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Estimates of heritabilities and genetic correlations for growth and carcass traits in gilthead seabream (*Sparus auratus* L.), under industrial conditions

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ABSTRACT

In this study, for the first time on gilthead seabream (*Sparus auratus* L.), genetic parameters for growth and carcass traits were estimated at 509 days (harvest size), and for growth only at another three ages (130, 165 and 330 days). A total of 867 offspring from an industrial mass spawning of 66 broodstocks were analysed. Parental assignment was inferred using the RimA multiplex PCR designed by Navarro et al. [Navarro, A., Badilla, R., Zamorano, M.J., Pasamontes, V., Hildebrandt, S., Sánchez, J.J., Afonso, J.M., 2008. Development of two new microsatellite multiplex PCRs for three sparid species: Gilthead seabream (*Sparus auratus* L.), red porgy (*Pagrus pagrus* L.) and redbanded seabream (*P. auriga*, Valenciennes, 1843) and their application to paternity studies. Aquaculture 285, 30–37.] and 100% success was obtained. Seventeen dams and 11 sires contributed to the spawn and a total of 89 full-sib families (eight paternal half-sib families and 16 maternal half-sib families) were represented. The heritability estimates at harvest were 0.34±0.06 for body weight, 0.33±0.07 for fork length, 0.13±0.04 for condition factor, 0.26±0.06 for gutted body weight, 0.15±0.04 for fillet weight, 0.31±0.07 for dressing percentage, and 0.12±0.03 for fillet percentage. For growth traits at different ages, heritabilities ranged from 0.28 to 0.34 for weight, from 0.27 to 0.35 for length, and from 0.05 to 0.13 for condition factor. At any age, the correlation between weight and length was close to one. Correlations for lengths or weights at two consecutive ages were also high but they decreased with increasing difference in age. Negative and medium genetic correlations between fillet percentage and growth traits (weight and length) were obtained, however these correlations were positive and high for fillet weight. These data suggest that direct selection of length, which is an easily measurable trait, also improves carcass traits. However, the inclusion of fillet percentage in breeding programmes is recommended due to the negative genetic correlation with length. These results highlight the potential for the gilthead seabream industry to improve its production not only through handling but also through the exploitation of additive genetic variation.

1. Introduction

Gilthead seabream (*Sparus auratus* L.) is a species with a wide geographical range in the wild (Lythageo and Lythageo, 1992; Moretti et al., 1999) whose eurytherm and euryhaline characteristics have led to the expansion and consolidation of its culture in nearly all Mediterranean and Mid-west Atlantic countries and to a growth in production at an annual rate of almost 15% in the last decade, reaching 124,640 tons in 2006 (APROMAR, 2007).

The growth and consolidation of the gilthead seabream industry have been accompanied by the stabilisation of the market prices in the last four years but with important seasonal fluctuations that have forced companies to optimise their yield and to plan their production more and more. In this sense, competitiveness among gilthead seabream companies has improved through higher farming pressure and intensity, minimising of costs and/or enhanced product value. With this aim, companies perform different courses of action related to nutrition, stock management, illness prevention or even the location of their facilities.

However, strategies that involve the development of selection schemes in gilthead seabream for traits of economic interest are scarce (Afonso et al., 1998; Montero et al., 2001; Gorshkov et al., 2002), partly due to the reproductive characteristics of the species. In commercial gilthead seabream broodstocks, effective population sizes are low due to the high fecundity rate, the high variance in family size and fewer males than females contributing in each mass-spawning (Brown et al., 2005). Nevertheless, mass-spawning is widely used among broodstocks ranging between 40 and 60 individuals in order to assure quality and offspring survival. From a genetic point of view, this industrial strategy has the advantage that common environmental sources are reduced, thus raising the precision of genetic parameter estimations (Herbinger et al., 1999). But on the other hand, it prevents knowing the genealogy of fish under culture conditions, which is

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absolutely necessary to estimate genetic parameters and to introduce selection programmes. For this reason studies related to genetic parameter estimations for traits of economic interest are scarce. Knibb et al. (1997) estimated realised heritability for weight at harvest size, after a single generation of mass selection. Montero et al. (2001) estimated the heritability of plasmatic cortisol measured after subjecting the fish to confinement stress. Castro et al. (2008) reported estimations of heritability for skeletal abnormalities (lordosis and lack of operculum) in fingerlings, on an experimental scale.

The introduction of breeding programmes in this kind of industrial production system needs both physical tagging and genetic identification of the exploited fish (Wesmajervi et al., 2006). In gilthead seabream, it is possible to physically identify fingerlings through Passive Integrated Transponder (PIT) tagging systems (Navarro et al., 2006). It is also possible to reconstruct parent–offspring relationships by analysing enough microsatellite markers (Batargias et al., 1999; Castro et al., 2007; Borrell et al., 2007), which can be combined in multiplex PCRs to reduce costs (Navarro et al., 2008).

Using industrial production systems and combining physical tagging and genetic identification of fish, the aim of this study was to estimate heritabilities and genetic correlations for growth and carcass traits at hatchery and harvest sizes from offspring of a commercial gilthead seabream broodstock.

