

BODY-SHAPE VARIATION BETWEEN TWO GENERATIONS OF REARED GILTHEAD SEA BREAM (*Sparus aurata*)

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Introduction

Although body shape is an important component of product quality in finfish Mediterranean aquaculture, it is rarely included in selective breeding programs (Kause et al., 2004). As in the case of other phenotypic characters (e.g. growth rate, food conversion ratio), body-shape is expected to be controlled by genetic and environmental factors, as well as by their interaction (Costa et al., 2010).

The aim of the present study was to compare the body shape between the first (G1) and the third (G3) generation of a gilthead sea bream population which has been subjected to selective breeding based on an index which includes growth rate, fat content and deformities.

Materials and methods

A group of 2214 animals from the G1 generation (1082 individuals, established in 2002) and from the G3 generation (1132 individuals, established in 2008) was provided from the genetic selection databank of a commercial farm (Andromeda S.A.). The same methodology was followed for both generations, during the hatchery and on-growing phases up to the mean standard length of 23.4cm (G1) and 24.7cm (G3). Shape analysis was performed on 13 landmark measurements which were taken on the digital photographs of anaesthetized individuals (figure 1). Specimens with severe skeletal deformities were excluded from the analysis (8% in total). The detailed methodology of the geometric morphometrics that implemented is presented elsewhere (e.g. Georgakopoulou et al., 2007).

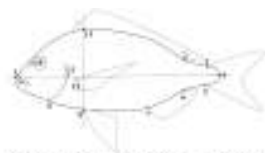


Fig. 1. Location of the 13 homologous landmarks used for the shape analysis.

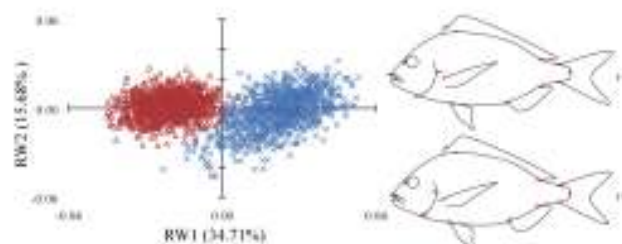


Fig. 2. The plot of the first two axes (RW1 vs RW2) of RWA ($\times G_1$, $\times G_3$). Vector diagrams were estimated relatively to the extreme values of RW1 (-1, +1).

The first two relative warps (RWs) from the relative warp analysis (RWA) explained 50.39% of total variation in body shape. Significant differences were found between the two generations in both RWs ($p < 0.001$) (figure 2). The coefficient of variation (CV*) of RW1 scores was larger in G1 (56.75%) than in G3 generation (42.36%). Both RWs were significantly independent from the centroid size (CS) ($p > 0.05$). Vector diagrams showed that when compared with the G1, the G3 specimens were characterized by an anterior shift of the upper jaw and an posterior shift of gill cover, a ventral distal shift of the anal fin-bases, a posterior transposition of the posterior base of the dorsal fin, an anterior shift of the base of the caudal fin and finally a posterior shift of the base of pectoral and pelvic fins (figure 2).

Canonical Variate Analysis (CVA) was applied for the comparison of body shape between the two groups. The distribution of the samples along the CV axis demonstrated a significant discrimination between the individuals of the two generations (Wilks' $\lambda = 0.095$, $p < 0.001$). The vector diagrams of CVA showed a similar pattern as those from RWA (data not shown). Our results indicate the significant shape variation between two generations of gilthead sea bream. Given that Andromeda's S.A. selective breeding program is based on an index that includes primarily the growth rate (among others), it can be assumed that the demonstrated shape variation might be attributed to this parameter. The increment of snout and gill-cover in G3 generation could at least partially support this hypothesis, as these characters are highly correlated with feeding and respiration capacity respectively. Indeed, our preliminary results show a significant correlation between the RW1 and the individual weight in each generation ($r = 0.25-0.26$, $p < 0.05$). Additionally, it could be assumed that the observed shape differences may be a result of environmental shifts (e.g. annual fluctuations of temperature during the on-growing phase), or/and an interaction between genetic background of the populations and the environment. Further analysis is required to determine the precise source of this variation.

As future aspects, we propose the body shape comparison between wild and reared populations, in order -primarily- to evaluate the best available reference point and secondarily to be included as a threshold in the selection criteria. The advantages of the use of geometric morphometrics in the study of shape variability in selective breeding programs are discussed by Loizides et al. (current volume).

This study was partially funded by the program NSRF 2007-2013, «Competitiveness & Entrepreneurship» (call Cooperation I, Project No 09SYN-24-619) of the Ministry of Education, Lifelong Learning and Religious Affairs, Greece.

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HERITABILITY OF BODY SHAPE IN GILTHEAD SEABREAM (*Sparus aurata*). A GEOMETRIC MORPHOMETRIC APPROACH

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Introduction

In order to establish genetic improvement programs it is crucial to estimate the genetic variation for traits of commercial interest. Regarding gilthead sea bream, existing relevant studies concern among other the estimation of genetic parameters for growth, visceral fat content and other composition and carcass traits and the development of skeletal deformities (Castro et al., 2008; Antonello et al., 2009; Navarro et al., 2009). However, to our knowledge no heritability estimations have been reported for the body shape of gilthead sea bream though is a basal component of product quality in Mediterranean finfish aquaculture.

