SUPPLEMENTARY INFORMATION

for

METAPOPULATION PATTERNS OF ADDITIVE AND NON-ADDITIVE GENETIC VARIANCE IN THE SEA BASS (*DICENTRARCHUS LABRAX*)

B. GUINAND, M. VANDEPUTTE, M. DUPONT-NIVET, A. VERGNET, P. HAFFRAY, H. CHAVANNE & B. CHATAIN

Supplementary Table S1: Pairwise F_{ST} ($\hat{\theta}$; *sensu* Weir & Cockerham, 1984) values based on seven microsatellite loci found among the wild samples of sea bass considered in this study (i.e. breeders that initiated the factorial diallel crosses; N = 101 correctly amplified individuals). The samples considered in this study represent the currently recognized subpopulations of sea bass (WEM: western Mediterranean [n = 32], SAT: southern Atlantic [n = 15], SEM: south eastern Mediterranean [n = 15], NEM: North Eastern Mediterranean [n = 15], NAT: northern Atlantic [n = 24]). Results agreed with previous studies that demonstrated significant nuclear genetic differentiation among the Mediterranean and Atlantic subpopulations (e.g., Quéré *et al*., 2012 and references therein), but genetic homogeneity between the NAT and SAT subpopulations (e.g., Fritsch *et al*., 2007). A Bonferroni correction for multiple tests was applied. See details in the text.

	SEM	**WEM**	**SAT**	**NAT**
NEM	0.0340***	0.0236***	0.0590***	0.0548***
SEM		0.0465***	0.0609***	0.0463***
WEM			0.0293***	0.0361***
SAT				0.0062^{NS}

***: P < 0.001; NS: not significant

Associated references:

Fritsch, M., Morizur, Y., Lambert, E., Bonhomme, F. &. Guinand, B. 2007 Assessment of sea bass (*Dicentrarchus labrax*, L.) stock delimitation in the Bay of Biscay and the English Channel based on mark-recapture and genetic data. *Fish. Res.* **83:** 123–132.

Quéré, N., Desmarais, E., Tsigenopoulos, C.S., Belkhir, K., Bonhomme, F. & Guinand, B. 2012. Gene flow at major transitional areas in sea bass (*Dicentrarchus labrax*) and the possible emergence of a hybrid swarm. *Ecol. Evol*. **2:** 3061-3078.

Weir, B.S. & Cockerham, C.C. 1984. Estimating *F*-statistics for the analysis of population structure. *Evolution* **38:** 1358–1370.

Figure Suppl. S1: Genetic differentiation among wild sea bass samples illustrated by the positions of male and female wild individual breeders that initiated the crosses considered in this experiment onto the map of a factorial correspondence analysis. Individual genotypes at seven microsatellite loci were used to generate this map. Analysis was performed with Genetix v4.05 (http://kimura.univ-montp2.fr/genetix/). The three first axis of the analysis summarise 83.91% of the total variance of the data set (axis 1: 40.04%; axis 2: 24.57%; axis 3: 19.30%). Details on significance of genetic differentiation for each pairwise population comparisons are reported in Suppl. Table S1. WEM: western Mediterranean, SAT: southern Atlantic, SEM: south eastern Mediterranean, NEM: North Eastern Mediterranean, NAT: northern Atlantic.

