Aquatic Living Resources

Note

Genetic variation for carcass quality traits in cultured sea bass (*Dicentrarchus labrax*)

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Abstract – Genetic parameters for carcass quality traits were estimated in 27 families of sea bass (3 dams × 9 sires factorial mating design), raised mixed in the same tanks starting before hatching. Offspring parentage was determined *a posteriori* using 6 microsatellite loci. Carcass quality traits were recorded at 818 days post fertilization (mean standard length: 32.6 ± 3.1 cm). Genetic parameters were estimated from the sire half sib variance and covariance components. Heritability of body weight (*BW*) and carcass processing traits (standardized to body weight) percent head weight (*Head%*), percent viscera weight (*Viscera%*) and percent visceral fat weight (*VisceFat%*) were relatively high ranging from 0.48 ± 0.15 (*Viscera%*) to 0.87 ± 0.23 (*Head%*); the estimate of heritability for fillet yield (*Fillet%*) was lower (0.25 ± 0.10) but was significantly greater than zero. Body weight was positively correlated to *Fillet%, Viscera%*, and *VisceFat%*, and negatively correlated to *Head%*. These results indicate that these carcass processing traits can be modified by directional selection and that selection for greater *BW* would lead to an increase of *Fillet%*, *Viscera%* and *VisceFat%* and a decrease of *Head%*.
Muscle lipid content (*MuscleLipid%*) was determined using two indirect methods: measurements with a Torry Fish Fatmeter® (*TorryLipid*) and determination of the percentage of dry matter content (*MuscleDry%*) via desiccation. Both measures were highly correlated to chemical measurements of *MuscleLipid%*. Regression analysis indicated a superior predictive value of *TorryLipid* suggesting that *MuscleLipid%* may be evaluated via rapid, non lethal measurements with a Torry Fish Fatmeter. Heritability estimates of *TorryLipid* and *MuscleDry%* differed significantly from zero (*TorryLipid*: 0.28 ± 0.12, *MuscleDry%*: 0.36 ± 0.14) indicating that *MuscleLipid%* could be lowered by directional selection. *TorryLipid* and *MuscleDry%* were weakly correlated to body weight and carcass processing traits suggesting that simultaneous improvement of *MuscleLipid%* and other carcass quality traits may require definition of multi-trait selection indices.

Key words: Heritability / Carcass quality / Microsatellites markers / Communal testing / *Dicentrarchus labrax*

1 Introduction

The European sea bass, *Dicentrarchus labrax* (L.), is a major species for marine aquaculture in the Mediterranean region. Initial aquaculture developments in this species relied on undomesticated breeders caught in the wild and conditioned for spawning in captivity (Garcia de Leon et al. 1998).

Development of breeding programs in order to improve phenotypic characters of interest for aquaculture production is now in progress in several aquaculture farms. Growth rate is usually of primary interest in those programs, as development of fast growing strains via selective breeding would allow lowering production costs significantly by reducing the duration of the rearing cycle. Carcass processing traits and body composition traits also are essential ingredients of economic profitableness as they influence the yield of final product, its quality, and its acceptance by the consumer (Neira et al. 2004; Kause et al. 2002). For example, fillet yield and gutted yield are primary components of economic gain when fish are marketed as pan

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fish or as gutted fish. The level of fat deposition in the flesh or in the visceral cavity also impacts carcass quality, including texture (Andersen et al. 1997) and storage characteristics of the fillet (Lie 2001), and ultimately acceptance of the product by the consumer. Thus, additional objectives for aquaculture production in sea bass may include increased gutted and fillet yields, lowered proportion of carcass waste products, and lowered fat deposition.

The design of efficient selective breeding programs aiming at improving multiple traits requires knowledge of the magnitude of heritability of individual traits and genetic correlations between traits (Falconer and McKay 1989). To date, estimates of genetic parameters in sea bass have been reported for growth (Saillant et al. 2006; Dupont-Nivet et al. 2008) but there is no published data on genetic parameters for additional carcass quality traits.

Here we report genetic parameters for carcass processing traits and fat deposition traits in 27 families of sea bass raised mixed in the same tanks from fertilization and using *a posteriori* parentage assignment with microsatellites. Using this approach, multiple families were tested under identical conditions (in the same tank) during the entire rearing cycle (Herbinger et al. 1995; Estoup et al. 1998; Garcia de Leon et al. 1998). Genetic parameters were thus estimated using a limited number of tanks and without confounding genetic effects with early common environment effects (Vandeputte et al. 2001). Heritability was estimated based on sire half sib families and using a restricted maximum likelihood algorithm. We also examined genetic correlation among traits in order to provide a first assessment of potential correlated responses to selective breeding for fast growth rate and evaluate potential for simultaneous improvement of multiple traits.

