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

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Carcass quality traits such as visceral fat and fish morphology have a direct influence on final product and consumer preferences, especially in species as sea bream that are sold as whole fish. Nevertheless, strategies that involve the development of selection schemes for these traits of economic interest in gilthead sea bream are limited. In this study the effect of the origin of the broodstock on carcass quality traits was analyzed in harvest size (690 days post-hatching) gilthead sea bream for the first time. For this purpose, a population (n = 890) of farmed gilthead sea bream obtained by industrial mass-spawnings from broodstocks from three different origins [Cantabrian Sea (CAN), the Atlantic Ocean (ATL) and Mediterranean Sea (MED)] was analyzed for condition factor, visceral fat content, dressing weight, dressing percentage, fillet weight and fillet percentage. Moreover, with the goal of estimating genetic parameters (heritabilities and genetic correlations) for carcass quality traits as well as their correlations with growth (harvest weight and length), a reconstruction of pedigree was carried out a posteriori. The origin had an effect on several carcass traits. Fish from ATL showed the lowest visceral fat percentage, dressing weight and percentage and those form CAN the lowest condition factor. These differences among origins can be explained through their different genetic backgrounds but also by environmental conditions in the initial facilities, where each origin was reared, and the derive genotype × environment interactions. All carcass traits showed medium heritabilities (ranging from 0.17 to 0.24) and were estimated with accuracy (standard errors from 0.05 to 0.07) except dressing (0.07 ± 0.05) and fillet (0.11 ± 0.05) percentage. Due to their genetic correlations, selection on weight could lead to an increase in condition factor (0.47 ± 0.21) but, at the same, to an undesirable increase in visceral fat (0.42 ± 0.20) and a decrease in fillet yield (−0.58 ± 0.09). However, selection on length could improve dressing (0.87 ± 0.07) and fillet weight (0.84 ± 0.09). Alternatively, visceral fat content could be decreased by selection through condition factor (−0.46 ± 0.16). 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 had an effect on different carcass traits. Moreover, genetic parameters are estimated for these traits which are scarce for this species.

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1. Introduction

Gilthead sea bream (Sparus aurata L.) is a member of the family Sparidae and one of the most important farmed fish in Europe, especially in the Mediterranean area. The main producer countries are Greece, Turkey and Spain that accounted for the 40.9%, 22.7% and 11.0% of total production, respectively. In Spain, this species is cultivated along the Mediterranean and Atlantic coasts although the 70% of total production is concentrated in the East coasts (APROMAR, 2013).

Although industry has focused their efforts mainly in the improvement of growth, nutrition and morphology parameters, quality traits...
are crucial for the achievement of high-quality products demanded by consumers. The knowledge about the genetic correlations between growth and carcass traits is important in order to make decisions in genetic selection processes. Therefore, these parameters should be incorporated into the goals of commercial breeding programs although the genetic information available for these types of traits in sea bream is limited. Consumers will not buy low-quality products, even at reduced prices. However, most consumers are usually unwilling to pay too high a price for superior quality (Gjedrem, 1997). In this regard, carcass quality traits directly influence yield of final product and consumer preferences (Neira et al., 2004). One important genetic factor is the fat that is concentrated inside the visceral cavity which has a negative effect on carcass quality traits for several reasons. Visceral fat affects carcass yield (Haffray et al., 2007; Kause et al., 2002; Neira et al., 2004; Rye and Gjerde, 1996) and the visual impression received by consumers, especially in species as gilthead sea bream which are mainly marketed as whole fish. Moreover, visceral fat could give a strong and unpleasant smell that often emanates from well-fed aquaculture fish (Grigorakis, 2007). Finally, it represents lost energy since the visceral fat is thrown away together with the intestines when the fish is gutted.

Other important carcass quality traits are dressing and fillet percentages since a high percentage means that a large part of the carcass is edible (Gjedrem, 2005) and because one of the aims of farmed fish production is to convert feed into muscle and decrease slaughter waste. Hence, the genetic improvement of fillet should be of high priority for breeders, although this is challenging in practice (Kause et al., 2011).

