

Estimation of genetic parameters of feed conversion ratio based on individual phenotypes and genomic data in sea bass

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Summary

We estimated genetic parameters of feed conversion ratio (FCR) and daily growth coefficient (DGC) using individual phenotypes measured in aquariums under a restricted feeding regime and genomic information on 2,722 SNP markers. The results showed a moderate heritability of both traits (0.26 for FCR and 0.41 for DGC) as well as close to unity negative genetic correlation between them. Thus, FCR of fish in aquariums could be improved by selecting fish for higher DGC. Nevertheless, these results must be taken with caution until we know whether individual FCR measured in aquariums also reflects the FCR of fish reared in groups.

Keywords: feed efficiency, fish, genomics

Introduction

Improving feed conversion ratio (FCR) is crucial to enhance the sustainability of fish farming (Besson *et al.*, 2017). Feed is indeed a major economic and environmental cost of fish production. Improving FCR by selective breeding has already been achieved in terrestrial livestock species (Cai *et al.*, 2008). However, breeding fish for better FCR is yet impossible because measuring individual feed intake accurately is problematic when fish are kept in groups. Hence, the aim of this study was to develop and implement a method to accurately phenotype individual fish for FCR by rearing fish in individual aquariums under restricted feeding. The fish phenotyped for individual FCR were genotyped for 2,722 SNPs markers in order to estimate the genomic heritability of individual FCR as well as genetic correlations between individual FCR and growth traits.

Material and Methods

Animals

Two females were mated with 30 males in a full factorial mating design. The fish produced were mixed and kept in 2 tanks at 48h post-fertilization. The parents came from two generations of divergent selection on weight loss during fasting. 15 males and 1 female were fish that lost more weight (J+) and 15 males and 1 female were fish that lost less weight (J-).

Individual phenotypes

Two hundred 10 l aquariums were used. European sea bass (25g on average) were first

reared in groups of five in each aquarium, to enable adaptation of the fish to the new environment. After 14 days, they were randomly split alone in aquariums. After 14 days in isolation, the fish were weighed (body weight, BW) in a “go, no go” biometrics. The fish that lost weight during this period were removed. The remaining ones were kept in aquariums for 2 more periods of 14 days. In total, a “successful” fish stayed 56 days in aquarium and was weighed 5 times (Figure 1) before being replaced by another fish in the aquarium. Thus, fish were phenotyped in successive and possibly overlapping batches.

Individual BW at each biometrics was used to estimate individual feeding ration for the following period. This ration (1.3% BW/day) was half the standard ration (2.6% BW/day) given by the feed manufacturer. Fish were fed automatically once a day in the morning. Every afternoon, the number of uneaten pellets was counted in each aquarium and converted to grams (1 pellet \approx 0.00925 g). We could then calculate the individual feed conversion ratio (FCR) of the fish for each period by dividing individual feed intake (FI) by body weight gain (BWG).

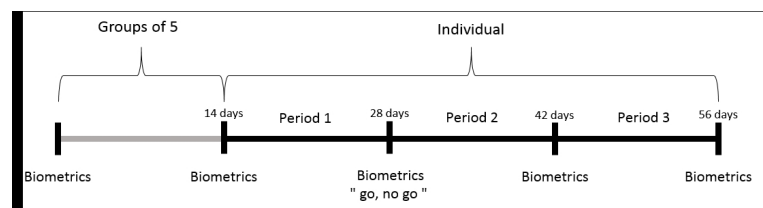


Figure 1. Experimental scheme.

Among the 831 fish tested in aquariums, 185 fish did not pass the “go, no go” biometrics. Thus 646 fish were evaluated for individual FCR for 3 periods. For those 646 fish, we calculated their cumulated FCR (noted as FCR) using their cumulated weight gain (BWG) and cumulated feed intake (FI) over periods 2 and 3. We excluded fish with aberrant performances: 6 fish with negative cumulated FCR and 52 fish with cumulated FCR higher than 2.60. Applying these thresholds, we could keep 588 fish with data available for FCR and DGC. DGC is the daily growth coefficient calculated for period 2 and 3 as:

$$(1)$$

Where initial BW_i is the weight at the beginning of period 2, final BW_f is the weight at the end of period 3 and D_{i-f} is 28 days, the cumulated duration of period 2 and 3. We also calculated the log-residual body weight gain (logRBW) based on the following linear regression:

$$(2)$$

Where e_i is the error term that represent the logRBW of fish i . We used log transform BWG and FI to estimate RBW in order to improve the homogeneity of variance throughout the regression.

Genotyping and parentage assignment

Fin clips from 400 out of 588 individually phenotyped fish and their 32 parents were

sent to LABOGENA for DNA extraction and genotyping for 2,722 SNP markers. After a quality control ignoring all monomorphic SNPs and all SNPs with a MAF below 5% and a call rate below 90%, we could keep 2,119 SNPs. We used VITASSIGN, an exclusion-based parentage assignment software adapted to SNP markers, to retrieve the pedigree of the 400 fish.