2 Materials and methods

2.1 Experimental groups

The studied groups included 27 families of sea bass raised mixed in the same tank beginning 48 h post fertilization (i.e. shortly before hatching) until sampling. The families were generated according to a full factorial mating design that involved 3 dams × 9 sires. All breeders had been caught in the wild (West Mediterranean) with the exception of two females of uncertain origin: the two females were either wild fish from West Mediterranean or cultured offspring from wild parents caught in this region. Embryos from each family were produced at the beginning of the natural spawning season (February): eggs were obtained from the three females by manual stripping following hormonal induction of ovulation, and individually fertilized with sperm from each of the 9 sires as described in Saillant et al. (2001a). All fertilizations were carried out within a three hours period. Floating (alive) and sinking (dead) eggs were separated at 48 h post fertilization by decanting at a salinity of 38‰ (Chatain 1994a). Three replicate groups were constituted at that stage. Each group received an equal volume of living eggs from each dam × sire combination as described in Saillant et al. (2002), thus resulting in an equal initial representation of the 27 families. Broodstock

management and protocols for hormonal induction of spawning, artificial fertilization and incubation of eggs are described in detail in Saillant et al. (2002).

Detailed protocols for subsequent rearing phases may also be found in Saillant et al. (2002) i.e. groups high temperature (HT). The three replicate groups (HT1, HT2, HT3) were maintained in separate tanks connected to the same water recirculating system and were treated identically throughout the experiment. Fish density was lowered on four occasions during fish growth by randomly discarding fish in each replicate. All the fish in replicate group HT1 died accidentally at 468 days post fertilization (dpf) due to accidental cut off of oxygen input in the tank. Replicate group HT1 was replaced by surplus fish from replicate tank HT2 obtained during the following density adjustment (at 504 dpf). The generated group (HT2b) was kept under the same conditions as the other two replicates (HT2, HT3) as indicated above until the end of the experiment. Fish were fed a commercial diet using an on-demand feeding system: Le Gouessant (Lamballe, France) for particles of a mean diameter < 2.5 mm and Biomar Ecolife (Biomar, Nersac, France) for larger pellets.

2.2 Samplings and measurements

Carcass quality traits were recorded when the fish reached the age of 818 dpf. A total of 709 fish were randomly sampled for genetic analysis. Sample sizes in individual replicates were 270, 284 and 155 in HT2, HT3 and HT2b, respectively.

Fish were killed a few at a time by immersion in a $400\ \mu$l L^{-1} solution of phenoxy-2-ethanol. Muscular fat content measurements were immediately taken with a Torry Fish Fat meter (see below). Fish were then weighed (body weight, *BW*) to the nearest g and measured (standard length, *SL*) to the nearest mm and dissected. All viscera (including visceral fact) were extracted and weighed. Visceral fat was separated from other visceral tissue and weighed individually. The phenotypic sex was identified by visual inspection of gonads as described in Saillant et al. (2002). No sign of active gametogenesis was observed at the time of sampling. Gonads and liver were also weighed separately but contributed a very small fraction of body weight (average 0.23 and 1.45% *BW*, respectively) and were not analyzed further. All gutted carcasses were then processed by the same experienced operator as follows: fillets were obtained by cutting along the rib cage and removing the skin from the flesh; the two fillets were weighed to the nearest gram and frozen for further analysis. The carcass was beheaded and fish head weighed individually. The other remains of the gutted carcasses ("filleting waste products" including skin, bones and fins) were pooled and weighed for each fish.

Muscle lipid content (*MuscleLipid%*) was evaluated by two indirect methods. Both methods exploit the approximately linear (negative) relationship between lipid and water content of fish tissues (Vogt et al. 2002). Determination of tissue water content (or dry matter content) thus provides an indirect measure of lipid content. *MuscleLipid%* was first measured on the carcass immediately after death with a Torry Fish Fatmeter 692 (Distell, Fauldhouse, UK). Measurement procedures followed directions from the manufacturer. Mean *MuscleLipid%* was estimated from the average of measurements implemented

at 5 different locations on the fillet as described in Douirin et al. (1998): three measurements were implemented along the longitudinal axis of the fish, 3 mm above the lateral line. The first one was located behind the gills, the second beneath the dorsal fins, and the third just behind the dorsal fins. The two additional measurements were located below the lateral line and were also taken along the longitudinal axis of the fish, one was just behind the pectoral fin and the second one above the anal fin. The percentage of dry matter content in the fillet flesh was also determined via direct desiccation of tissue samples. Frozen fillets obtained as above were thawed and ground in order to obtain a homogeneous mixture. Three aliquots (1–3 g) were sub-sampled from the mixture and weighed to the nearest 10^{-2} g (wet weight, *WW*). The aliquots were then dried at 105 °C for 24 hours and weighed to determine the dry weight (*DW*). The percent dry matter (*MuscleDry%*) was calculated as $MuscleDry\% = 100 \times \frac{DW}{WW}$ and averaged over the three sub-samples.