On the other hand, the morphology of the fish, which is reflected in the condition factor, is also an important trait influencing the final decision by the consumer and the price of species that are sold as whole fish (Navarro et al., 2009a). The morphology affects the consumer impression i.e. it plays a role in the visual sense.

Strategies for the implementation of selection schemes for economically important traits 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. Molecular markers such as microsatellites are useful tools to assign parentage and to estimate genetic parameters (Castro et al., 2008; Lee-Montero et al., 2013).

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). Different degrees of genetic differentiation between sea bream populations inferred by microsatellites have been found (Alarcón et al., 2004; Ben-Slimen et al., 2004; De Innocentiis et al., 2004; Šešić-Bubić et al., 2011). However, we did not find works in which the relationship between the origin of the broodstock and carcass quality traits had been studied in this species.

Considering all these circumstances, the aims of this research were: A) To study the effect of the origin of the broodstock on carcass quality traits (condition factor, visceral fat content, dressing weight, dressing percentage, fillet weight and fillet percentage) as well as to estimate the phenotypic correlations between them and with growth traits (harvest weight and length). B) To estimate genetic parameters (heritabilities and genetic correlations) for growth and these carcass quality traits in a population of gilthead sea bream sourced from broodstock from three origins.

2. Materials and methods

2.1. Broodstocks and offspring. 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 more detail in Garcia-Celdrán et al. (2015).

2.2. Analyzed traits

Body weight and fork length were measured and condition factor was determined (100 × body weight × fork length⁻³). All individual were inspected and all of them were sexual immature. Visceral fat deposts were manually removed, weighed and expressed as a percentage of the body weight; then gutted body weight was recorded (dressing weight) and also expressed as a percentage of the body weight (dressing percentage). Fish were manually skinned and filleted and both fillets were weighed together (fillet weight) and also expressed as a percentage of the body weight (fillet percentage).

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. Analysis data

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

\[ y_{ij} = \mu + \text{origin}_i + \beta \times \text{body weight}_j + e_{ij} \]

in which \( y \) is the data recorded for the analyzed variable, \( \mu \) is the overall mean, origin is the effect of the broodstock origin (\( i = \text{CAN, ATL and MED} \)), \( \beta \) is the regression coefficient between the analyzed variable and the covariate body weight and \( e_{ij} \) is a random residual error.

Pearson correlation was carried out to determine phenotypic correlations among the analyzed parameters. The level of significant difference was set at \( P < 0.05 \).

Bivariate analyses were carried out using a Restricted Maximum Likelihood (REML) algorithm to obtain (co)variance components through the following animal linear model, with body weight as a co-variate for carcass quality traits:

\[ y = X\beta + Zu + e \]

where \( y \) is the recorded data on the studied traits, \( \beta \) the fixed broodstock origin effect, \( u \) the random animal effect and \( e \) the error. Non-genetic maternal and/or paternal effects were not significant for the studied traits so they were removed from the model when analyzing carcass traits. The model was resolved with the software package VCE (v 6.0) (Groeneveld et al., 2010). 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 (N > 0.65). Correlations were classified as low (0–0.40), medium (0.45–0.55) and high (0.60–1), regardless of the sign (Navarro et al., 2009a,b).

3. Results and discussion

3.1. Phenotypic results

The effect of the broodstock origin of the fingerlings on carcass quality traits was assessed in gilthead sea bream for the first time in this study. Due to the wide range of values observed for weight, discussed in detail in García-Celdrán et al. (2015a), phenotypic results for carcass traits (Table 1) were adjusted to a constant final weight (232.5 g) to be compared. However, due to the requirements of the project (PROGENSA®, http://www.progensa.eu) it was not possible to obtain a commercial size of 300 g at slaughter. All studied traits showed significant differences (P ≤ 0.05) among origins except fillet weight and percentage (P = 0.08). The covariate fish weight was positive and highly significant (P ≤ 0.01) for all studied traits. Thus, when the final weight increased 10 grams, condition factor increased 0.01, visceral fat 0.06%, dressing weight 7.7 grams, dressing percentage 0.3%, fillet weight 3.8 grams and fillet percentage 0.1%. Other authors (Ginés et al., 2004; Grigorakis and Alexis, 2005) have also reported positive correlation between fish weight and the amount of visceral fat.