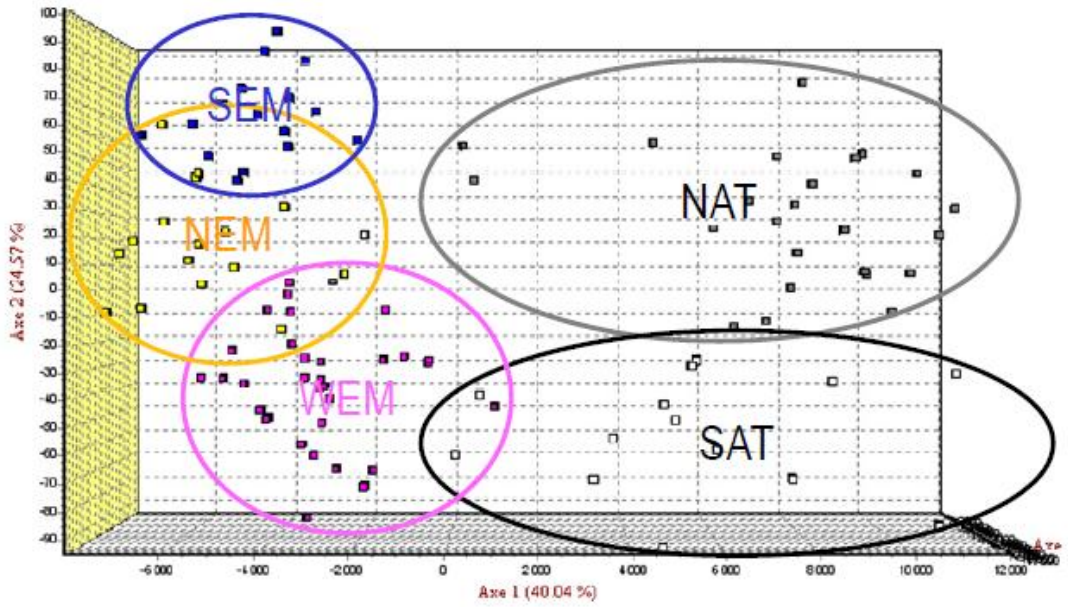
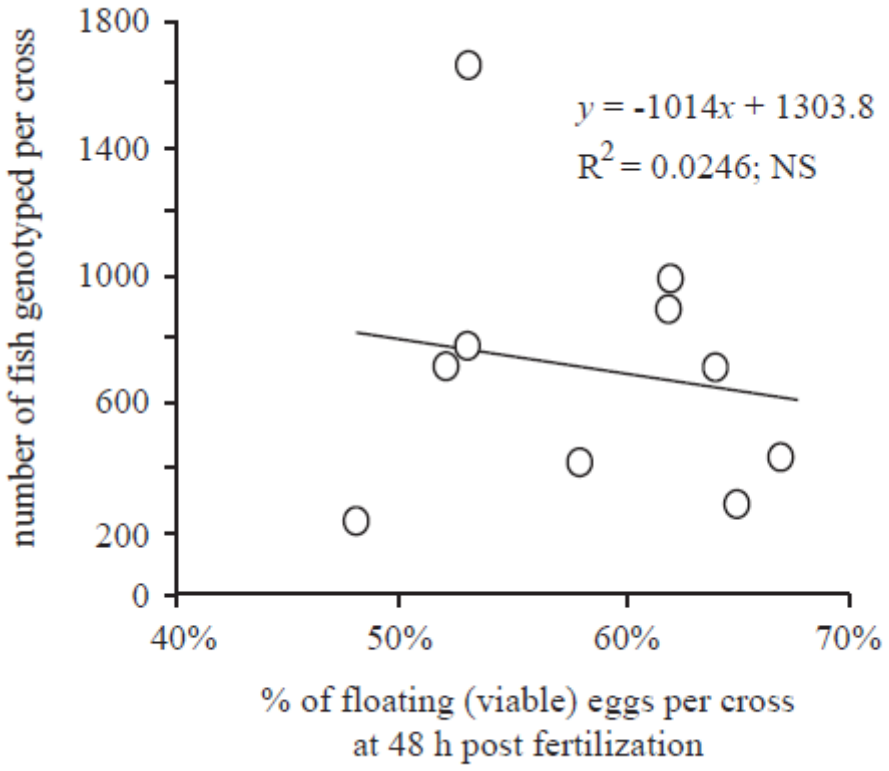


Figure Suppl. S2: Number of fish per cross at tagging (mean individual weight ~20g; 187 dpf in Israel; 216 dpf in Portugal) in relation to the percentage of floating eggs at 48 hours post-fertilization. The percentage of floating eggs is an indicator of the fertilization rate (Carillo *et al*., 1989). No significant relationship was demonstrated, showing that fertilization/hatching rate is not linked to survival during larval rearing. Significant heterosis detected in the data is then not biased by difference in fertilization or hatching rates.