In order to evaluate the reliability of estimation of lipid content of the muscle by the two indirect methods implemented during the study, *MuscleLipid%* was measured directly by a biochemical method for a sub-sample of 30 randomly chosen individuals. Biochemical measurements were performed at the "Centre d'évaluation et de valorisation des produits de la mer" (Boulogne-sur-Mer, France). Total lipids were extracted by the Folch method (Folch et al. 1957), and pre- and post-extraction weights were used to derive lipid content.

A small piece of fin (ca. 25 mm^2) was sampled and kept in 95% ethyl alcohol for further genotyping. Fin clips had been taken from the three dams and the nine sires previously.

2.3 Genotyping and pedigree analysis

Deoxyribonucleic acid (DNA) isolations and microsatellite assays were performed at LABOGENA laboratory (Jouy-en-Josas, France). Nuclear DNA was extracted from the fin clips using an alkaline lysis protocol as described in Saillant et al. (2002). Parents and offspring were assayed at 3 or 6 microsatellite loci described by Garcia de Leon et al. (1995). The loci were combined in two multiplex panels (multiplex-1: *Labrax 3*, *Labrax 13* and *Labrax 29*; multiplex-2: *Labrax 6*, *Labrax 8* and *Labrax 17*) for polymerase chain reaction (PCR) amplification and electrophoresis on an automatic sequencer ABI 377 (Perkins Elmer, Courtaboeuf, France). Primer labeling, multiplex PCR amplification and electrophoresis, and analysis of electrophoregrams followed procedures detailed in Saillant et al. (2002). Multilocus genotypes were used to assign offspring to parents based on Mendelian principles and using a personal Excel macro (Microsoft, Redmond CA, USA): based on genotypes at multiplex-1 or the combination of multiplex-1 and multiplex-2, parental origin could be traced unambiguously for 98.1% of the fish sampled.

2.4 Data analysis

The following carcass quality traits derived from the measurements taken on the fish were evaluated in statistical analysis: body weight (*BW*), body standard length (*SL*), total viscera weight (*Viscera*), visceral fat weight (*VisceFat*), overall fillet (both fillets summed) weight (*Fillet*), head weight (*Head*), filleting waste products weight (*FilletWaste*), mean *MuscleLipid%* as evaluated from Torry Fish Fatmeter measurements (*TorryLipid*), and mean muscle dry matter content (*MuscleDry%*). Weights of total viscera, visceral fat, fillets, head and filleting waste products were also standardized to body weight resulting in the following traits: *Viscera%*, *VisceFat%*, *Fillet%*, *Head%*, *FilletWaste%*.

Fish condition coefficient (*K*) was estimated as described in Blanc and Poisson (2006); principal component analysis (PCA) was applied to the bivariate distribution of Naperian logarithms of weight and length, and individual fish coordinates along the second principal component were taken as a measure of *K*. PCA computations were implemented in PROC FACTOR of SAS$^{\circledR}$ (SAS Institute Inc., Cary, NC, USA).

Correlation between the direct measure of *MuscleLipid%* and *TorryLipid* or *MuscleDry%* was estimated using Pearson's linear correlation coefficient as implemented in PROC CORR of SAS$^{\circledR}$. The quality of the prediction of *MuscleLipid%* by the two indirect measures was assessed by regression analysis as implemented in PROC CORR of SAS$^{\circledR}$.

Transformation was necessary to stabilize heterogeneity of variances for some of the traits examined. However, analysis of transformed and untransformed data yielded nearly identical results for all traits. Therefore only results obtained on untransformed data are presented.

Variance and covariance components and their standard errors for all traits were estimated using the restricted maximum likelihood method (REML) as implemented in VCE 5.0$^{\circledR}$ (Neumaier and Groeneveld 1998). Both univariate and bivariate analyses were implemented using the following mixed model:

$$y_{ijklm} = \mu + Se_i + s_j + d_k + T_l + e_{ijklm} \tag{1}$$

where y_{ijklm} is an observation on individual m, μ is the overall mean, Se_i is the fixed effect of phenotypic sex i, s_j is the random additive effect of sire j, d_k is the random additive effect of dam k, T_l is the fixed effect of replicate tank l, and e_{ijklm} is the residual random error term associated with y_{ijklm}.

