

Estimates of heritabilities and genetic correlations of carcass quality traits in a reared gilthead seabream (*Sparus aurata* L.) population sourced from three broodstocks

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Resumen

La calidad de la canal tiene una influencia directa en el producto final y en las preferencias de los consumidores, especialmente en especies como la dorada que son vendidas como pez entero. En este trabajo se estudió el efecto del origen de los reproductores sobre caracteres de calidad de canal. Para ello, una población de dorada cultivada obtenida a partir de lotes de reproductores de diferentes orígenes [mar Cantábrico (CAN), Océano Atlántico (ATL), mar Mediterráneo (MED)] fue analizada para estas características a talla de sacrificio. Además, para estimar heredabilidades y correlaciones genéticas para caracteres de canal así como su correlación con caracteres de crecimiento, realizamos una reconstrucción genealógica. El origen tuvo un efecto en varios caracteres. Los peces del ATL presentaron el menor porcentaje de grasa visceral; los del CAN el menor factor de condición. Todas las variables de canal presentaron heredabilidad media (0.17-0.24) excepto rendimiento canal (0.07±0.05) y filete (0.11±0.05). Dada su correlación genética, seleccionar por peso aumentaría el factor de condición (0.47±0.21) pero también la indeseable grasa visceral (0.42±0.20) disminuyendo el rendimiento filete (-0.58±0.09). Seleccionar por longitud mejoraría el peso canal (0.87±0.07) y filete (0.84±0.09). Alternativamente, el contenido de grasa visceral disminuiría seleccionando por factor de condición (-0.46±0.16).

Palabras clave: Origen de los reproductores; grasa visceral; factor de condición; dorada.

Abstract

Carcass quality traits have a direct influence on final product and consumer preferences, especially in species as seabream that are sold as whole fish. In this study the effect of the origin of the broodstock on carcass quality traits was studied. For this purpose, a population of farmed gilthead seabream obtained from broodstocks from three origins [Cantabrian Sea (CAN), the Atlantic Ocean (ATL), Mediterranean Sea (MED)] was analyzed for these traits at harvest size. Moreover, to estimate heritabilities and genetic correlations for carcass quality traits as well as their correlations with growth traits, a reconstruction of pedigree was carried out. The origin had an effect on several carcass traits. Fish from ATL showed the lowest visceral fat percentage and those from CAN the lowest condition factor. All carcass traits showed medium heritabilities (0.17-0.24) 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 also to an undesirable increase in visceral fat (0.42±0.20) and a decrease in fillet yield (-0.58±0.09). 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).

Keywords: Broodstock origin; visceral fat; condition factor; gilthead seabream

1. Introduction

Gilthead seabream (*Sparus aurata* L.) is one of the most important farmed fish in Europe, especially in the Mediterranean area. Carcass quality traits such as visceral fat and fish morphology, which is reflected in the condition factor, have a direct influence on final product and consumer preferences, especially in species as seabream that are sold as whole fish. Nevertheless, strategies that involve the

development of selection schemes for these traits of economic interest in gilthead seabream are limited. 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 [1]. 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) in a population of gilthead seabream sourced from broodstock from three origins. B) To estimate genetic parameters (heritabilities and genetic correlations) for growth and these carcass quality traits

2. Materials and methods

2.1 Broodstocks and offspring

Initially, samples of seabream were captured from wild populations from three geographically differentiated origins; 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 2,500 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. Fry were individually tagged for individual identification and then randomly distributed in tanks and reared under communal conditions. At 325 dph about 2,000 specimens were moved to a cage in the Mediterranean Sea and reared under intensive conditions. At harvest size (690 dph), the fish were slaughtered and transported to the laboratory for assays.

2.2 Analyzed traits

Body weight and fork length were measured and condition factor was determined ($100 \times \text{body weight} \times \text{fork length}^{-3}$). Visceral fat deposits 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 [2].

2.4 Analysis data

Data were analyzed using SPSS® by the General Liner Model:

$$y = \mu + \text{origin} + \beta * \text{body weight} + e$$

in which y is the data recorded for the analyzed variable, μ is the overall mean, origin the effect of the broodstock origin (CAN, ATL and MED), β was regression coefficient between the analyzed variable and the covariate body weight and e is a random residual error. Pearson correlation was carried out to determine phenotypic correlations among the analyzed parameters. Bivariate analyses were carried out using a Restricted Maximum Likelihood (REML) algorithm to obtain (co)variance components through the following animal linear model, resolved with the software VCE, with body weight as a covariate for carcass quality traits:

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

where y is the recorded data on the studied traits, β the fixed broodstock origin effect, u the random animal effect and e the error.

3. Results and Discussion

All studied traits showed significant differences among origins (Table 1) except fillet weight and percentage ($P=0.08$). Fish from ATL showed the lowest visceral fat percentage and those from CAN the lowest condition factor. The covariate fish weight was positive and highly significant ($P \leq 0.01$) for all studied traits.

All carcass traits, except dressing and fillet percentages, showed medium heritabilities (Table 2) that could allow genetic improvements through implementation of selection programs. However, the moderate genetic variance for carcass and fillet yield 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 [3].