Regarding condition factor, Glover et al. (2009) compared salmon of farmed, wild and hybrid origin in a simulated aquaculture production cycle. At slaughter, they found that this trait was considerably higher in farmed contra wild salmon, with hybrids displaying intermediate or similar values. Vandeputte et al. (2014) compared five wild populations of sea bass founding differences in shape. In the present research, fish from CAN showed a lower value for condition factor than those from ATL and MED pointing out an effect of the origin of the broodstocks on this trait. Other factors have shown an effect on this parameter as well. An increase of condition factor with intensification of culture has been observed for gilthead sea bream (Flors et al., 2002; Francescon et al., 1988; Navarro et al., 2009b; Sahujo et al., 1993), while condition factor reduces during food deprivation (Grigorakis and Alexis, 2005).

The broodstock origin had an effect on visceral fat percentage in the present study with fish from ATL showing the lowest percentage (5.7% lower than the overall average). Visceral fat content is influenced by a variety of factors related to diet (Grigorakis and Alexis, 2002; Navarro et al., 2009b) and sex (Kause et al., 2002; Neira et al., 2004). In the case of gilthead sea bream reported values for this trait ranged from 0.79% to 2.98% (Grigorakis and Alexis, 2005; Grigorakis et al., 2002; Navarro et al., 2009b; Santinha et al., 1999). Our results showed a high visceral fat deposition (about 6% in all or- gins) and were in the upper range of values reported for the former origins in 12 tanks during the pre-on-growing period since the genetic basis of carcass quality trait for sea bream, we found refer- ences for other species.

In the present study, fish were held in the same station the majority of their life raised under the same conditions. Moreover, they were slaughtered and stored the same way. Differences observed in them seem to be the results of differences in their genetic backgrounds. However, larvae from each origin were reared in different facilities until 84 dph. Despite that the rearing protocol was standardized some environmental perturbations could happen which may be expressed as geno- type × environment interaction. The same could happen after mixing of the origins in 12 tanks during the pre-on-growing period since the tank effect cannot be analyzed.

3.2. Heritability of carcass quality traits

Heritabilities and their corresponding standard errors (h2 ± SE) of carcass traits (Table 2) were estimated in 890 individuals correctly assigned to a unique parental couple using the SMsa1. All carcass traits, except dressing and fillet percentages, showed medium heritabilities that could allow genetic improvements through implementation of selection programs. Although few researches have been found regarding the genetic basis of carcass quality trait for sea bream, we found references for other species.

The estimate of heritability for condition factor was 0.18 ± 0.07 and was in the range of estimates reported in sea bream (Navarro et al., 2009a) and sea bass (Dupont-Nivet et al., 2008; Saillant et al., 2009). However, higher genetic variance has been observed for this trait in other species including Atlantic salmon (Rye and Gjerde, 1996), common carp (Vandeputte et al., 2004), rainbow trout (Kause et al., 2002) and European whitefish (Kause et al., 2011) with values ranging from
0.31 to 0.49 respectively. The lower heritabilities of condition factor in comparison with other species can be explained because gilthead sea bream presents, proportionally, a greater growth in height than in length (Navarro et al., 2009a).

- **Visceral fat** showed medium heritability (0.20 ± 0.06). Higher values have been found for this trait in gilthead sea bream (Navarro et al., 2009b) as well as in other species with heritabilities ranging from 0.30 to 0.68; Rye and Gjerde (1996) in Atlantic salmon, Gjerde and Schaeffer (1989) in rainbow trout and Saillant et al. (2009) in sea bass, highlight the genetic basis for this trait so that selection for decreased fat content is feasible.