Preliminary analysis revealed that the dam × sire interaction was not significant for any of the traits studied. This effect was therefore not included in the final model (1) employed to estimate genetic parameters.

The additive genetic variance (σ_A^2) was estimated from the sire component of variance (σ_s^2) through the relationship $\sigma_A^2 = 4\sigma_s^2$ (Becker 1984), and heritability was calculated as the ratio $h^2 = \sigma_A^2/\sigma_P^2$. Phenotypic ($r_p$) and additive genetic correlations (r_a) between traits were estimated as the ratio of the phenotypic or genetic (sire) covariance to the product of the square root of the estimated phenotypic or sire variances as obtained during bivariate analyses.

The magnitude of the effect of sex on all traits was estimated as the difference between the best linear unbiased estimator (BLUE) of the mean trait value for male offspring and the BLUE of the mean trait value for female offspring; BLUE values and their standard errors were generated in PEST 4.2.6 (Groeneveld and Kovac 1990) and were based on (1).

Table 1. Phenotypic mean (± standard deviation) and heritability estimates (h^2 ± standard error, SE) for carcass quality traits recorded in 694 sea bass *Dicentrarchus labrax*. See text for detailed trait definitions.

Trait	Tank 1	Tank 2	Tank 3	Overall	h^2 (± SE)
n	269	273	152	694	
BW (g)	727.1 ± 233.6	744.2 ± 225.4	741.9 ± 247.5	741.9 ± 233.4	0.63 ± 0.23
SL (cm)	32.6 ± 3.2	32.6 ± 2.8	32.6 ± 3.2	32.6 ± 3.1	0.40 ± 0.16
Viscera (g)	78.2 ± 33.1	77.1 ± 28.5	80.9 ± 34.4	78.3 ± 31.7	0.86 ± 0.25
Viscera%	10.6 ± 2.3	10.3 ± 2.0	10.8 ± 2.6	10.5 ± 2.3	0.48 ± 0.15
VisceFat (g)	50.1 ± 25.7	51.5 ± 23.0	55.2 ± 27.6	51.8 ± 25.2	0.91 ± 0.27
VisceFat%	6.7 ± 2.1	6.8 ± 1.9	7.2 ± 2.1	6.9 ± 2.0	0.68 ± 0.19
Fillet (g)	247.7 ± 80.2	247.5 ± 77.7	247.8 ± 87.0	247.6 ± 80.7	0.63 ± 0.23
Fillet%	34.1 ± 2.2	33.4 ± 2.4	33.3 ± 2.5	33.7 ± 2.4	0.25 ± 0.10
Head (g)	149.5 ± 47.5	153.9 ± 46.5	151.6 ± 49.6	151.7 ± 47.6	0.36 ± 0.15
Head%	20.7 ± 1.9	20.8 ± 2.1	20.6 ± 1.6	20.7 ± 1.9	0.87 ± 0.23
FilletWaste (g)	242.5 ± 78.9	258.2 ± 77.1	254.1 ± 82.6	251.2 ± 79.3	0.54 ± 0.20
FilletWaste%	33.9 ± 2.0	34.6 ± 1.9	34.4 ± 2.1	34.3 ± 2.0	0.18 ± 0.08
K	–0.1 ± 1.0	0.1 ± 1.0	0.0 ± 1.0	0.0 ± 1.0	0.10 ± 0.05
MuscleDry%	29.2 ± 2.3	29.7 ± 2.2	29.6 ± 2.2	29.5 ± 2.3	0.36 ± 0.14
TorryLipid (%)	5.9 ± 1.8	6.1 ± 1.8	6.2 ± 1.8	6.0 ± 1.8	0.28 ± 0.12

3 Results

Thirteen individuals (1.9%) could not be assigned to dam or sire due to unsuccessful PCR amplification. Phenotypic sex was not available for another two individuals. The 15 individuals were discarded from further analysis. Ultimately records were available for 694 fish. A significant excess of males was found in all three replicate groups (average 65%, contingency *G* test of association: $G = 26.44$, $df = 1$, $p < 0.001$). Detailed contributions of individual families to each group are available from the authors upon request. Offspring from one of the three dams was underrepresented in all three replicate groups (16% of the offspring sampled) whereas 47 and 37% of the offspring were assigned to the other two dams. The proportions of offspring assigned to individual sires varied from 2- to 16%.

