

# THE ESTIMATION OF GENETIC DETERMINISM FOR BIOECONOMIC AND ECOECONOMIC TRAITS IN FISH - BASIS FOR GENETIC IMPROVEMENT

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## Abstract

Establish the genetic determinism is a very important step in animal breeding, including fish. Result of the selection of fish depends directly on the statistical relationship between the coefficient of heritability and phenotype. According to heritability value is underlie the breeding system, selection purposes and method. Furthermore the heritability is a part of any mathematical relation in animal breeding (estimation of breeding value, genetic gain). The work consists in identifying the methods used at international level for determining heritability of fish. The development of methodology for determining the genetic determinism is a basis for genetic improvement programs. A properly chosen and applied methodology can have a positive impact on bioeconomic and economic traits in fish.

**Key words:** fish, genetic improvement, heritability

## INTRODUCTION

Genetic improvement of fish can be defined as a process of change, by specific means and methods of genetic structure of populations, in the direction desired by the man, taking into account the characteristics of the species and the environment [13].

In this sense, the purpose of quantitative genetics is to identify and quantify the elements involved in the formation of bio- and eco-economic characters useful, as well as to determine in which measure the value of a character shall be transmitted to descendants [14].

The effective of getting genetic progress for each generation, depends on heritability, number of deemed traits and the interdependency between them.

The results obtained as a result of identifying heritability characters may be suggestive of genetic improvement process, the premises for the desired objectives.

## MATERIAL AND METHODS

Heritability ( $h^2$ ) is defined as the rate of additive genetic variance of the phenotypic variance. Since the selection and breeding programmes can act only on the additive genetic variation within the population, the other components of the genetic variation of raw material being limited and particular environment in which the experiment takes place, the estimates coefficients for heritability are considered as having no practical importance as indicators for the results of these programmes [12].

Methods for estimating the heritability that applies to fish is one of the points of departure of genetic improvement programmes.

The study was based on the identification of these methods used in national and international, in consultation with the literature.

Over time, various researchers have developed and use different methods for estimating the heritability of the various characters to fish.

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## RESULTS AND DISCUSSIONS

In planning the selective growth of a species or breeds, the analysis of the genetic determinism, peoples becomes critical.

Knowledge of the heritability, in order to express heritability, it is very important for breeders in the selection remains primarily additive variance or variance value of improvements. Thus, the higher its weight, the selection is considered more efficient [8].

Analyzing studies aimed at estimating the heritability have identified a number of ways, including:

1. *Determination of the „realized heritability” made on the basis of the effectiveness of the selection.* The method takes into account the difference between parental selection differential pairs (S) and the corresponding difference between their descendants and the response to selection (R). The report shows that RS is the fraction of the difference between parents kept the descendants, this representing a heritable component [2]. This value was made called "realized heritability".

The characters used for the determination of „realized heritability” made by this method would have been some tangible weight and dimensions, measured at two different generations of fish, in order to normalize and standardize conditions of fish growth, particularly in terms of density and feeding conditions. The calculation of „realized heritability” becomes much more accurate if you use three or more successive generations.

2. *Determination of heritability by regression between parents and their offspring.* This method requires the calculation of the coefficient of the regression line (**b**) which shows how much you change the value of a character in descendants for change by one of the parents. Linear regression equation may be used in almost all cases:

$$y = a + bx,$$

where **x** and **y** are the average values of the character for parents and children, **a** constant, reflecting differences in terms of expressing intergenerational nature, and **b** is the coefficient of regression.

If the independent variable (performance of parents) is the average of the values recorded for each parent, then heritability is equal to the coefficient of regression:

$$h^2 = b$$

If the independent variable is represented only by the performance of one of the parents then heritability will be equal to twice the value of the regression, i.e.:

$$h^2 = 2b$$

3. *Determination of heritability by referencing the values of the characters from close relatives.* You can use three groups of relatives, to calculate the correlation: parents and descendants, sibs (FB-SB) and half sibs (SF-SS).

