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Study on Identification of Selection Indices for a Single Character to Increase Meat Production in a Population of Ropsa Carp

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Abstract

In the context of ensuring bio resources for future generations, scientific research of carp culture have shown that it can realize high meat production, if it respects certain conditions of race performance and the growth medium. The genetic improvement objective is to increase meat production, based on maximizing meat production per female of breeding stock. Estimation of genetic progress using the character selection requires the use of selection indices. The study consists in identifications of the selection indices of some morphological traits which can lead to maximizing the meat production in a population of Ropsa carp. In the structure of selection index was measured the characters on live animal: weight (W), body depth (BD) and standard length (SL). The biologic material was represented by 50 individuals of Ropsa carp from 5 families, each family consisting of a mother and two fathers. Individuals were reared intensively in the same environmental conditions, since juvenile stage until the age of three summers. For each selection index was determined line vector of partial regression coefficients and the hierarchy was based on the accuracy of genetic evaluation and genetic progress provided by each variant. After calculating indices for each character considered, it was found that selection to maximize meat production of Ropsa carp population can be done on the basis of selection for live weight character (selection accuracy is 52.22%). This provides a genetic gain of 60.6318 grams for live weight. By transformation of morphological traits of individuals in the population of cyprinids can increase the quantity of meat/individual and contribute to sustainable aquaculture development and traceability.

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1. Introduction

In order to ensure the bioresources for future generations and to preserve the natural resources and our planet, researches have shown that carp breeding can determine high yields of meat, when it complies with certain conditions of race used performance and growing medium (Grosu, Oltenacu et. al., 2005).

At national level it is found a lack of national fish genetic breeding programs similar to other domestic species of economic interest. The applications of selection in genetic breeding determine a constant and real production growth by exploiting an improved genetic material. In this way it contributes to the development of aquaculture sustainability and traceability.

As concerning the cyprinids, the literature cites performing hybridization, but not referring to selection plans associated with genitor populations, which are important to fundament coherent breeding plans (Nicolae et al., 2012).

The present study fits in the scientific research area of animal biodiversity development and preservation by applying a genetic amelioration for improvement the food resources for humanity. Knowing the fish origin contributes to fish and fishery products distribution chain development and traceability, including all links from the production point to the final consumer (Nicolae et al., 2014).

2. Research Methods

The study is focused to identify the selection indicators of morphological traits measured on live animal. These characters can lead to meat production maximizing in a population of Ropsa cyprinids (Nicolae et al., 2012).

The Ropsa breed is characterized by a high precocity, vigor, feed conversion, productivity, adaptation to unfavorable environmental conditions. The Ropsa carp is approved by breeders because it has an increased adaptability to environmental conditions and feeding (Nicolae, 2004). It is also preferred by buyers due to its similarity with wild carp.

The research was initiated with 5 lots of larvae (7 days age), belonging to 5 families of Ropsa breed carp, each family consisting in a female and 2 males. Those lots were monitored until the age of two years and one summer. The followed characters were: live weight (W), body depth BD and standard length (SL); measured by conventional methodology (Lustun, 1985). The morphological characters listed above (quantitative characters) are the performance of Ropsa cyprinid breed, which give information about meat production.

In the first summer of growth the larvae were reared in pens. Populating with 7-day larvae was made in early summer. The summer juveniles were growing in pens until autumn, when before placing at wintering place, they were marked, weighed and measured. The following spring, juveniles were raised in pens thus they benefit from the same environmental and feeding conditions. By the age of two years and one summer there was used the same protocol of maintenance and measurement of characters as in the first year of growth.

Optimization of genetic improvement objective in the analyzed population was done by using the “selection indexes”. In principle, selection index theory refers to the simultaneous selection for several traits (n) using a linear function of the measured performance of individual and/or its relatives. Estimation of the genetic progress, especially when using multiple traits, requires the use of concepts “Aggregate Genotype” and “Selection Index” concepts introduced by Hazel and Lush (1943), cited by Popescu-Vifor (1990).