- Within livestock breeding programs the yield of the final product is a highly desirable trait, and is commonly a target for selection (Powell et al., 2008). In the present research, medium heritability was observed for dressing weight (0.24 ± 0.06), for the first time reported in sea bream, while heritability for dressing percentage was low (0.07 ± 0.05) in accordance with previous results in salmon. In this regard, Powell et al. (2008) found high genetic variation for carcass weight (0.51) but low for carcass yield (0.02) and Neira et al. (2004) observed medium heritability for carcass weight. However, higher genetic variance for dressing percentage than those estimated in the present research has been reported with considerable variation among studies ranging from medium heritabilities (0.20; Rye and Gjerde, 1996; 0.23–0.33; Neira et al., 2004; 0.31; Navarro et al., 2009a,b; 0.36; Gjerde and Schaeffer, 1989) to high (0.45; Kause et al., 2002) and very high (0.58 to 0.74; Haffray et al., 2007) estimates.

- Regarding fillet traits, we observed medium heritability for fillet weight (0.17 ± 0.05) in agreement with results obtained by Kause et al. (2002, 2007), while for fillet percentage the estimated heritability was lower (0.11 ± 0.05). In this regard, medium genetic variance for fillet yield have been found in black sea bream (0.30; Doupe and Lymberry, 2005), common carp (0.21; Kocour et al., 2007) and in rainbow trout (0.33; Kause et al., 2002). The higher heritability for fillet weight than for fillet percentage reported here is in accordance with those obtained in sea bream (Navarro et al., 2009a) as well as in other species (Kause et al., 2011; Neira et al., 2004; Powell et al., 2008; Rutten et al., 2005; Saillant et al., 2009).

- The moderate genetic variance for carcass and fillet yield observed in our study suggests that response to selection for increasing yields would be slow. This is probably due to a low degree of repeatability of the processes of gutting and filleting without skin leading to variations in these data (Kocour et al., 2007). Variability in genetic parameters (heritabilities and genetic correlations) among studies may also result from genotype by environment interactions. Such variability highlights the fact that these parameters are population and environment specific (Kause et al., 2002). In this regard, there was considerable variation among the estimated correlations between pairs of traits among species.

### Table 2

<table>
<thead>
<tr>
<th>Condition Factor</th>
<th>Visceral fat</th>
<th>Dressing (%)</th>
<th>Fillet (%)</th>
<th>Weight</th>
<th>Lenght</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Condition Factor</strong></td>
<td>0.18 ± 0.07</td>
<td>−0.46 ± 0.16</td>
<td>−0.62 ± 0.16</td>
<td>−0.10 ± 0.84</td>
<td>−0.15 ± 0.23</td>
</tr>
<tr>
<td>Visceral fat</td>
<td>0.76** ± 0.02</td>
<td><strong>0.20</strong> ± 0.06</td>
<td>0.62 ± 0.15</td>
<td>0.50 ± 0.25</td>
<td>0.53 ± 0.17</td>
</tr>
<tr>
<td>Dressing (%)</td>
<td>0.47 ± 0.03</td>
<td>0.47 ± 0.03</td>
<td><strong>0.24</strong> ± 0.06</td>
<td>0.82 ± 0.99</td>
<td>0.01 ± 0.99</td>
</tr>
<tr>
<td>Fillet (%)</td>
<td>0.94* ± 0.01</td>
<td>0.79** ± 0.03</td>
<td>0.62** ± 0.03</td>
<td><strong>0.07</strong> ± 0.05</td>
<td>0.99 ± 0.98</td>
</tr>
<tr>
<td>Fillet weight</td>
<td>−0.02 ± 0.03</td>
<td>0.12 ± 0.03</td>
<td>0.26 ± 0.02</td>
<td>0.15 ± 0.03</td>
<td>0.17 ± 0.05</td>
</tr>
<tr>
<td>Weight</td>
<td>0.99** ± 0.01</td>
<td>0.76** ± 0.02</td>
<td>0.47 ± 0.03</td>
<td>0.94** ± 0.01</td>
<td>−0.02 ± 0.01</td>
</tr>
<tr>
<td>Lenght</td>
<td>0.82** ± 0.02</td>
<td>0.60** ± 0.03</td>
<td>−0.03 ± 0.02</td>
<td>0.77** ± 0.02</td>
<td>−0.02 ± 0.02</td>
</tr>
</tbody>
</table>

**Significant Pearson correlations between carcass quality traits (P < 0.01).**

- Denotes the correlation that we were unable to estimate due to convergence problems.