The coefficient's heritability species (breeds) of fish shall be calculated, in general, by referencing the parents with the offspring. Both parents and only one, you can compare with the offspring. According to this, heritability is calculated by the formula:

$$h^2 = r \quad \text{or} \quad h^2 = 2r$$

Correlation method has been used for the calculation of the coefficient of heritability for the number of dorsal fin of common carp [7].

4. *Determination of heritability by the phenotypic variance expansion difference, using analysis of variance.* The method has been proposed and used in his works of *Nenashev* (1966, 1969). The method involves the simultaneous production of a sufficient number of descendants from the same parents is a lot known and a population of fish [10, 11]. Offspring are produced both by diallel crosses and on the basis of the so-called complex hierarchical.

The first experiences, which used complex hierarchical, had as its object the common carp. In the hierarchy of the offspring produced by *Nenashev*, a female with several different males are half sibs, while individuals in each progeny are sibs. For the analysis of variance is calculated, first, the sum of squared residuals raised (the sum of squares), separately for females, for males with the same female in different nests and for all the fish measured.

The calculation is done using the following formula:

$$SP_{\varphi\varphi} = ab \sum (\bar{X}_{\varphi} - \bar{X})^2;$$

$$SP_{\delta\delta} = n \sum (\bar{X}_w - \bar{X}_{\varphi})^2;$$

$$SP_w = \sum (X - \bar{X}_w)^2;$$

$$SP_{ph} = \sum (X - \bar{X})^2.$$

where  $\bar{X}$  is average for all fish,  $\bar{X}_w$ , the average value for different descendants,  $\bar{X}_{\varphi}$ , the average value for different descendants from the same female,  $X$  represents the individual measurements, where  $n$  is the number of individuals from a descent time,  $a$  is the number of female and  $b$  is the number of males cross with a female.

Sums of squares obtained shall be divided by the degrees of freedom corresponding to each source of variation ( $a - 1$ ) for  $SP_{\varphi\varphi}$ ,  $a(b - 1)$  for  $SP_{\delta\delta}$ ,  $ab(n - 1)$  for  $SP_w$ , yielding the averages of the squares:  $MP_{\varphi\varphi}$  or  $MP_D$ -for females,  $MP_{\delta\delta}$  or  $MP_S$ -for males cross with a female,  $MP_R$  or  $MP_S$ -for separate descendants;  $MP_{ph}$ -for all descendants.

Whereas the averages of the squares on the sources of variance are the variance of its own, each containing a number of parts of different origin:

$$S^2_D = \sigma^2_w + n \sigma^2_s + bn \sigma^2_D;$$

$$S^2_s = \sigma^2_w + n \sigma^2;$$

$$S^2_w = \sigma^2_w.$$

it is necessary to calculate variances on sources using the following formula:

$$\sigma^2_s = \frac{V_s - V_w}{n}; \quad \sigma^2_D = \frac{V_D - V_s}{bn}$$

Each of the  $\sigma^2_s$  and  $\sigma^2_D$  contain variances, as it has been calculated, a quarter of the additive genetic variance of parents. Heritability can be obtained from the formulas:

$$h^2_{\delta} = \frac{4\sigma^2_S}{\sigma^2_{Ph}}; \quad h^2_{\varphi} = \frac{4\sigma^2_D}{\sigma^2_{Ph}};$$

$$h^2_{\delta\varphi} = \frac{2(\sigma^2_S - \sigma^2_D)}{\sigma^2_{Ph}}.$$

*Kirpichnikov (1981)* has chosen a complex hierarchical simplified with three females, three males for every female and three descendants of each mating (Table 1). Heritability in females was larger than the males, often in the case of fish. Heritability increased in females is usually explained by

the existence of a "shared" environment for all offspring produced by a female. This environment is hard to describe, but it increases the apparent "variation of females" and increase the amount of the variance.

Complex hierarchy created cannot be the variance results from the interaction of genotypes of the females and males to be assessed on its own, being an integral part of  $\sigma^2_s$  and  $\sigma^2_D$ . This leads to a decrease in the accuracy of determination of heritability by using the hierarchical scheme.

In another study of its, *Kirpichnikov (1981)* used a scheme for the calculation of body weight by using heritability in matting of type- 2 x 2, as shown in table 2.