For each index variant was determined the line vector of partial regression coefficients and hierarchy was based on the accuracy of genetic evaluation ($r_{I,H}$) and genetic progress (ΔH) offered by each variant, using the formulas (1; 2):

$$r_{I,H} = \sqrt{\frac{S_I^2}{S_H^2}} = \sqrt{\frac{b'Vb}{v'Gv}} = \sqrt{\frac{b'Cv}{v'Gv}} \quad (1)$$

$$\Delta H = i \cdot r_{I,H} \cdot S_H \quad (2)$$

3. Results and Discussions

The growing need in human nutrition for animal proteins also determines an increasing of meat production and quality in fish and others animals. Maximizing meat production based on maximizing production of meat per female breeding stock is the main objective of breeding of Ropsa cyprinids.

The selection criteria to optimize the genetic progress are represented by the selection indices, which were calculated for a single morphological trait considered character of production. Using the working methodology described and economic proportion of 100% for each character, it was designed three selection indices to identify the variant selection index which maximizes genetic progress (Grosu, Oltenacu et. al., 2005).

The first determined index was *the selection index for the live weight*. As mentioned above, in the case of selection for a single economic trait, the economic value (v) is equal to unit, so that the system of equations is (3):

$$[V \cdot b = G \cdot v] \text{ will be } [V \cdot b = G], \text{ respectively: } 49442 \cdot b_1 = 13482 \quad (3)$$

Hence, the regression will be quite the value of heritability ($b_1 = h^2 = 0.2727$).

The selection index will have the simple form (4):

$$I = 0.2727 \cdot P_1 \quad (4)$$

The selection index variable (S_1^2) was as following formula (5):

$$S_1^2 = b' \cdot V \cdot b = 0.2727 \cdot 49442 \cdot 0.2727 = 3676.2 \quad (5)$$

with an error (S_I) = 60.6318.

The aggregate genotype variance (S_H^2) was (6):

$$S_H^2 = v' \cdot G \cdot v = 1 \cdot 13482 \cdot 1 = 13482 \quad (6)$$

associated with an error (S_H) of 116.1111, using the formula (7):

$$S_H = \sqrt{S_H^2} = \sqrt{13482} = 116.1111 \quad (7)$$

The selection accuracy is estimated by the correlation between genotype and phenotype, using the formula (8):

$$r_{IH} = \sqrt{\frac{S_1^2}{S_H^2}} = \sqrt{\frac{3676.2}{13482}} = 0.5222 \quad (8)$$

This means that the aggregate genotype can be predicted with a probability of 52.22% if in practice is using the selection index considered, *the selection index for the live weight* respectively.

The expected genetic progress on the aggregate genotype based on this selection index will be 60.6318 units of selection intensity (9):

$$\Delta H = r_{IH} \cdot i \cdot S_H = 0.5222 \cdot i \cdot 116.1111 = 60.6318 \cdot i \quad (9)$$

where i is the selection intensity.

In conclusion, the genetic progress per generation is 60.6318 grams for life weight.

At the selection index for the body depth, the system of equations $[V \cdot b = G \cdot v]$ will be $[V \cdot b = G]$, respectively: $227.6894 \cdot b_1 = 52.3564$. Hence, the regression will be even heritability ($b_1 = h^2 = 0.2299$).

The selection index will have the simple form (10):

$$I = 0.2299 \cdot P_1 \quad (10)$$

The selection index variable (S_I^2) was as following formula (11):

$$S_I^2 = b' \cdot V \cdot b = 0.2299 \cdot 227.6894 \cdot 0.2299 = 12.0392 \quad (11)$$

with an error (S_I) = 3.4698.

As regarding the aggregate genotype variance, (S_H^2) this was following formula (12):

$$S_H^2 = v' \cdot G \cdot v = 1 \cdot 52.3564 \cdot 1 = 52.3564 \quad (12)$$

associated with an error (S_H) of 7.2358 (13):

$$S_H = \sqrt{S_H^2} = \sqrt{52.3564} = 7.2358. \quad (13)$$

The selection accuracy is estimated by the correlation between genotype and phenotype (14):

$$r_{IH} = \sqrt{\frac{S_I^2}{S_H^2}} = \sqrt{\frac{12.0392}{52.3564}} = 0.4795 \quad (14)$$

These data shown that the aggregate genotype can be predicted with a probability of 47.95 % if the practice were used selection index considered, *the selection index for the body depth* respectively.

