

GENETIC PARAMETERS OF BODY WEIGHT, FEMALE SPAWNING DATE, AND AGE AT SEXUAL MATURATION IN RAINBOW TROUT

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INTRODUCTION

A synthetic strain of rainbow trout (*Oncorhynchus mykiss*) characterised by fast growth, a spring spawning season, and a low incidence of precocious maturation is being developed for Ontario aquaculture. Faster growth reduces costs by decreasing the amount of time required to rear fish to market size. Spawning time also affects production since the seasonal reproductive cycle causes corresponding fluctuations in product availability and facility use. Rates of pre-harvest maturation (especially precocious males) affect return, since the small size and poor flesh quality of mature trout make these animals essentially unmarketable. In Ontario, there are currently no rainbow trout strains available that perform well for these three traits. Availability of this synthetic strain would give farmers a more flexible production schedule and increase efficiency.

An essential step in the development of this strain is estimation of the genetic parameters of these important traits. In this paper, we discuss the results of two studies that estimated genetic parameters for weight at 2 years of age, female spawning date at 3 and 4 years of age, and age at sexual maturation. These results were used to determine the most efficient breeding scheme to develop a synthetic strain of rainbow trout exhibiting the desired characteristics.

MATERIALS AND METHODS

Experimental Design and Husbandry. The study was conducted at the Alma Aquaculture Research Station, University of Guelph, Guelph, Ontario, Canada. Fertilised eggs from three diverse farmed strains of rainbow trout were brought to the research station in 1991 to form a base population (G0) (McMillan and McKay, 1992; McKay and McMillan, 1997). From November 1995 to March 1996, a series of individual matings were done among the three G0 strains to form a complete diallel cross (G1). All reciprocal crosses were made, forming nine strain combinations.

G0 and G1 were raised indoors under similar optimal conditions (McMillan and McKay, 1992; McKay and McMillan, 1997), including constant 8.5°C water temperature and simulated natural photoperiod. Males and females were housed together. Individuals were marked with passive integrated transponder (PIT) tags prior to the first spawning season. After tagging, all fish were individually weighed and checked for gamete production every three months until the beginning of the first female spawning season. Female spawn dates were recorded for individuals of each year class at 3 and/or 4 years of age. Imminent spawning was assessed in anaesthetised females by colour, look and feel of the abdomen, and vent extension. Females judged close to spawning were checked weekly for ripeness. Ripe females (those from whom eggs were easily stripped) were anaesthetised and eggs stripped by manual pressure to the

abdomen. G1 families had been pooled together after fertilisation, so exact parentage of G1 individuals was determined from microsatellite DNA analysis (McDonald, 2001), revealing 29 maternal half-sib families, 38 paternal half-sib families, and 182 full-sib families in this year class. The G1 generation consisted of 567 individuals.

Statistics. In G0, 2-year old weight was defined as the individual's body weight measured between May 11 and 15, 1993. In G1, 2-year old weight was estimated from individual weights taken between 570 and 970 days post-fertilisation (approximately 4 weighs per fish). For each G1 individual, a linear regression of weight on age in days was used to estimate weight at 730 days post-fertilisation (2 years old). Female spawn dates at 3 and 4 years of age were defined as the period after October 1, in days, that eggs were stripped from a particular female. Age at sexual maturation (ASM) was a categorical trait defined as the year in which an individual first produced gametes. There were 4 levels of ASM: males that matured at 2, males that matured at 3, females that matured at 3, and females that matured at 4 years of age.

Genetic parameters for all traits were calculated using VCE4 (Neumaier and Groeneveld, 1998) with restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) animal model. Heritability and correlations of 2-year old weight, spawn date at 3 years old, and spawn date at 4 years old were estimated with the following model:

$$y_{ijkl} = \mu + GS_i + X_j + A_k + e_{ijkl}$$

where y_{ijkl} was an observation of 2-year old weight, 3-year old spawn date, or 4-year old spawn date for individual k ; μ is the population mean, GS_i was the fixed effect of the animal's combined generation and strain i ($i=1, \dots, 12$), X_j was the fixed effect of the animal's sex j ($j=1,2$), A_k was the additive genetic value of individual k , and e_{ijkl} was the residual error associated with observation $ijkl$. Heritability of ASM and correlations of ASM with weight at 2 years of age were estimated with the same model, except y_{ijkl} was an observation of 2-year old weight or ASM. Correlations between ASM and weight at 2 years old were also estimated separately for males and females using the same model, but with the effect of sex removed.

