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GENOTYPE x ENVIRONMENT INTERACTIONS FOR GROWTH RATE IN EUROPEAN SEA BASS (*Dicentrarchus labrax*)

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Introduction

The European sea bass is a major aquaculture species in the North-East Atlantic and in the Mediterranean. Rearing systems and environments are very diverse, with different structures (raceways, ponds, cages) and temperature ranges. It has been shown recently that the sea bass has a very good potential for selective breeding (Dupont-Nivet et al., 2008). The question naturally arises whether selecting fish in a single environment will yield good results in other conditions. This question can be answered by the evaluation of genotype by environment (GxE) interactions, which quantify the re-ranking of families performances in different environments, and then allow the prediction of selection response when fish are selected in one environment but reared in another one. GxE interactions are moderate for slaughter weight in sea bass (Dupont-Nivet et al, 2008). This paper evaluates them on growth rate at the population and family levels.

Material and methods

Broodstock were collected from five populations (North Atlantic – NAT, South Atlantic – SAT, West Mediterranean – WEM, North-East Mediterranean – NEM and South-East Mediterranean – SEM). Males were collected in all five populations, while females came from two origins (NAT and WEM). A full factorial mating was performed between 15 sires per population and 9 NAT and 17 WEM dams. They were all reared as a single batch. Family (and population) origins were reconstructed *a posteriori* using seven microsatellite markers, with a single assignment rate of 98.9%.

Four sites (A, B, C, D) were chosen with contrasted situations: site A had sea cages in tropical waters (20-28°C), site B had on-shore tanks fed with constant temperature (22°C) borehole water, site C was temperate with on-shore tanks and natural temperature sea water (15-27°C) and in site D fish were raised in tidal earthen ponds with natural temperature (13-25°C).

Larval rearing and pre-growing was performed in tanks in site D. A random sample of fish was sent to site A at a mean weight of 1g (111 dpf). 1,800 of them were individually PIT-tagged and weighed at 23g mean weight and further grown in site A. Another random sample of fish was grown until 20g in site D, and 5,400 were tagged and sent to sites B, C and D (1,800 in each site). When an estimated 200 g mean weight was reached, the remaining fish in each site were individually weighed and a sub-sample (on average 700 per site) was sexed.

Growth rate was measured as thermal growth coefficient (TGC) between tagging at *ca.* 20g and slaughtering at *ca.* 200g. Analysis of data involved mixed models with site, sex, sire and dam populations as fixed effects, and sire and dam as random effects using SAS-

Proc Mixed. GxE interactions were evaluated considering TGC in each environment as a separate trait using VCE6 (Groeneveld et al, 2008) with an animal model, with sex, sire and dam populations as fixed effects.

Results

A total of 6024 fish were analyzed. At the sire population level, there was a significant GxE interaction between site A and the other three ($P<0.01$). In site A, the fastest growers were the offspring of NEM and SEM. NAT and WEM were the slowest growers while SAT was in-between. In sites B, C and D, the fastest growers were NEM and SAT, the slowest growers were SEM and WEM while NAT was in-between. The differences between populations were relatively moderate (8% difference in TGC between the best and the worst population).

Table I. Heritabilities of TGC between 20 and 200 g (in bold on the diagonal) in each rearing site and genetic correlations for TGC between sites (\pm SE). The difference in mean rearing temperature between sites is given in italics

	Site A	Site B	Site C	Site D
Site A	0.41±0.04	0.64±0.09 <i>2.4°C</i>	0.46±0.11 <i>4.1°C</i>	0.39±0.12 <i>5.3°C</i>
Site B		0.48±0.05	0.72±0.07 <i>1.7°C</i>	0.57±0.07 <i>2.9°C</i>
Site C			0.40±0.04	0.63±0.09 <i>1.2°C</i>
Site D				0.39±0.03

Heritabilities of TGC were high (Table 1), confirming good prospects to select for growth rate in sea bass. Genetic correlations were moderate, and higher for sites exhibiting smaller differences in mean rearing temperatures (Mantel test, $P<0.05$). GxE interactions on weight at tagging showed that fish pre-grown in site A from 1 to 20g already differed in family rankings at 20 g mean weight when compared with fish pre-grown in site D (genetic correlation between pre-growing sites=0.64±0.09), showing that shorter common life could also explain higher GxE between site A and the others.

Conclusion

In this study, we showed that GxE interaction for growth rate exists in seabass, and is larger when the difference in rearing temperature between sites increases and when duration of common life decreases. Selective breeding for faster growth in seabass then has to be done at a temperature as close as possible to the temperature of the ongrowing sites. Still other factors not studied here (density, feed, water quality) could also participate to the interactions observed.

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