Associated reference:

Carrillo, M., Bromage, N., Zanuy, S., Serrano, R. & Prat, F. 1989. The effect of modifications in photoperiod on spawning time, ovarian development and egg quality in the sea bass (*Dicentrarchus labrax* L.). *Aquaculture* **81:** 351–365.

Figure Suppl. S3: Number of fish per cross at tagging in relation to the manipulation order at 48 hours post-fertilization. As the relationship was not found significant, eggs manipulated later during the experiment did not suffered from unfavourable holding conditions that may have substantially impacted their survival. Significant non-additive interaction effect detected in the data is then not biased by manipulation of crosses.

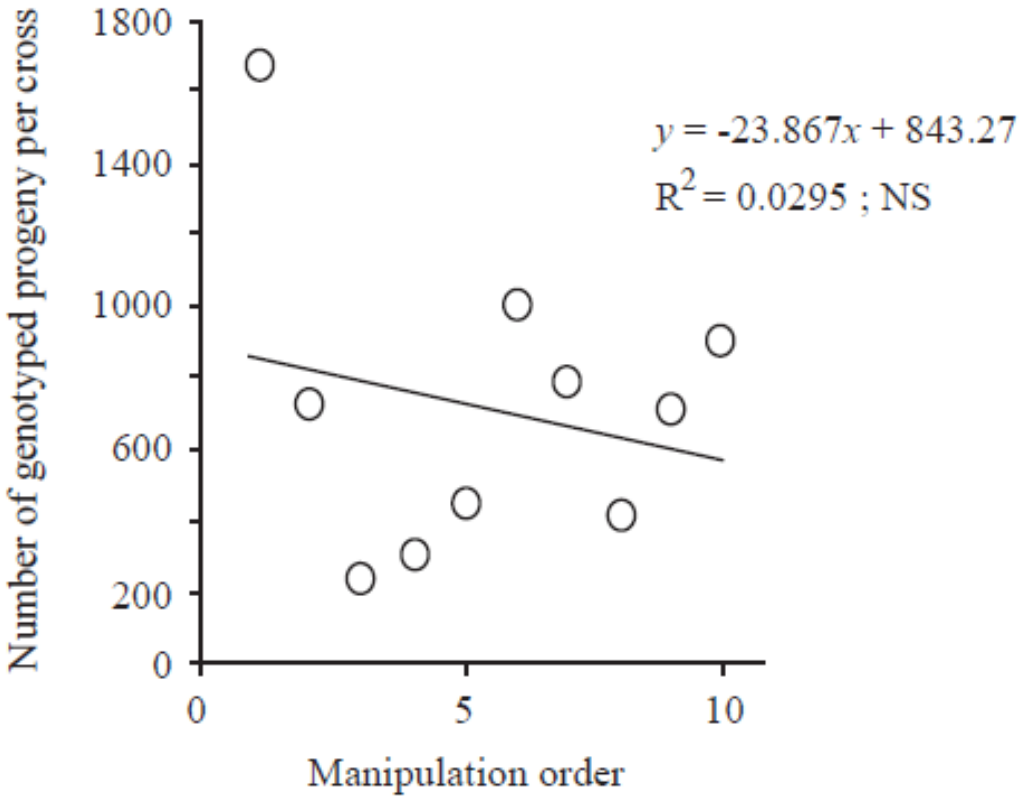
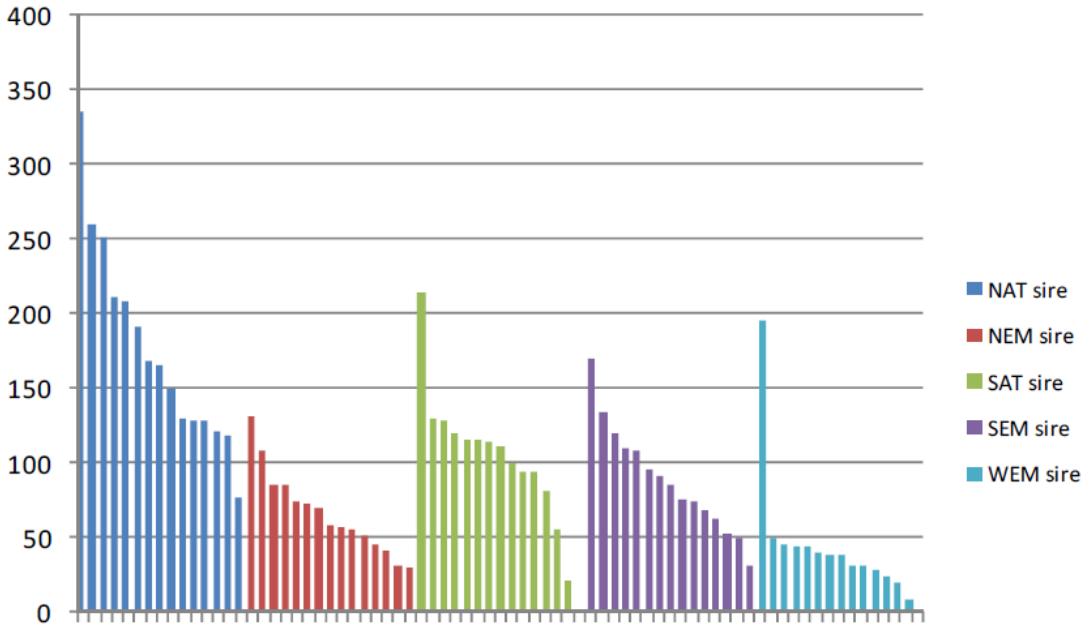