### 3.3. Correlations between growth traits and carcass quality traits

Due to the fact that growth is the most economically important objective in the majority of fish genetic selection programs (Saillant et al., 2006) it is important to study its genetic correlations with carcass traits in order to make decisions in selection processes. Moreover, the evaluation of carcass traits, which are laborious to record, requires technical skills and the slaughter of the fish, whereas growth traits can easily be measured in the field and allows the evaluation of a high number of fish per time unit (Kause et al., 2007).

- Body weight was phenotypically positively correlated with all carcass traits (P < 0.01) except with dressing weight and fillet weight.

- Regarding genetic correlations, weight was positively correlated with condition factor in concordance with previous results (Kause et al., 2002; Kause et al., 2011; Rye and Gjerde, 1996; Saillant et al., 2009). However, the correlation between length and condition factor was close to zero although imprecise due to the high standard error in line with results obtained previously in sea bream (Navarro et al., 2009a) and sea bass (Dupont-Nivet et al., 2008) suggesting that improvements in growth would produce no change in fish conformation.

The genetic correlation between weight and visceral fat was in the upper range of those previously reported in the same species (Navarro et al., 2009b) indicating an undesirable increase of fat with selection for growth in the population under study in agreement with Rye and Gjerde (1996) and Saillant et al. (2009). The correlation between length and visceral fat was imprecise and it was not possible to draw any conclusion about them.

- Due to convergence problems, the genetic correlation between harvest weight and dressing weight could not be estimated. However, dressing weight and length were positively correlated in line with results reported by Powell et al. (2008) showing that dressing weight increase as length increases. In this regard, strong genetic correlations between body weight and carcass weight have been obtained in other species (Doupe and Lymberry, 2005; Neira et al., 2004).

- The genetic correlations between growth traits and dressing percentage were close to zero in accordance with those obtained by Navarro et al. (2009b) questioning the use of yield traits in selection criteria. In fact, the results are inconsistent among species ranging from medium and negative (Kause et al., 2011; Neira et al., 2004) to high and positive (Rye and Gjerde, 1996) correlations.

- Positive and high phenotypic and genetic correlations between growth and fillet weight have been found in sea bream (Navarro et al., 2009a) as well as in other species (Kause et al., 2002; Kause et al., 2007, 2011; Powell et al., 2008; Rutten et al., 2005) indicating the potential for using easily recorded weight as a selection criterion for improved meat weight of fish at harvest. We were unable to estimate the genetic correlation between harvest weight and fillet weight due to convergence problems. However, fillet weight was strongly genetically correlated to length suggesting that fillet weight would...
could be controlled in fish with improved length and therefore, its inclusion in breeding programmes might be recommended. Regarding growth and fillet percentage, negative genetic correlation were obtained in the present study in agreement with Navarro et al. (2009a) but with low consistency in the case of length due to the high standard error. The results are not consistent among species ranging from genetic correlations close to zero (Kause et al., 2007, 2011) to medium (Kause et al., 2002; Saillant et al., 2009) to high (Doupé and Lembersy, 2005; Kocour et al., 2007; Neira et al., 2004; Rutten et al., 2005).

Weight and length showed mediumheritabilities at harvest and both traits were phenotypically and genetically correlated suggesting that both traits could be useful criterion for selection. In fact, Navarro et al. (2009a) and Vandeputte et al. (2008) proposed using length instead of weight since it is easy to measure in the field and more repeatable.

