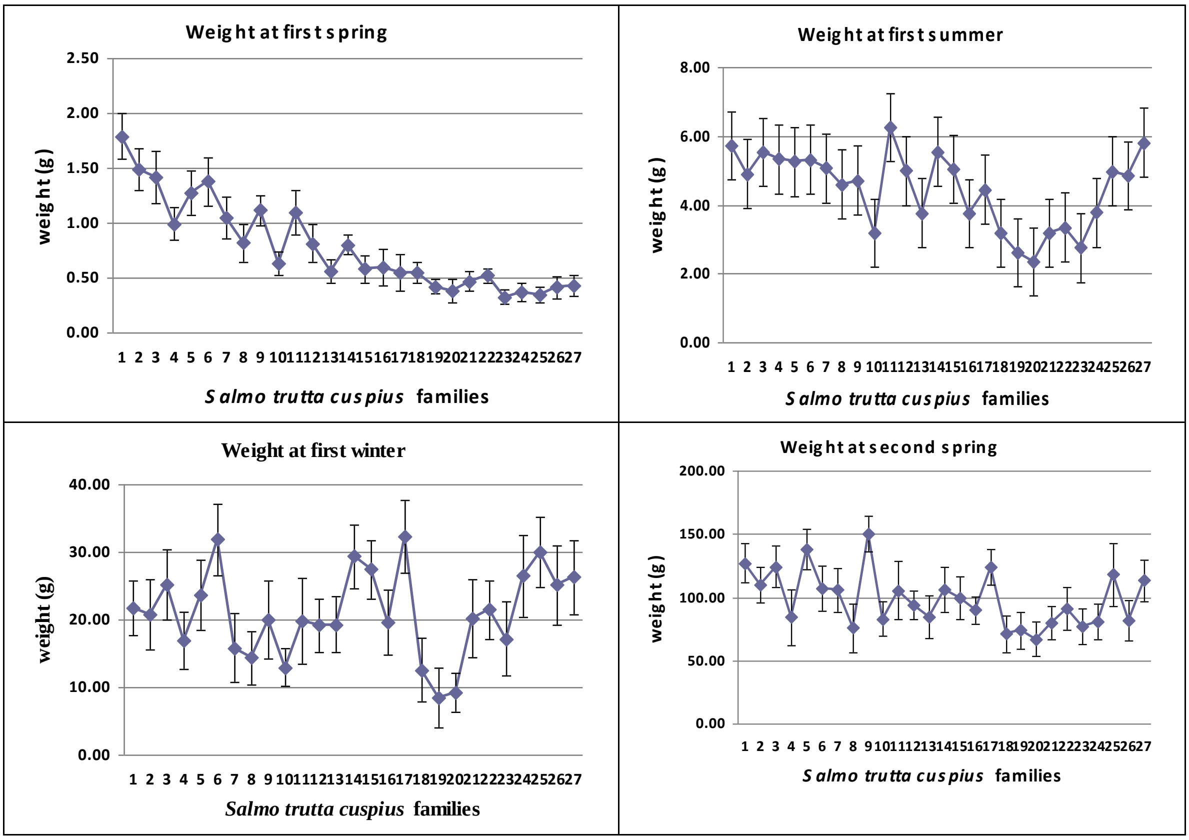

Figure 1: The variation in fish weight at different stage of sampling between 27 families of *Salmo trutta Caspius*

Discussion

Genetic studies have revealed moderate levels of genetic variation for growth rates of salmonids, allowing its genetic improvement (Gjerde and Schaeffer, 1989; Crandell and Gall, 1993b; Elvingson and Johansson, 1993; Winkelman and Peterson, 1994). The estimation of heritability at different stages of rearing and condition were varied based on the several experimental works done on Salmonids. According to McKay et al., (1986), the heritability estimated in rainbow trout for weight and length ranged from 0.13±0.17 to 0.38±0.22, respectively. Heritability based on the sire component of variance for rainbow trout traits were 0.21 for body weight and 0.18 for body length (Gjerde and Schaeffer, 1989) (Crandell and Gall, 1993a). The heritability at swim-up in brown trout (*salmo truta fario* L.) for initial weights was $h^2= 0.23\pm0.13$ (Vandeputte et al., 2002). In spite of the high variation in genetic components of Salmonids, in the present work the heritability at different times of sampling was approximately in the same range.

There was high family variation on first stages of growth in *salmo trutta Caspius* (0.3-1.8 g). Several factors may have affected the creation of this high variation. The variable between different family individuals may be considered as dominance effects, inherited from different breeders to offspring. Dominance effects for all individual variables were moderate to large (0.14-0.39) for brown trout (*salmo trutta fario L.)* which is concluded in the work of Vandeputte et al., 2002.

In spite of having the experiment in a common environment and randomizing the experiment to eliminate environmental effects, yet the eggs of each family were incubated separately, which may have permitted the onset of a common environment different for each family. The large dominance effect is based on the fact that accelerated larval growth allows an earlier onset of exogenous feeding, and improves the survival during this phase (Wallace and Aasjord, 1984; Vandeputte et al., 2002).

The breeders used in the present experiment had a different age and weight, therefore the eggs of some females were smaller than the others, consequently such effect persisted at swim-up stage. Analysis variance also revealed significant differences between different families. In addition, the basic protein energy requirements of Salmonids showed that a significant growth improvement can be obtained when using specific diets with protein corresponding to the requirement of the species. In this experiment we used the trout diets, which may be far from the optimum need of brown trout. Up to now, precise monitoring of the food conversion index for Brown trout of the Caspian Sea was not obtained precisely by experimentation. Therefore, the experiment may not have been performed under optimum environment conditions to estimate the correct heritability for this fish.

The effect of breeders may also be explained by the effect of inbreeding depression which occurred in offspring, that is in accordance with Quillet, 1994. He stated the fact that growth rate is especially affected by inbreeding depression during early stages which is linked to the existence of oriented dominance variation.

The lower variability and heritability of domesticated strain in many cases of Salmonids indicates that they were propagated with small effective numbers of breeders, resulting in some inbreeding. This initial inbreeding in the domesticated strains could somehow hamper the possibilities of genetic gain from selective breeding (Vandeputte, 2002).

The Brown trout of the Caspian Sea is quite distant from other species of brown trout in Europe and may then have conserved different alleles influencing the species with high genetic variability or/and heritability which in this species may be a good material to start selective breeding programs with.

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