5. *Determination of heritability for the size of the spawning* starts from the premise that the variation of all oocytes from the females ovary is due to environment.

If its extract the variance associated with this variance of the total phenotypic variance of spawning several different females, obtain a pure genotypic [16]. Hence,

$$h^2 = \frac{\sigma^2_{Ph} - \sigma^2_E}{\sigma^2_{Ph}}$$

where  $\sigma^2_{ph}$  is the variance of the size of eggs in a population,  $\sigma^2_E$  is the variance of the size of the eggs for a single female.

*Rokitsky (1974)* propose a determination that is associated with the use of complex hierarchical [15]. This makes it possible to use a direct comparison between same sex parents to their offspring.

Heritability is determined by the significance of the correlation between a class and the value obtained shall be multiplied by 4:

$$h^2 = \frac{4\sigma^2_S}{\sigma^2_s + \sigma^2_w}$$

The numerator of this formula is the variance of males multiplied by 4, and the denominator is the sum of the variances of the "male" and "between individuals" to each descendant. Calculation of heritability by this technique gives a result about. This technique has been used so far in raising the fish.

Table 1 The calculation of the heritability body weight using complex hierarchical (Kirpichnikov, 1981)

Specification	♀ <sub>1</sub>			♀ <sub>2</sub>			♀ <sub>3</sub>			SP	GL	MP
	σ̂ <sub>1</sub>	σ̂ <sub>2</sub>	σ̂ <sub>3</sub>	σ̂ <sub>4</sub>	σ̂ <sub>5</sub>	σ̂ <sub>6</sub>	σ̂ <sub>7</sub>	σ̂ <sub>8</sub>	σ̂ <sub>9</sub>			
Descendants weight (g)	4.0 6.0 8.0	5.0 7.5 10.0	6.0 8.0 13.0	9.0 11.0 13.0	8.0 11.0 11.0	4.0 7.0 10.0	8.0 10.5 13.0	10.0 16.0 11.0	7.0			
$\bar{X}$ of descendants	6.0	7.5	9.0	11.0	9.0	7.0	10.5	12.0	9.0			
$\bar{X}$ of descendants /♀	7.5									10.5		
$\bar{X}$ for all individuals	9.0											
Deviations for σ̂ <sub>1</sub>	-1.5 2.25	0										
Deviations for σ̂ <sub>2</sub>	0	0	1.5 2.25	2.0 4.0	0	-2.0 4.0	0	1.5 2.25	-1.25 2.25	2	4.50x9=40.5	MP <sub>♀</sub> = 20.25
Random deviations for σ̂ <sub>3</sub>	-2.0;2 4;0;4	-2.5;0;2.5 6.25;0;6.25	-3;-1;4 9;1;16	-2;0;2 4;0;4	-1;1;2 1;1;4	-3;0;3 9;0;9	-2.5;0;2.5 6.25;0;6.25	-2;-2;4 4;4;16	-2;0;2 4;0;4	6	17x3=51	MP <sub>σ̂<sub>3</sub></sub> = 8.50
Total deviations	-5;-3;-1 25;9;1	-4;-1;5;1 16;2.25;1	-3;-1;4 9;1;16	0;2;4 0;4;16	-1;-1;2 1;1;4	-5;-2;1 25;4;1	-1;-1;5;4 1;2.25;16	1;1;7 1;1;49	-2;0;2 4;0;4	18	214.5	MP <sub>Ph</sub> = 8.25

Table 2 The calculation of the heritability body weight using type cross 2x2 (the complete dispersion bifactoriale) (Kirpichnikov, 1981)

