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Estimates of heritabilities and genetic correlations of raw flesh quality traits in a reared gilthead sea bream (*Sparus aurata* L.) population sourced from broodstocks along the Spanish coasts

M. García-Celdrán [a], G. Ramis [b], M. Manchado [c], A. Estévez [d], A. Navarro [e], E. Armero [a,*]

[a] Department of Agricultural Science and Technology, Technical University of Cartagena, Paseo Alfonso XIII 48, 30203 Cartagena, Spain
[b] Departamento de Producción Animal, Facultad de Veterinaria, Universidad de Murcia, Campus de Espinardo, 3100 Murcia, Spain
[c] Centro IFAPA El Toruño, Camino de Tiro Pichón, Puerto de Santa María, Cádiz, 11500, Spain
[d] Centro de Acuicultura, Institut de Recerca i Tecnologia Agroalimentáries (IRTA), Ctra. Poble Nou Km 6, San Carlos de la Rápita, Tarragona, 43540, Spain
[e] Grupo de Investigación en Acuicultura (GIA), Instituto Universitario de Sanidad Animal y Seguridad Alimentaria (IUSA), Instituto Canario de Ciencias Marinas (ICCM), Universidad de Las Palmas de Gran Canaria (ULPGC), Carretera Trasmontaña s/n, Arucas, Las Palmas, 35413, Spain

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ABSTRACT

In gilthead sea bream, flesh quality traits such as body composition and texture directly influence yield of final product and consumer preferences so they should be considered in the breeding goal. However, strategies that involve the development of selection schemes for these traits of economic interest are scarce. Taking into account these circumstances, in this study the effect of the origin of the broodstock on the major flesh quality traits was analyzed at harvest size (690 days post-hatching) and genetic parameters (heritabilities and genetic correlations) were estimated as well as their correlations with harvest weight. For this purpose, a population of farmed gilthead sea bream was obtained from three broodstock of different geographical origins along the Spanish coast [Cantabrian Sea (CAN), the Atlantic Ocean (ATL) and Mediterranean Sea (MED)]. Parental assignments between breeders and their offspring were carried out *a posteriori* using a microsatellite multiplex (SMsa1). In the offspring, raw flesh composition (muscular collagen, fat, moisture and protein contents) were determined ($n = 700$). Textural parameters (hardness, cohesiveness and derived traits) were measured in an industry relevant number of offspring ($n = 890$) for the first time in this species. The origin had an effect on muscular fat content as well as on hardness and derived textural parameters. Fish from MED showed the lowest fat percentage and those from CAN the highest values for textural parameters. Differences among origins could be explained through their different genetic backgrounds. However, the effect of the origin could be affected by environmental conditions in the initial facilities, where each origin was reared separately, and by genotype x environment interactions. Heritabilities were medium for muscular fat (0.31 ± 0.08) and moisture (0.24 ± 0.07). The genetic correlation between them was very high and negative (−0.99 ± 0.02). Selection for harvest weight may lead to an increase in fillet fat percentage due to the genetic correlation between the two traits (0.29 ± 0.14). Hardness showed a medium heritability (0.21 ± 0.06) and an unfavourable negative genetic correlation with harvest weight (−0.34 ± 0.14). All findings reported in this study should be relevant for the establishment of successful breeding programs in aquaculture of this species.

Statement of relevance

This study proves the importance of the acquisition of a stock in sea bream since the studied origins of the broodstock has an effect on muscular fat content and textural parameters. Moreover, genetic parameters are estimated for this traits which are scarce in this species.

1. Introduction

The gilthead sea bream (*Sparus aurata* L.) is one of the most important farmed fish in Europe, especially in the Mediterranean area. Total worldwide production reached 176,191 metric Tonnes (mT) with Greece (40.9%), Turkey (22.7%) and Spain (11.0%) as the major producers. In our country four regions share 100% of the gilthead sea bream production with Murcia being the second producer (APROMAR, 2013).

Due to consumer demands, quality traits have become an important parameter for the gilthead sea bream industries and therefore they

* Corresponding author. Tel.: +34 968 325538; fax: +34 968 327046.
E-mail address: eva.armero@upct.es (E. Armero).

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should be considered in the breeding goal. Body composition and texture of flesh directly influence yield of final product and consumer preferences (Neira et al., 2004). In this regard, muscle composition plays an important role in aspects related to flesh quality such as flavour, juiciness, texture and appearance, and changes in these parameters may have consequences for the market. Specifically, flavour and juiciness are highly and positively correlated with fat content in the muscle (Grigorakis, 2007). On the other hand, between 3% and 10% of the protein content is collagen, which constitutes the connective tissue among cells and is related to fillet texture. Fillets with lower collagen content are tender since collagen has a positive and significant correlation with the firmness of raw flesh (Hatae et al., 1986). Flesh composition in gilthead sea bream is influenced by a variety of environmental factors such as abiotic (Ginés et al., 2004), nutrition (Izquierdo et al., 2005; Nasopoulou et al., 2011; Suárez et al., 2010), or factors related to the farming system (Grigorakis and Alexis, 2005; Grigorakis et al., 2002). However, genetic determination for flesh quality traits has been poorly studied in this species (Navarro et al., 2009).