Summary statistics for all phenotypic traits recorded are reported in Table 1. Mean body weight and standard length (± SE) were 737.0 ± 233.4 g and 32.6 ± 3.1 cm, respectively. The weight of total viscera, visceral fat, fillets, fish head and filleting waste products represented on average 10.5, 6.9, 33.7, 20.7, and 34.3 percent of body weight respectively (Table 1). Variations among the three replicate tanks were low for all traits (range 0–2%). Both indirect measures of *MuscleLipid%* were significantly correlated to the direct biochemical measurement ($r = 0.73$, $p < 0.0001$ for *MuscleDry%*; $r = 0.82$, $p < 0.0001$ for *TorryLipid*). The regression parameters for the prediction of *MuscleLipid%* by the two indirect measurements were

$$MuscleLipid\% = 1.475 TorryLipid + 0.493 \ (R^2 = 0.72)$$
$$MuscleLipid\% = 0.776 MuscleDry\% - 13.515 \ (R^2 = 0.53)$$

3.1 Heritability estimates

Heritability estimates for non standardized carcass processing traits (*BW*, *SL*, *Viscera*, *VisceFat*, *Fillet*, *Head*, *FilletWaste*) ranged between 0.36 ± 0.15 (*Head*) and 0.91 ± 0.27

(*VisceFat*). All estimates differed significantly (>1.65 SE) from zero (Table 1).

Estimates of heritability for standardized traits also differed significantly from zero (Table 1). The highest heritability estimate was obtained for *Head%* (0.87 ± 0.23) followed by *VisceFat%* (0.68 ± 0.19) and *Viscera%* (0.48 ± 0.15). Estimates of h^2 for *Fillet%* (0.25 ± 0.10), *K* (0.10 ± 0.05), and FilletWaste% (0.18 ± 0.08) were lower but were significantly greater than zero (Table 1).

Both indirect measures of *MuscleLipid%* gave significant h^2 estimates. Estimates (0.36 ± 0.14 for *MuscleDry%* *versus* 0.28 ± 0.12 for *TorryLipid*) were very similar and did not differ significantly (difference < 1.96 SE) from one another.

Estimates of the dam component of variance represented on average 14.6% of the phenotypic variance and ranged between 0% (*FilletWaste*) and 29% (*Head*). The difference between estimates of the dam and sire components of variance (in % of the phenotypic variance) ranged between 0.1% (*K*) and 20.6% (*TorryLipid*) and averaged 11.1%. The estimate of the sire component of variance was greater for *BW*, *SL*, *Fillet*, *Head*, *FilletWaste*, *MuscleDry%* and *TorryLipid* and lower for the remaining traits. Because estimates of the dam (co)variance components were based on three dams only, they are not detailed further.

3.2 Correlations among traits

All non standardized carcass processing traits were highly correlated to body weight (phenotypic correlations 0.78 < r_p < 0.98, genetic correlations 0.95 < r_g < 1.00), suggesting that response to selection for those traits would essentially parallel response to selection observed in body weight. Because selective breeding programs for sea bass would likely include growth rate (e.g. body weight at a given age) as a primary selection criterion, we focused description of genetic and phenotypic correlations on traits standardized to body weight in order to evaluate potential for simultaneous improvement of body weight and those quality traits.

Table 2. Genetic (above diagonal) and phenotypic (below diagonal) correlations between body weight (*BW*), standardized carcass traits, and measures of muscle lipid content. See text for detailed trait definitions.

	BW	*Viscera%*	*VisceFat%*	*Fillet%*	*Head%*	*FilletWaste%*	*K*	*MuscleDry%*	*TorryLipid*
BW		0.83 ± 0.09	0.83 ± 0.08	0.47 ± 0.25	–0.83 ± 0.09	–0.82 ± 0.14	1.00*	0.37 ± 0.23	0.30 ± 0.25
Viscera%	0.26		1.00 ± 0.00	0.50 ± 0.22	–0.95 ± 0.04	–0.84 ± 0.13	0.80 ± 0.16	0.09 ± 0.26	–0.05 ± 0.28
VisceFat%	0.34	0.92		0.58 ± 0.21	–0.96 ± 0.03	–0.92*	0.87*	0.08 ± 0.26	–0.02 ± 0.27
Fillet%	0.17	–0.08	–0.04		–0.73 ± 0.15	–0.89 ± 0.08	0.82 ± 0.20	–0.15 ± 0.29	0.14 ± 0.27
Head%	–0.41	–0.62	–0.65	–0.29		0.90 ± 0.1	–0.96 ± 0.16	0.14 ± 0.26	0.18 ± 0.26
FilletWaste%	–0.17	–0.31	–0.30	–0.62	0.23		–1.00*	–0.32*	–0.54 ± 0.21
K	0.12	0.27	0.25	–0.19	–0.14	0.04		0.51 ± 0.26	0.59 ± 0.24
MuscleDry%	0.31	0.35	0.34	0.17	–0.40	–0.17	0.07		0.94 ± 0.04
TorryLipid	0.31	0.34	0.36	0.13	–0.41	–0.12	0.09	0.79	

* Standard error could not be estimated during optimization of the bivariate model.