Specification	♂ <sub>1</sub>		♂ <sub>2</sub>		SP	GL	MP	σ <sup>2</sup>
	σ̂ <sub>1</sub>	σ̂ <sub>2</sub>	σ̂ <sub>1</sub>	σ̂ <sub>2</sub>				
Descendants weight (g)	10;15;20	8;14;20	13;16;25	11;16;21				
$\bar{X}$ of descendants	15.0	14.0	18.0	16.0				
$\bar{X}$ for families ♀	14.5				17.0			
$\bar{X}$ for families ♂	16.5		16.5		15.0			
$\bar{X}$ for all individuals	15.75							
Deviations for σ̂ <sub>1</sub>	-1.25 1.5625x3	-1.25 1.5625x3	+1.25 1.5625x3	+1.25 1.5625x3	18.75	1	18.75	3.00
Deviations for σ̂ <sub>2</sub>	+0.75 0.5625x3	-0.75 0.5625x3	+0.75 0.5625x3	-0.75 0.5625x3	6.75	1	6.75	1.00
Deviations due to Interactions	-0.75+1.25-0.75 0.0625x3	-1.75+1.25+0.75 0.0625x3	+2.25-1.25+0.75 0.0625x3	+0.25-1.25+0.75 0.0625x3	0.75	1	0.75	-10.17
Random deviations	-5;0;+5 25;0;25	-6;0;+6 36;0;36	-5;-2;+7 25;4;49	-5;0;+5 25;0;25	250.00	8	31.25	31.25
Total deviations	33.0625;0.5625;18.0625	-7.75;-1.75;+4.25 60.0625;3.0625;18.0625	-2.75;+0.25;+5.25 7.5625;0.0625;8.5625	-4.75;+0.25;+5.25 22.5625;0.0625;27.5625	276.25	11	25.11	-

6. *Method for determining heritability for the viability and resistance to diseases using analysis of variance.* In this case, they used no more than 3 determinations replicate during the period of growth. Character taken into account in these cases appears in quantities relative to survivors or dead fish [9]. Situations of this type tend to vary quite a lot, depending on the value of the character, representing the percentage of survival.

To cancel this dependence of mortality, some authors have used in experimental work at salmon formula [3, 6]:  $y = \arcsin \sqrt{x}$

In those cases, *Boygo* and *Becker* (1965) recommended for use the following formulas: [1]:

$$h^2_s = \frac{4\sigma_s^2}{0,25 + \sigma_s^2 + \sigma_D^2} \text{ or}$$

$$h^2_D = \frac{4\sigma_D^2}{0,25 + \sigma_s^2 + \sigma_D^2}$$

Methods of calculating the heritability take into account the predominantly just a fraction of the genetic variance, additive effect associated with the gene. Estimation of genetic variance in total (including variances are due to the left, over-dominance and epistasy) can be obtained by using a special approach. Variance due to the overdominance plays an important role in many species of fish. It was established in particular that most of the variance of genetic variation in body weight, body size and viability of the *Ciprinidae* and *Salmonidae* is represented by the variance associated with over dominance [5, 17]. A more accurate analysis of neaditive variance components are one of the most important issues in relation to future studies on the variation of fish.

7. *Estimation methods based on a restricted maximum likelihood (REML)* routine combining estimates from different relationships, suitably weighted, to provide the best estimate of heritability. Estimations in REML are done by iteration based on a mixed model. The iterative process involves two steps. First - the value of  $\lambda$ , a derivation of the

heritability, is calculated from estimates of genetic and phenotypic variances, and the mixed model equations are solved for the fixed effects and the breeding values. Second - updated estimates of the genetic and phenotypic variances are determined from the predicted breeding values. Both steps are repeated until the estimates converge [4].

Unfortunately, as shown in *Kirpichnikov* (1981), some works contain many errors. According to *Kirpichnikov*, "Heritability indexes" set of *Plokhinsky* (1964) which is based on the proportion of the total amount of biases, without any expansion of the variance, there aren't recommended to be used. All these indices do not describe the heritability within the meaning of the word genetic; they do not define the additive genetic variance fraction of total variation. Often, these indices produce erroneous estimates. [15].

## CONCLUSIONS

Estimation of genetic determinism for bio- and eco-economics characters to fish includes the following:

- identification and selection of the character bio- and eco-economics with the high value of breeding;
- an estimate of the expected effect of the selection, and genetic progress;
- estimating the value of improving breeding;
- choice of the method of selection;
- choice of improvement;
- duration of improvement variable, depending on the value of the heritability.

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