### 3.4. Correlations between carcass quality traits

Genetic correlations between carcass quality traits were imprecise in many cases, especially those between dressing and fillet percentages and the rest of analyzed traits as was indicated by their large standard errors (Table 2) probably due to the low heritability of these traits (Kause et al., 2011). However, phenotypic correlations were very precise in all cases due to the large number of samples analyzed.

Regarding condition factor, Kause et al. (2002), Grigorakis and Alexis (2005), Navarro et al. (2009b) and Saillant et al. (2009) reported positive phenotypic correlations with visceral fat. We found that both traits were highly and significantly correlated at the phenotypic level as well, being our results much higher. Previous researches have reported high and positive genetic correlations between these both traits (Navarro et al., 2009b; Rye and Gjerde, 1996; Saillant et al., 2009) while we found this correlation medium and negative in agreement with Kause et al. (2002). Therefore, due to the medium heritability shown for both traits and due to their genetic correlation, it seems that condition factor could be useful as a non-invasive index for predicting the response of fish fat deposit content in a breeding programme. Moreover, this parameter could easily be measured on the live breeding candidates which is effective in the case of individual selection. However, because the evaluation of visceral fat is lethal for breeding candidates, this implies that selection through fat should be done on the basis of slaughtering traits of their relatives. This practice would require identification of families, either by separate rearing or by genotyping (Kocour et al., 2007).

We found some conflicting result in the present research. Condition factor was negatively correlated with visceral fat and positively correlated with weight. Nevertheless, we observed a negative correlation between weight and visceral fat, as we said before. Therefore, further studies are necessary to draw more precise conclusions about these correlations.

The genetic correlation between condition factor and dressing weight was high and negative so selection for increasing condition factor may also lead to a decrease in dressing weight in the population under study. The rest of the genetic correlations for condition factor and carcass traits were found to be inconsistent although the phenotypic correlation between condition factor and dressing and fillet percentages were found to be high and significant (P < 0.01).

Regarding the genetic correlations between visceral fat with dressing and fillet weight, high and medium values were obtained respectively. In spite of their high phenotypic correlation, the genetic correlations between visceral fat with dressing and fillet percentages were inconsistent in accordance with Kause et al. (2002) and Saillant et al. (2009). However, Haffray et al. (2007) and Navarro et al. (2009a) reported very high and negative genetic correlation between visceral fat and dressing yield.

Concerning carcass weight, it was highly and positively correlated with dressing percentage at the phenotypic level although its genetic correlations with dressing percentage and the rest of carcass trait analyzed were imprecise as was denoted by their large standard errors.

Dressing and fillet percentage showed a strong phenotypic correlation while the genetic correlations among dressing yield and the rest of carcass traits studied were imprecise as well as the genetic correlation between fillet weight and percentage.

### 4. Conclusions

Our results highlight that the acquisition of a stock is an important aspect of broodstock management in sea bream since the different origins presented in the studied population had an effect on important carcass traits. Regarding these traits, juveniles from ATL broodstock were the best performers since fingerlings from that origin showed the highest condition factor and the lowest visceral fat percentage. These differences among origins may be explained through their different genetic backgrounds. However, the effect of the origin could be affected by environmental conditions in the initial facilities and by genotype × environment interactions.

All carcass traits, except dressing and fillet percentages, showed medium heritability and could be included in a selection breeding program. Growth traits are the traits assigned the highest importance in selection programs. As a result of their genetic correlations, selection on weight could lead to an increase in condition factor but, at the same, to an undesirable increase in visceral fat and a decrease in fillet yield so these traits need to be controlled. However, other carcass traits such as dressing and fillet weight could be improved through direct selection of length.

The evaluation of carcass traits requires the slaughter of the fish and technical skills. Therefore, condition factor is shown as an interesting alternative trait to be included in a breeding programme since it is easy to measure and allows a non-invasive measurement in living candidates. Selection for this trait could lead to a decrease in the undesirable visceral and to an increase in weight, due to the genetic correlations between these traits. All these findings should be relevant for the establishment of successful breeding programs in aquaculture of this species.

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