Viscera% and *VisceFat%* were highly correlated to each other ($r_p = 0.92$, $r_g = 1$) and the two traits were positively correlated to body weight ($r_p = 0.26$–0.34, $r_g = 0.83$, Table 2). Phenotypic correlations between *Fillet%* and *BW*, *Viscera%*, and *VisceFat%* were close to zero. Corresponding genetic correlations however were positive (range 0.47–0.58) and significantly greater than zero.

Head% was positively correlated to *FilletWaste%* ($r_p = 0.23$, $r_g = 0.90$) and the two traits were negatively correlated to *BW*, *Viscera%*, *VisceFat%*, and *Fillet%* with genetic correlations approaching –1 (Table 2).

Phenotypic correlations between *K* and other traits were low (range –0.19–0.27). However, genetic correlations between *K* and *BW*, *Viscera%*, *VisceFat%*, and *Fillet%* were close to 1 and those between *K* and *Head%* and *FilletWaste%* approached –1.

Both phenotypic and genetic correlations between the two indirect measures of *MuscleLipid%* were high ($r_p = 0.79$; $r_g = 0.94$). Both traits were positively correlated (phenotypic correlations r_p) with *BW*, *Viscera%*, *VisceFat%*, *Fillet%*, and *K* and negatively correlated to *Head%* and *FilletWaste%*; however corresponding genetic correlation estimates did not differ significantly from zero except for the correlations between *TorryLipid* and *K* (0.59 ± 0.24), and *TorryLipid* and *FilletWaste%* (−0.54 ± 0.21) (Table 2).

3.3 Effect of phenotypic sex

Females were significantly larger than males (BLUE of body weight of 840.3 ± 68.5 and 627.8 ± 67.9 for females and males respectively). The dimorphism in body weight (100 × [BLUE females – BLUE males]/BLUE males) was 33.8%. The sexual dimorphism was significant for all non standardized carcass processing traits and was similar in magnitude to the dimorphism in body weight (range 29.6–37.9%).

The effect of sex was significant on *Fillet%*: fillet yield in Females was lower than in Males (–2.4%, BLUE estimates 32.7 ± 0.4 in females and 33.5 ± 0.4 in males). Females also tended to have greater condition coefficient (0.20 ± 0.17 *versus* −0.03 ± 0.16), higher standardized head weight (21.0 ± 0.4 *versus* 20.5 ± 0.4, +2.4%) and lower *MuscleLipid%* (*MuscleDry%*: 28.8 ± 0.7 *versus* 29.7 ± 0.7, –3.0%; *TorryLipid*: 5.2 ± 0.7 *versus* 6.4 ± 0.6, –18.8%). BLUE estimates for males and females

differed by less than one standard error for *Viscera%*, *VisceFat%* and *FilletWaste%*.

4 Discussion

The objective of this work was to evaluate genetic effects on a panel of carcass quality traits important for aquaculture production. Estimates of additive genetic variance and heritability were derived from the variance among paternal half sibs in a mixture of 27 families raised mixed in the same tanks (i.e. in a common environment) throughout the rearing cycle.

The estimate of heritability of body weight (0.63 ± 0.22) was in the upper range of estimates reported in cultured fishes (Saillant et al. 2006) and was significantly greater than zero indicating that selection for increased body weight would be successful as previously reported in sea bass (Saillant et al. 2006; Dupont-Nivet et al. 2008). Non standardized carcass processing traits (*Viscera*, *VisceFat*, *Head*, *Fillet*, *FilletWaste*) were highly correlated to *BW* and showed similar heritability estimates, suggesting that response to selection in those traits would essentially parallel response observed on body weight. We therefore focus further discussion below on carcass processing traits standardized to body weight.