Fig. Suppl. S4 : Contribution of sire and dam to the progenies at tagging (216 days post-fertilization)

A : Representation of the 73 sires in the progenies at tagging. Two sires over 75 considered in this study have no progeny (SAT#04 and WEM#14). The ordinate axis represents the number of offspring produced by each sire. Labels as in Fig. 1.



B : Representation of the 26 dams in the progenies at tagging (~20g). Labels as in Fig. 1.

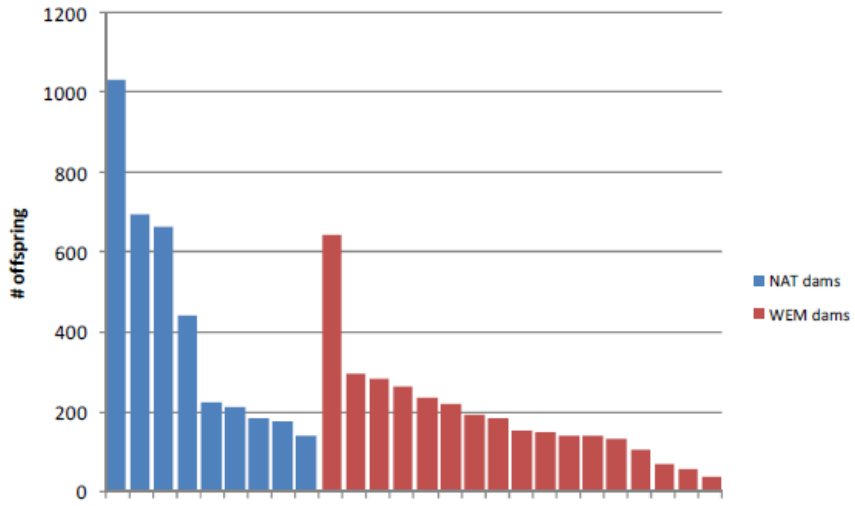


Fig. Suppl. S5 : Relationship between the number of progeny by sire and the mean body mass of progenies at tagging (216 days post-fertilization). Regression lines are reported for each sire's population, together with significance of the linear relationship. Labels as in Fig. 1.