Growth is the most economically important objective in the majority of fish genetic selection programs so it is important to study its genetic correlations with carcass traits. Weight was positively correlated with condition factor as in [4]. The genetic correlation between weight and visceral fat was in the upper range of those previously reported in seabream [5] indicating an undesirable increase of fat with selection for growth in our population. The genetic correlation between harvest and dressing weight could not be estimated. However, dressing weight and length were positively correlated in line with previous results [6] showing that dressing weight increase as length increases. Fillet weight was strongly genetically correlated to length suggesting that fillet weight could be controlled

in fish with improved length. Therefore, the inclusion of length in breeding programmes might be recommended. Regarding growth and fillet percentage, negative genetic correlations were obtained in agreement with previous studies [7] but with low consistency for length due to the high standard error. The correlation between condition factor and visceral fat was negative as in [8]. Therefore condition factor could be useful as a non-invasive index for predicting the response of fish fat deposit content in a breeding programme. 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 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 [3].

4. Conclusions

The acquisition of a stock is an important aspect of broodstock management in seabream since the different origins presented in the studied population had an effect on important carcass traits. Except dressing and fillet percentages, all carcass traits showed medium heritability and could be included in a selection breeding program. 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. Dressing and fillet weigh could be improved through direct selection of length. Condition factor is shown as an interesting alternative trait to be included in a breeding programme. Selection for this trait could lead to a decrease in the undesirable visceral fat and to an increase in weight. All these findings should be relevant for the establishment of successful breeding programs in aquaculture of this species.

Table 1: Phenotypic results (least square means \pm standard error) for weight, condition factor and carcass traits for gilthead seabream from three

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6. References

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- broodstock origins at harvest age (690 days post-hatching) adjusted to a final fish weight of 232.53 grams

Broodstock origin	CAN	ATL	MED	Covariate ²
N	424	245	221	890
Condition Factor (g cm⁻³)	1.56 ^a ± 0.010	1.71 ^b ± 0.015	1.67 ^b ± 0.015	0.001 ^{**} ± 0.000
Visceral fat (%)	6.24 ^a ± 0.052	5.89 ^b ± 0.077	6.26 ^a ± 0.078	0.006 ^{**} ± 0.001
Dressing weight (g)	204.4 ^a ± 0.71	199.2 ^b ± 1.06	205.3 ^a ± 1.08	0.772 ^{**} ± 0.011
Dressing percentage (%)	88.0 ^a ± 0.23	86.5 ^b ± 0.35	88.3 ^a ± 0.35	0.034 ^{**} ± 0.004
Fillet weight (g)	85.5 ± 0.50	83.8 ± 0.75	85.5 ± 0.76	0.380 ^{**} ± 0.008
Fillet percentage (%)	36.8 ± 0.22	36.0 ± 0.32	36.4 ± 0.33	0.009 ^{**} ± 0.003

¹Broodstock origin: CAN = Cantabrian Sea, ATL = The Atlantic Ocean, MED = Mediterranean Sea; ²Regression coefficient for the covariate fish weight, units are the unit of each trait per gram of fish weight, and standard error (***P* < 0.01); ^{abc}Different superscripts within each row indicate significant differences among origins (*P* < 0.05)

Table 2: Genetic correlations ± standard error (above the diagonal), phenotypic correlations ± standard error (below the diagonal) and heritabilities ± standard errors (in bold at the diagonal) of condition factor, carcass and growth traits estimated from 890 gilthead seabream at harvest age (690 days post-hatching)

	Condition Factor	Visceral fat	Dressing weight	Dressing (%)	Fillet weight	Fillet (%)	Weight	Lenght
Condition Factor	0.18±0.07	-0.46±0.16	-0.62±0.16	-0.10±0.84	-0.15±0.23	0.23±0.92	0.47±0.21	0.01±0.18
Visceral fat	0.76 ^{**} ±0.02	0.20±0.06	0.62±0.15	0.50±0.25	0.53±0.17	-0.23±0.95	0.42±0.20	0.33±0.23
Dressing weight	0.47±0.03	0.47±0.03	0.24±0.06	0.82±0.99	0.01±0.99	0.01±0.99	-	0.87±0.07
Dressing (%)	0.94 ^{**} ±0.01	0.79 ^{**} ±0.03	0.62 ^{**} ±0.03	0.07±0.05	0.99±0.98	0.96±0.99	0.01±0.11	0.01±0.12
Fillet weight	-0.02±0.03	0.12±0.03	0.26±0.02	0.15±0.03	0.17±0.05	0.99±0.98	-	0.84±0.09
Fillet (%)	0.92 ^{**} ±0.01	0.75 ^{**} ±0.02	0.54±0.03	0.93 ^{**} ±0.02	0.38±0.03	0.11±0.05	-0.58±0.09	0.59±0.50
Weight	0.99 [*] ±0.01	0.76 ^{**} ±0.02	0.47±0.03	0.94 ^{**} ±0.01	-0.02±0.01	0.92 ^{**} ±0.01	0.25±0.07	0.86±0.05
Lenght	0.82 ^{**} ±0.02	0.60 ^{**} ±0.03	-0.03±0.02	0.77 ^{**} ±0.02	-0.02±0.02	0.75 ^{**} ±0.02	0.82 ^{**} ±0.02	0.22±0.07

^{**} Significant Pearson correlations between carcass quality traits (*P* < 0.01); - Denotes the correlation that we were unable to estimate due to convergence problems.