Heritability estimates were significantly greater than zero for the standardized carcass processing traits *Fillet%*, *Viscera%*, *VisceFat%*, *Head%*, and *FilletWaste%* indicating that genetic progress towards desirable phenotypes could be achieved via directional selection for each of these traits. The estimate of heritability for *Viscera%* and *VisceFat%* were 0.48 ± 0.15 and 0.68 ± 0.19 respectively and were in the upper range of heritability values reported for these two traits in other fishes, e.g. *Viscera%*: 0.20–0.38 in *Cyprinus carpio* (Kocour et al. 2007); 0.33–0.45 in *Oncorhynchus mykiss* (Gjerde and Schaeffer 1989; Kause et al. 2002), *Viscefat%*: 0.03–0.47 in various salmonids (Gjedrem 2000; Kause et al. 2002; Neira et al. 2004); 0.42 in *Ictalurus punctatus* (Bosworth et al. 2007). The relatively high estimated heritability values suggest that rapid reduction of the proportion of viscera (i.e. increase in gutted yield), and reduction of percent visceral fat could be achieved via directional selection. In addition, both genetic and phenotypic correlations between *Viscera%* and *VisceFat%* were close to one, indicating that higher *Viscera%* was essentially

due to greater amount of fat deposition in the viscera. A high correlation between the two traits was also reported in channel catfish (Bosworth et al. 2007) and rainbow trout (Kause et al. 2007a) and is likely due, for a large part, to occurrence of very large amounts of visceral fat in farmed sea bass (6.9% of the overall body weight, 66% of the overall viscera weight in our study). The positive correlation between *Viscera%* and *BW*, and *VisceFat%* and *BW* also suggests that *Viscera%* and *VisceFat%* would increase relatively rapidly following selection for fast growth rate (i.e. for a greater *BW* at the age of sampling) leading to decreased gutted yield. Similar observations were made in salmonids (Kause et al. 2007b; Powell et al. 2008). An increase in *VisceFat%*, in addition to contributing to decreasing gutted yield, may also impact negatively acceptance of farmed sea bass by consumers if sold as whole fish.

The estimate of heritability for *Fillet%* was 0.25 ± 0.10 and was in the range of estimates reported in other species including *Oreochromis niloticus* (0.12, Rutten et al. 2005), *C. carpio* (0.28, Kocour et al. 2007), or *O. mykiss* (0.33, Kause et al. 2002). The moderate h^2 value for *Fillet%* suggests that response to selection for increased fillet yield would be slow, a prediction that is consistent with observations reported during studies on pedigreed farmed populations of salmonids (Kause et al. 2007a; Powell et al. 2008). However, genetic and phenotypic correlations between *Fillet%* and *BW* were positive indicating that selection for increased *BW* would not lead to an unfavorable response in *Fillet%* but rather may lead to a slight increase in this trait.

The estimate of heritability for *Head%* was high (0.87 ± 0.23) and indicates occurrence of significant genetic variation for the relative size of fish head. Estimates of heritability for this trait in other species are generally significantly greater than zero and range from moderate (0.15 in *O. niloticus*, Rutten et al. 2005) to high (e.g. 0.52 for h^2 of relative head length in *C. carpio*, Kocour et al. 2007). *Head%* was strongly negatively correlated to *BW* and the carcass processing traits discussed above suggesting that selection for increased body weight would lead to a rapid decrease of the relative size of fish head together with an increase of viscera and fillet yields. Heritability of the relative weight of the remaining carcass waste product (*FilletWaste%*) differed significantly from zero but was moderate (0.18 ± 0.08). However *FilletWaste%* was positively correlated to *Head%* (genetic correlation 0.90 ± 0.10) and negatively correlated to body weight, *Fillet%*, *Viscera%* and *VisceFat%*. These correlation estimates suggest that selection for increased body weight may lead to a reduction of *Head%* and *FilletWaste%*; reduction of the contribution of these two carcass waste products to the overall carcass weight may in turn contribute to the overall expected increase in fillet yield discussed above. The negative correlation between *FilletWaste%* and *Fillet%* likely reflects in part easier filleting of larger fish leading to lower filleting waste products for those fish. However, the occurrence of a significant genetic correlation between *Head%* and *Fillet%* also suggests that conformation traits contribute to increasing fillet yield. Identification of such conformation traits would be useful in sea bass as they would allow indirect, non lethal evaluation of genetic values for fillet yield (see Rutten et al. 2004). Fish conformation was also evaluated using the condition coefficient (*K*) in our study. Estimates of genetic correlations between *K* and *BW*, *Viscera*, *VisceFat%* and *Fillet%* were close to 1 while correlations between *K* and *Head%* or *FilletWaste%* were close to –1 suggesting that condition may be used as a (non invasive) predictor of genetic values for these carcass quality traits. The estimate of h^2 for *K* was however low (0.10 ± 0.05), predicting a slow response to selection and likely reflecting the fact that *K* is a relatively poor indicator of body shape that potentially integrates the effects of several variables including skeletal deformities which are frequently reported in cultured sea bass (Chatain 1994b). Further assessment of genetic variation in conformation and skeletal deformities, using more reliable descriptors, and correlations of these characters with carcass processing traits is warranted. We note that our standardization of the weight of body compartments was calculated as a simple ratio to *BW*. Issues associated with selective breeding for ratio traits were discussed by Gjerde and Schaeffer (1989) and Rutten et al. (2005) and include potentially low and erratic response to selection. This potential problem may be in part mitigated by improving trait standardization to *BW* (e.g. by including *BW* as a covariate in analysis models and applying an allometric transformation). The efficiency of such approaches in sea bass may be evaluated in future studies when larger datasets will become available.