The expected genetic progress on the aggregate genotype based on this selection index will be 3.4698 units of selection intensity (15):

$$\Delta H = r_{IH} \cdot i \cdot S_H = 0.4795 \cdot i \cdot 7.2358 = 3.4698 \cdot i \quad (15)$$

where i is the selection intensity.

In conclusion, the genetic progress per generation is 3.4698 mm for body depth.

For the third character, the system of equations for *the selection index for the standard length* will be: $1977.7 \cdot b_1 = 458.4445$. Hence, the regression will be the same as heritability ($b_1 = h^2 = 0.2318$).

The selection index will have the simple form (16):

$$I = 0.2318 \cdot P_1 \quad (16)$$

The selection index variable (S_I^2) was as follow formula (17):

$$S_I^2 = b' \cdot V \cdot b = 0.2318 \cdot 1977.7 \cdot 0.2318 = 106.2699 \quad (17)$$

with an error (S_I) = 10.3087.

The aggregate genotype variance (S_H^2) was the formula (18):

$$S_H^2 = v' \cdot G \cdot v = 1 \cdot 458.4445 \cdot 1 = 458.4445 \tag{18}$$

with an error (S_H) of 21.4113 (19):

$$S_H = \sqrt{S_H^2} = \sqrt{458.4445} = 21.4113 \tag{19}$$

The selection accuracy is estimated by the correlation between genotype and phenotype (20):

$$r_{IH} = \sqrt{\frac{S_I^2}{S_H^2}} = \sqrt{\frac{106.2699}{458.4445}} = 0.4815 \tag{20}$$

This means that the aggregate genotype can be predicted with a probability of 48.15% if the practice were used selection index considered, *the selection index for the standard length* respectively.

The expected genetic progress on the aggregate genotype based on this selection index will be 10.3087 units of selection intensity (21):

$$\Delta H = r_{IH} \cdot i \cdot S_H = 0.4815 \cdot i \cdot 21.4113 = 10.3087 \cdot i \tag{21}$$

where *i* is the selection intensity.

In conclusion, the genetic progress per generation is 10.3087 mm for standard length.

Summarizing the data after compiling the three variants of indices, it was proceed to identify the optimal variant, that which ensures the highest precision, expressed by the correlation between genotype and phenotype value. The results are described in Table 1 below.

Table 1. The Comparative Data of Selection Indices for a Single Morphological Trait in Ropsa Carp

Considered Traits	The Regression (b)	The Index Variance (S_I^2)	The Aggregate Genotype Variance (S_H^2)	Selection Accuracy ($r_{H,I}$)	The Global Genetic Progress (ΔH)	The Partial Genetic Progress (ΔG_i)
The Live Weight (W)	$b_1 = 0.2727$	3676.2	13482	0.5222	-	$\Delta G_1 = 60.6318$
The Body Depth BD	$b_2 = 0.2299$	12.0392	52.3564	0.4795	-	$\Delta G_2 = 3.4698$
The Standard Length (SL)	$b_3 = 0.2318$	106.2699	458.4445	0.4815	-	$\Delta G_3 = 10.3087$

4. Conclusions and Recommendations

By using the selection indices that have been determined, the conclusions are:

- In the case of separate selection by one character the best results were obtained for the live weight selection (the selection accuracy was 52.22%). The estimated genetic progress per generation will be 60.6318 grams for life weight.
- The lowest result was recorded for selection for the body depth (47.95%).
- The indices values of the analyzed characters refer only to the study over the population and environmental conditions in which it has evolved.

The recommendation is that genetic improvement programs to be properly implemented so as to allow increased production of fish meat at a low price. This will a clear benefit for producers and consumers leading to the

emergence of new market opportunities, variety of quality products with greater frequency on the market; ensuring food safety.

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