Texture is also an important trait related to flesh quality in fish (Ayala et al., 2010; Gjedrem, 2005). The use of different systems of handling postharved (refrigeration, freezing, etc.) influences significantly on the post-mortem degradation and hence, on the flesh quality (Ayala et al., 2010). These changes in the texture can be monitored by instrumental techniques, using a texturometer. A widely used test is the Texture Profile Analysis (TPA), which rely on compression. This test consists of two identical cycles which reproduce the process of chewing food in the mouth, obtaining a curve (force *vs.* time), from which properties are calculated as chewiness, gumminess, adhesiveness, hardness, and elasticity (Friedman et al., 1963; Szczesniak et al., 1963).

The use of different rearing systems and broodstocks to produce commercial fish usually causes great variability of the production i.e. in the growth rates and the overall quality of the end product (Ayala et al., 2010). However, we did not find works in which the relationship between the origin of the broodstock and flesh quality traits had been studied in this species.

Growth rate is usually the first goal in breeding programs of different species. Nevertheless, the effect of selecting for increased body weight on other commercially important traits such as body composition and flesh needs to be considered (Powell et al., 2008). Strategies that involve the development of selection schemes for these traits of economic interest in gilthead sea bream are still scarce due to the biological characteristic of this species. Gilthead sea bream is a mass-spawning species in which individuals are males during the first two years of life and then gradually become females. Mass spawning prevents knowing the genealogy of fish under culture conditions which is essential to estimate genetic parameters and to introduce selective programs. The use of molecular markers such as microsatellites is a useful tool for addressing these matters (Castro et al., 2008).

Taking into account all the circumstances mentioned above, the main goals of this research were: A) To study the effect of that origin of the broodstock on major raw flesh quality traits (muscle composition and textural parameters) as well as to estimate the phenotypic correlation between them and harvest weight. B) To estimate genetic parameters (heritabilities and genetic correlations) for major flesh quality traits and for harvest weight in a population of gilthead sea bream sourced from broodstocks from three origins.

2. Materials and methods

2.1. Rearing conditions

Initially, samples of sea bream were captured from wild populations from three geographically differentiated origins along the Spanish coast; Cantabrian Sea (CAN), the Atlantic Ocean (ATL), and Mediterranean Sea (MED). From these samples, three broodstocks were established in different Spanish facilities where fingerlings were obtained and reared in the same conditions. At 84 days post-hatching (dph) a random sample of 2500 individuals, in which all origins were represented, was taken to the on-growing facilities of the Centro de Cultivos Marinos de la Región de Murcia. Fingerlings were individually tagged in the abdominal cavity for individual identification and then randomly distributed in 12 tanks and reared under communal conditions. At 325 dph the majority of the fish (about 2000 specimens) were moved to the facilities of the company Servicios Atuneros del Mediterraneo S.L. (San Pedro del Pinatar, Murcia, Spain) where they were reared in a cage in the Mediterranean sea under intensive conditions. At harvest size (690 dph), the fish were slaughtered and transported to the laboratory for assays. Specimens were kept on ice during the study at 4 °C refrigeration until the moment of their analyses.

The establishment of broodstocks, the conditions of spawn, the rearing conditions and the slaughter process are explained in depth in García-Celdrán et al. (2015).

2.2. Analyzed traits

Texture profile analysis (TPA) was measured on the back of the whole fish (Fig. 1) as described in Ginés et al. (2002) for two post-mortem storage periods of two days ($n = 890$). For this purpose we used a texture analyser QTS-25 (Brookfield CNS Farnell, Borehamwood, Hertfordshire, England) equipped with a load cell of 25 kg and Texture Pro V.2.1 software. The samples were compressed perpendicular to the muscle fibres with a 25 mm diameter cylindrical probe. The testing conditions were: 20 °C room temperature; two consecutive cycles of 50% compression; cross-head moved at a constant speed of 5 mm/s and a trigger point of 0.5 N. Texture variables, hardness (peak force of the first compression cycle; expressed as N), cohesiveness (ratio of positive force area during the second compression compared to that during the first compression; no units), springiness (height that the food recovers during the time that elapses between the two compression cycles expressed as mm), gumminess (hardness multiplied by cohesiveness; N) and chewiness (hardness multiplied by cohesiveness multiplied by springiness; N mm), were calculated as described by Bourne (1978).

Body harvest weight was also measured. Fish were then manually skinned and filleted (Fig. 1). Thereafter these raw fillets were vacuum-packed using a packaging INELVI VISC 500 (Industrial eléctrica Vilar S.L, Barcelona, España) and frozen (−20 °C) prior to compositional analysis. Flesh composition (muscular collagen, fat, moisture and protein contents) was determined ($n = 700$) by the indirect method Near Infrared Spectroscopy, NIR, using the FoodScan ™ equipment at IRTA.

2.3. PCR reaction and genotyping

The genetic characterization of breeders and juveniles and the parental assignments between them were conducted according to García-Celdrán et al. (2015).

2.4. Data analysis

All data were tested for normality and homogeneity of variances using SPSS® (v.19.0) (SPSS, Chicago, IL, USA) and then analyzed using the next General Liner Model:

$$y_{ijk} = \mu + \text{origin}_j + \text{time of storage}_k + \beta^* \text{ body weight} + e_{ijk}$$

in which y_{ijk} is an observation of an individual i^{th} from the origin j^{th} and with time of storage k^{th}, μ is the overall mean, origin is the effect of the broodstock origin of the fingerlings (j = CAN, ATL and MED), time of storage was included only for texture variables (j = 1 day or 2 days post-mortem), β is the regression coefficient between the analyzed