MuscleDry% and *TorryLipid* both were highly correlated to direct measurement of *MuscleLipid%* suggesting that both traits could be used as indirect selection criteria in a breeding program aiming at lowering *MuscleLipid%* in sea bass. The quality of the prediction of *MuscleLipid%* was however greater with *TorryLipid* as indicated by regression analysis suggesting increased efficiency in the evaluation of phenotypic and genetic values. Overall, use of *TorryLipid* seems therefore the most cost effective approach for practical field genetic evaluation given that this method is non lethal and provides an instantaneous measure of *MuscleLipid%*, while invasive and likely lethal sampling of muscle tissue coupled with significant laboratory work are needed to estimate *MuscleDry%*. The heritability estimates for *TorryLipid* and *MuscleDry%* were intermediate and differed significantly from zero ($h^2 = 0.28 \pm 0.12$ for *TorryLipid*, 0.36 ± 0.14 for *MuscleDry%*) indicating that both traits and *MuscleLipid%* could be improved via directional selection. Significant heritability of *MuscleLipid%* is in accordance with observations in other species, e.g. 0.25–0.72 in *O. mykiss* (Quillet et al. 2005; Tobin et al. 2006); 0.17–0.26 in *O. kisutch* (Neira et al. 2004); 0.58 in *C. carpio* (Kocour et al. 2007). Phenotypic and genetic correlations between *TorryLipid* or *MuscleDry%* and other carcass quality traits were low and the estimates of genetic correlations did not differ significantly from zero except for a significant negative correlation between *TorryLipid* and *FilletWaste%* and a significant positive correlation between *TorryLipid* and *K*; the latter two genetic correlations were intermediate in magnitude (-0.54 ± 0.21 and 0.59 ± 0.24 respectively). Altogether these results indicate that selection for increased body weight would not impact negatively *MuscleLipid%* and that simultaneous improvement of the latter trait and other carcass processing traits in a multi-trait selection approach would require separate genetic evaluation of breeders for *MuscleLipid%*. In addition, we observed a weak correlation between *MuscleLipid%*

and *VisceFat%* (r_p between 0.34–0.36, r_g between 0.02–0.08). *VisceFat%* shows a strong positive correlation to *BW* as discussed above that was not found for *MuscleLipid%*. These results highlight that *VisceFat%* and *MuscleLipid%* are different lipid traits that would both need to be accounted for in a breeding program in order to control lipid deposition in selected strains. Similar findings were recently reported in *O. mykiss* by Tobin et al. (2006) and Kause et al. (2007b).

Design of optimal selection strategies in order to improve simultaneously multiple carcass quality traits in sea bass will require accurate estimates of genetic parameter (heritability and genetic correlations) in order to define efficient selection indices. Our estimates are based on a relatively limited number of families (27 families and 9 sires) leading to a low precision as indicated by the relatively large standard errors obtained; further study using a more robust experimental design is warranted and in progress. We also note that our results suggest that the relative weight of the various body parts examined during this work may evolve rapidly as responses to direct selection on these traits, or simply as the result of correlated responses to selection for fast growth rate. Potential consequences of these modifications (e.g. reduction of gutted yield and fish head size) on physiological integrity of selected fish will require further evaluation.

Finally the effect of phenotypic sex on body size was significant as previously documented in sea bass (Carillo et al. 1993; Saillant et al. 2001b; Saillant et al. 2003). The sexual dimorphism in weight was 33.8% and translated in a similar (29.6–37.9%) relative advantage for females in all non standardized carcass processing traits. Females also had a lower fillet yield as reported previously in sea bass (Peruzzi et al. 2004) and tended to exhibit greater condition coefficient, greater relative weight of the head, and lower *MuscleLipid%*. Greater condition coefficient and relative size of the head suggest occurrence of differences in conformation between sexes as previously reported in sea bass (Barnabé 1976; Peruzzi et al. 2004); differences in conformation between sexes might thus be involved in the lower fillet yield reported for females. Lower *MuscleLipid%* in females was also reported previously in sea bass (Saillant et al. 2001) and would be a favorable response to breeding monosex female populations

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