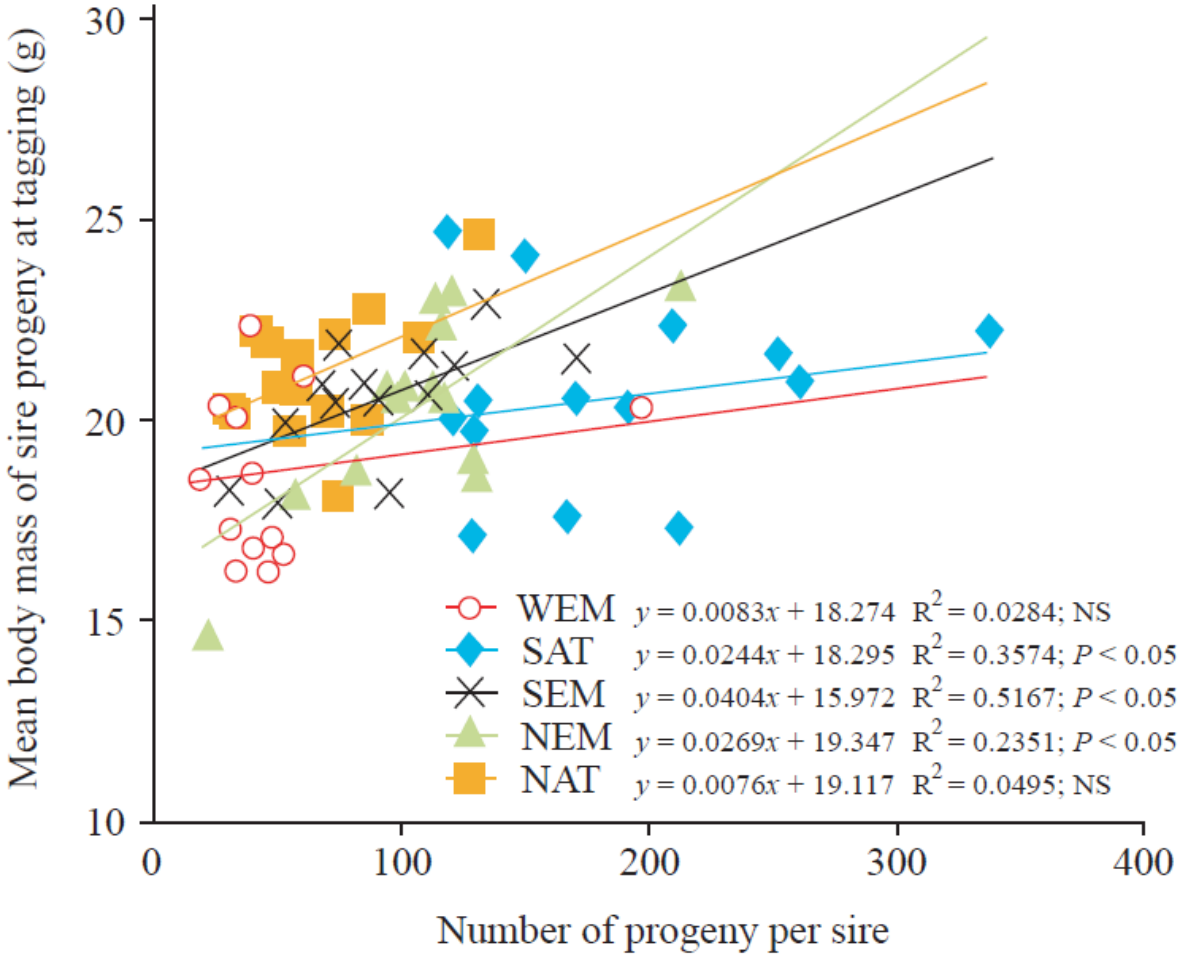


Fig. Suppl. S6 : Sex ratio as measured by the proportion of females in each of the ten sire × dam crosses. Labels as in Fig. 1.