Genetic parameters

Variance components were estimated based on multivariate linear mixed animal models fitted by restricted maximum likelihood in AIREMLF90, using the genomic relationship matrix obtained from the 2,119 SNP genotypes:

$$(3)$$

Where Y_{ijkl} is the observed trait ($\log(\text{FCR})$, $\log(\text{DGC})$ or $\log(\text{RBW})$) of individual i from Origin j , reared in tank k before tagging and phenotyped in aquariums in batch l . We used log transformed FCR and DGC in order to linearize the relationships between the traits. μ is the overall mean, origin_j is the genetic group of fish (1 for fish with two J+ parents, 2 for fish with one J+ and one J- parent, 3 for fish with two J- parents), tank_k is the fixed effect of the rearing tank of the fish before tagging (tank 1 or 2), batch_l is the fixed effect of the batch in which the fish has been phenotyped in aquariums (1 to 10), animal_i is the additive genetic effect of animal i and ε_{ijkl} is the random residual.

Results

The average FCR was estimated to be 1.46 with a CV of 0.22. There were strong negative phenotypic correlations between $\log(\text{FCR})$, $\log(\text{DGC})$ and $\log(\text{RBW})$ meaning that the fish with the best feed efficiency were the fish that grew faster in aquariums. There was also a moderate phenotypic correlation between $\log(\text{DGC})$ and $\log(\text{RBW})$ (Figure 2). The three traits showed moderate heritability and strong genetic correlations (Table 1). We also calculated the correlation between the FCR measured in period 2 and period 3 and found a strong positive genetic correlation of 0.96 (se = 0.43).

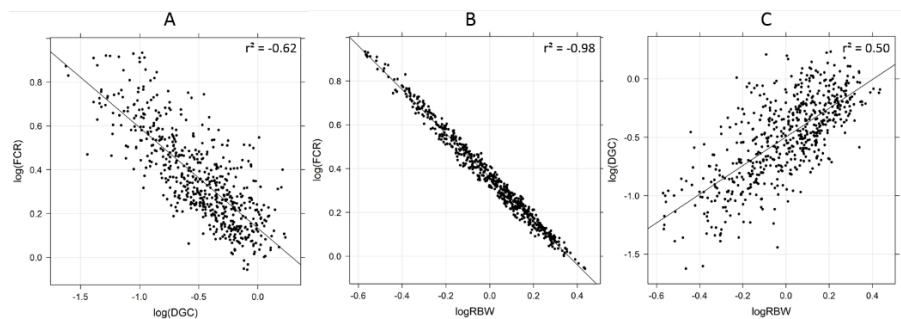


Figure 2. Linear regression of $\log(\text{FCR})$ on $\log(\text{DGC})$ in panel A, of $\log(\text{FCR})$ on $\log(\text{RBW})$ in panel B and of $\log(\text{DGC})$ on $\log(\text{RBW})$ in panel C. In the upper right corner of panels is the coefficient of determination (r^2) of the regressions.

Table 1. Heritability of $\log(\text{FCR})$, $\log(\text{DGC})$ and $\log(\text{RBW})$ on the diagonal, genetic correlations above the diagonal and phenotypic correlations below the diagonal. Standard

errors are between brackets.

	log(FCR)	log(DGC)	logRBW
log(FCR)	0.26 (0.06)	-0.99 (0.10)	-0.94 (0.39)
log(DGC)	-0.78	0.41 (0.08)	0.99 (0.03)
logRBW	-0.99	0.71	0.20 (0.05)

Discussion

This is the first study presenting a method to evaluate the genetic variation of individual feed intake and FCR in European sea bass. Compared to other methods, such as X-ray analysis, phenotyping individuals in aquariums allows to estimate FCR over a continuous period of several weeks with a very precise estimate of feed intake. With this new method, we found phenotypic variability in FCR and also in DGC. The phenotypic coefficient of variation for FCR was close to that observed in Nile tilapia also phenotyped individually by video observation (de Verdal *et al.*, 2017).

The genetic analysis showed that log(FCR), log(DGC) and logRBW measured in aquariums are all heritable and are also strongly genetically correlated. The strong phenotypic and genetic correlations between the traits could be explained by the setup of the experiment. Indeed, we chose to estimate FCR under restricted feeding. When the ration is restricted, the fish that grow faster are consequently more efficient fish. Thus, in these conditions, selection for better DGC in aquariums would lead to lower FCR in aquariums. This trend was also found by Drouilhet *et al.* (2015) on rabbits who showed that selection for average daily gain under restricted feeding regime lead to a reduction of FCR. Our results suggest also that the response to selection in FCR would be larger when selecting on DGC rather than selecting on FCR due to the higher heritability of DGC and the close to unity genetic correlation between them.

This is an encouraging result towards possible genetic improvement of feed efficiency in fish. Nevertheless, we do not yet know whether the individual FCR measured in aquariums does reflect the performance of the fish reared in groups – which is our final target trait. Thus in a second experiment, we will test the relationship between individual and group FCR by evaluating the FCR of groups of fish constituted according to their individual FCR.

Acknowledgements

This work is part of the EMBRIC project, funded by the European Union under H2020 under grant agreement No 654008.

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