2. Materials and methods

2.1. Rearing conditions and analysed traits

An egg batch obtained from 66 breeders of the Tinamenor S.A. company (San Vicente de la Barquera, Cantabria, Spain) was cultured in the industrial-like facilities of the Instituto Canario de Ciencias Marinas (ICCM, Gran Canaria, Spain). Eggs and larvae were reared in the conditions described by Roo et al. (1999). Fingerlings were not graded in terms of deformities due to the stock's good quality (Afonso and Roo, 2007). At 130 days post-hatching (4.8±1.1 g) (mean±standard deviation), all fish were taken to the facilities of the Playa de Vargas 2001 S.L. Company (PLV2001, Gran Canaria, Spain), except a sample of 472 individuals, which remained in the on-growing facilities of the ICCM.

The fish that remained in the ICCM were individually tagged (130 days post-hatching) in the abdominal cavity with a Passive Integrated Transponder (PIT; Trovan Daimler-Benz), following the tagging protocol described by Navarro et al. (2006), and were distributed in three 1000-l tanks where they were reared under intensive conditions to commercial size (300–500 g). Food was provided through self-feeders using commercial fish feed (Proaqua S.A., Dueñas-Palencia, Spain). Water temperature ranged from 19.3±0.2 °C in March to 25.0±0.3 °C in September. Values for dissolved oxygen and water flow were 6.0±0.5 ppm and 21 l min^{-1}, respectively. Fish density ranged from 2.3±0.1 kg m^{-3} at the beginning of the experiment to 35.0±3.9 kg m^{-3} at the end. At the ages of 130, 165, 330 days post-hatching, the body weight and fork length of all fish were measured; 130 and 165 days are approximately the sale ages for fingerlings (2–20 g). 165 days is also the age at which the industry carries out the final reorganisation of their fish baths and/or the removal of deformed fish. The age of 330 days corresponded to the reproductive season and was chosen because at this point an incipient sexual maturity exists (Zohar et al., 1978; Micale and Perdichizzi, 1990) that might negatively interfere with growth (Ginés et al., 2003).

The fish at PLV2001 were reared in a cage and fed with commercial fish feed (Proaqua S.A., Dueñas-Palencia, Spain and BioMar A/S, Brande, Denmark) at a daily specific feed rate of 5.6–1% per body weight. Fish densities ranged from 1 kg m^{-3} during the hatchery period to 25 kg m^{-3} at the end of the on-growing period, and dissolved oxygen in the water had an average value of 7 ppm.

At harvest size (509 days post-hatching), at the end of July, fish from ICCM (472 fish) and a sample of fish from PLV2001 (395 fish) were slaughtered and the following traits were recorded: body weight, fork length and gutted body weight. Fish were manually skinned and filleted without including the nape and the belly flap. Both fillets were weighed together. Derived traits were also calculated as follows: dressing percentage (100×gutted body weight×body $weight^{-1}$), fillet percentage (100×fillet weight×body $weight^{-1}$) and condition factor (100×body weight×$fork\ length^{-3}$).

2.2. Genotyping and parental assignment

All 867 offspring and 66 breeders were genetically characterised using the nine microsatellite markers RimA multiplex designed by Navarro et al. (2008). A fragment of the caudal fin was preserved in 1 ml of absolute ethanol until DNA extractions. DNA was extracted following the phenol–chloroform method (Sambrook et al., 1989). DNA was stored at 4 °C in 50 µl of TE 1X solution. Amplification, running and reading conditions for the microsatellite markers are described in Navarro et al. (2008). Familial assignments for gilthead seabream broodstock of unknown gender were determined using the exclusion method with non-commercial software provided by Dr. J. Fernández (INIA-Madrid, Spain).

2.3. Data analysis

All data were tested for normality and homogeneity of variances, and then analysed using a General Linear Model, in order to detect the effects of facility and tank, using SPSS (v. 15.0) (SPSS, Chicago, IL, USA). Then, variance components for body weight, fork length, condition factor, gutted body weight, fillet weight, dressing percentage and fillet percentage were estimated by Restricted Maximum Likelihood (REML) using the following linear model:

$$y = X\beta + Zu + e$$

where y was the data recorded for the studied traits, β the fixed effects (facility and tank) and u the random animal genetic effect. The model was resolved with the software package VCE (v. 5.1.2) (Kovač et al., 2002). The magnitude of estimated heritability was established, following the classification of Cardellino and Rovira (1987), as low (0.05–0.15), medium (0.20–0.40), high (0.45–0.60), and very high (>0.65). Correlations were classed as low (0–0.40), medium (0.45–0.55) and high (0.60–1), regardless of the sign.

Genotype–environment interactions (G×E) were estimated through genetic correlations between a trait in the PLV2001 facility and the same trait in the ICCM facility, using VCE (v. 5.1.2) (Kovač et al., 2002).

3. Results

3.1. Genotyping and parental assignment

One hundred percent success in familial assignment (each offspring was assigned to a single parent pair) was obtained with RimA, using the exclusion method with one tolerated error. After revising genotypes, all errors were identified as null alleles. Within broodstocks, only marker *PbMS2* showed null alleles with a frequency of 5.36%. In offspring, as expected under the Hardy–Weinberg equilibrium, this frequency was very similar, at 5.07%, indicating that there was no mutation rate activity during segregation. Only 28 fish, 17 females and 11 males, out of the 66 breeders, contributed to the spawn. A total of 89 full-sib families (eight paternal half-sib families and 16 maternal half-sib families) were represented in the 867 offspring sample, with a mean of 9.7 descendents per family (ranging between 1 and 53).

3.2. Growth and carcass traits, and GxE interactions

At 130 days both the individuals sent to the company and those which remained in the ICCM showed the same values for body weight, fork length and condition factor. Table 1 depicts these growth