RESULTS AND DISCUSSION

Heritability estimates. Two-year old weight, spawn date, and ASM heritability estimates ranged from 0.258 to 0.659 (Table 1), so these traits should all respond well to selection. Published weight heritabilities for this age are usually around 0.2 (e.g. Gjerde and Gjedrem, 1984; McKay *et al.*, 1986; Gall and Huang, 1988; Crandell and Gall, 1993). The higher estimate from this study may have been partly due to the high genetic and phenotypic diversity of the crossed population. Spawning time and ASM heritability estimates from these studies are similar to other published estimates (e.g. Gjerde and Gjedrem, 1984; McKay *et al.*, 1986; Siitonen and Gall, 1989; Su *et al.*, 1997).

Correlations between traits. Phenotypic correlations between 2-year old weight and spawn date were low and negative, but genetic correlations between these traits were close to zero. Therefore, there was no relationship between an animal's additive genetic value for weight and its additive genetic value for spawn date and it is unlikely that genes controlling these traits are

linked. Published phenotypic and genetic correlations between weight and spawning time have been positive and low to moderate (Su *et al.*, 1997; Huang and Gall, 1990), but have been estimated from selected lines raised in warmer water and maturing earlier than those in this project.

Phenotypic and genetic correlations between weight at 2 years old and ASM were moderate and negative. Estimates for males and females were very similar. Selection for high weight will cause undesirable higher rates of precocious maturation in the population, and culling early-maturing animals will slow the rate of progress of weight. The correlations, however, are not very strong, so there are animals with suitable breeding values for weight and maturation. Published phenotypic and genetic correlations between weight and maturity have been low and positive (Gjerde and Gjedrem, 1984).

Phenotypic and genetic correlations between spawn date at 3 years old and spawn date at 4 years old were very high and positive. The phenotypic correlation of 0.82 may be considered an estimate of the repeatability of spawn date. Genetically, correlations between traits are due mainly to pleiotropy (Falconer and Mackay, 1996), so it is probable that the same genes control spawning time from year to year.

Table 1. Estimated genetic parameters^A for 2-year old weight (2YWT), female spawning dates at 3 and 4 years old (3YSP, 4YSP), age at sexual maturation (ASM), and male and female age at sexual maturation (MASM, FASM)

	2YWT	3YSP	4YSP	ASM	MASM	FASM
2YWT (g)	0.490	-0.002	-0.019	-0.412	-0.326	-0.349
3YSP (d)	-0.200	0.659	0.916			
4YSP (d)	-0.169	0.821	0.458			
ASM	-0.236			0.258		
MASM	-0.280				NE	
FASM	-0.254					NE

^AHeritabilities are on the diagonal (NE = not estimated); genetic and phenotypic correlations are above and below the diagonals, respectively.

CONCLUSION

Selection would be an appropriate strategy to change growth, spawning time, and rates of precocious maturation. Due to negative phenotypic correlations among some traits, simultaneous phenotypic selection on all three traits may not be an effective method to produce a strain with fast growth, delayed spawning, and a low rate of precocious maturation. Since there was no genetic correlation between weight and spawn date, simultaneous selection on BLUP-generated estimated breeding values (EBVs) for weight and spawn date would be more efficient than phenotypic selection in improving these two traits. There should be more potential parents with good EBVs for weight and spawn date since these are not related. In addition, males could also be selected for spawning time. More intense selection could be applied with this method, resulting in faster genetic progress. Since there are negative genetic correlations between weight and age at maturation, care should be taken that not too much

emphasis be placed on weight improvement, since it is likely to have undesirable effects on maturation rates. Further study is needed to determine the genetic relationship between spawning time and age at maturation.

ACKNOWLEDGEMENTS

The authors wish to acknowledge the staff Alma Aquaculture Research Station, assistance from V.M. Quinton, and contributions by Aqua-Cage Fisheries Ltd. and Blue Spring Trout Farms Ltd. This research was funded by the Ontario Ministry of Agriculture, Food and Rural Affairs through the Applied Fish Production Research Program.

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