The aim of the present study was to report the heritability estimates of body shape in reared gilthead sea bream and to investigate the use of geometric morphometrics (GM) in selective breeding programs.

Materials and methods

A group of 2153 animals was sampled at mean weight of ca 437g, from the genetic selection databank of a commercial farm (Andromeda S.A.). All fish originated from a mass spawning event of two broodstock tanks (n=34 each). Rearing took place according to the standard production procedure of the company with the exception of grading. After PIT tagging and fin clipping, the fish (~65g) were transferred to a common cage and the pedigree was constructed from a commercial company using microsatellite markers.

Body shape analysis was based on the landmark configuration of Loizides et al. (current volume). The relative warp analysis (RWA) and the GM methodology that were implemented are presented elsewhere (e.g. Georgakopoulou et al., 2007). The variance components of the first four relative warps (RWs) were estimated by Restricted Maximum Likelihood (REML) under an animal model: $y = X\beta + Zu + e$; where y is the vector of RW scores, β is the vector of the fixed effect (cage of origin= broodstock) and u the vector random additive genetic effects.

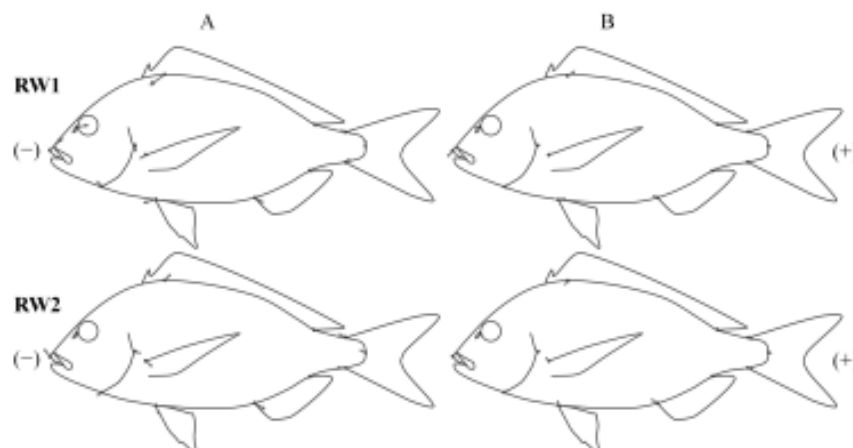


Fig. 1. Vector diagrams of the first two RWs, relative to their extreme values (-, +). A, B indicate the two distinct landmark configurations.

Results and Discussion

The first four RWs explained the 52.80% of the total variation of body shape. All RWs were significantly independent from the centroid size (CS) and the standard length of the individuals (all $p > 0.05$). Vector diagrams demonstrated that the shape variation along the RW1 was mainly attributed to shifts of the pre-anal area landmarks. The range of this variation was defined by two distinct landmark configurations, A and B (figure 1, RW1). Compared with the B configuration, A configuration was mainly related to a dorso-posterior shift of the upper jaw, a ventro-anterior shift of the distal dorsal margin of the body at the level of the pelvic fins, a posterior shift of the anterior tip of the eye, a distal shift of the pelvic

fin-base and the anterior base of the anal-fin (figure 1, RW1). Concerning the body-shape variation along the RW2, besides the anatomical shifts of the pre-anal landmarks, shifts of caudal-fin landmarks were observed as well (figure 1, RW2).

The heritability estimates for the RWs were as follows ($h^2 \pm SE$): for RW1 0.30 ± 0.09 , for RW2 0.36 ± 0.10 , for RW3 0.14 ± 0.06 and for RW4 0.19 ± 0.06 . The estimations of RW1 and RW2 are a lower but of the same magnitude as in sea bass (Castro et al., 2008). These estimations of the shape heritability show that there is a considerable genetic component promising for using it in a selective breeding program.

To our knowledge, this is the first study which clearly demonstrates the significance of genetic background for the body shape of gilthead sea bream. The phenotypic variation was estimated by the use of the GM methodology. Compared with the traditional morphometric approaches, the selected methodology allows the independent examination of the variance of each anatomical part (landmark), as well as the visualization of the overall shape variance (discussed by Georgakopoulou et al., 2007).

Although GM is a powerful tool for the study of body-shape variation, the implementation in selective breeding of gilthead sea bream would constrain the program to distinct shape phenotypes which are related to the extreme values of specific RWs (figure 1). Such a restriction could be omitted by the partition of shape variability into specific distance measurements (traits) according to the GM landmark configurations, and the sequent estimation of the heritability for each trait separately.

This study was partially funded by the program NSRF 2007-2013, «Competitiveness & Entrepreneurship» (call Cooperation I, Project No 09SYN-24-619) of the Ministry of Education, Lifelong Learning and Religious Affairs, Greece.

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