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 Europe. Rearing systems and environments are very diverse, with different structures (raceways, ponds, cages) and temperature ranges. For selective breeding, it is important to know whether the same genotypes will perform well or not in different rearing environments. This is evaluated through genotype by environment (GxE) interactions which quantify the re-ranking of genotypes among environments. We studied this for 5 populations (figure 1), and the families within, in 4 rearing systems, using *a posteriori* parentage assignment with microsatellites.

***Figure 1:** origin of the 5 wild populations of sea bass studied*

Material and Methods

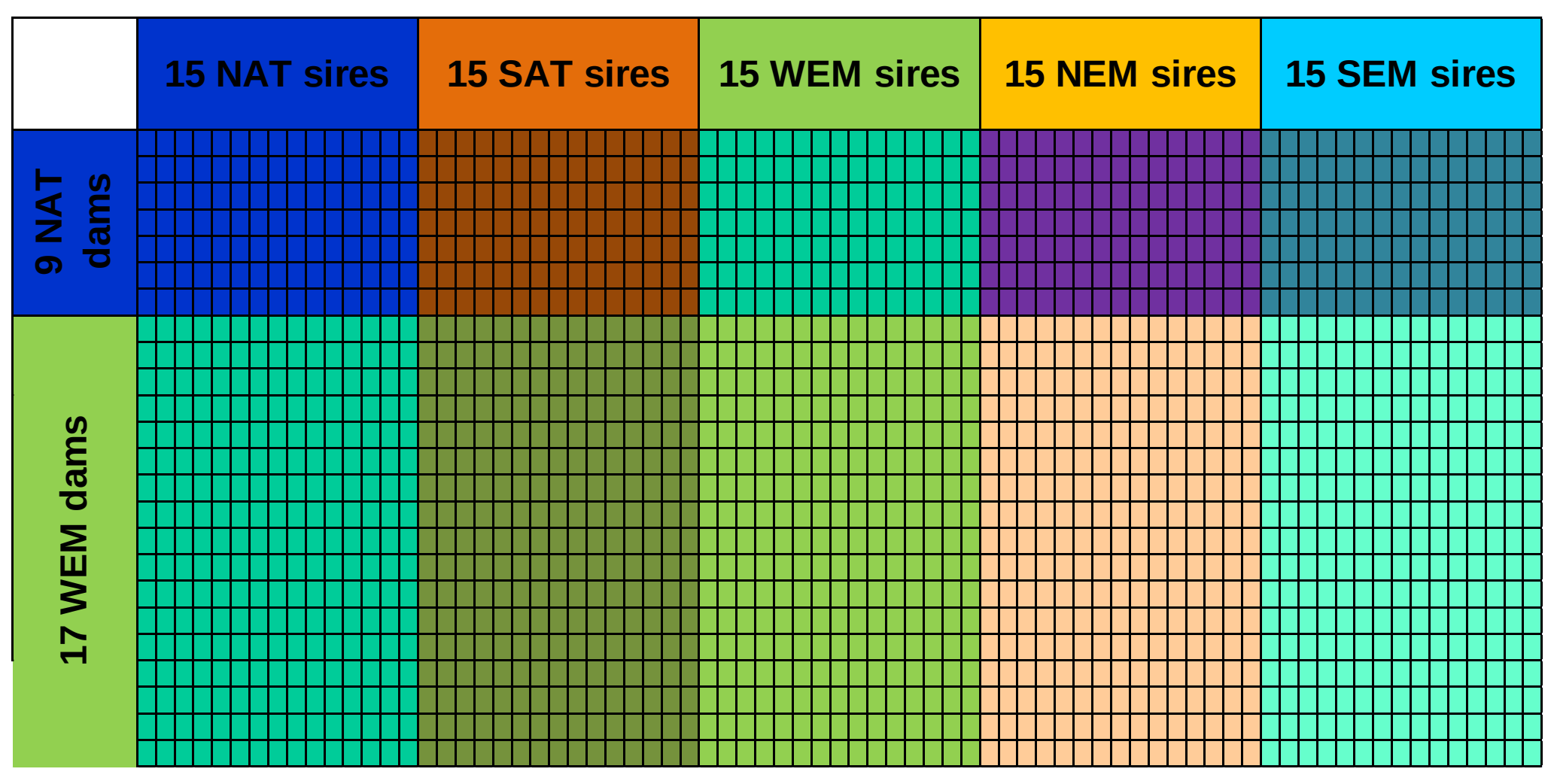

***Figure 2:** Mating design used*

- ○Five broodstock populations collected (figure 1).
- ○Factorial mating design with 5 male origins and 2 dam origins (figure 2).
- ○Fish reared as a single batch, individually tagged at *ca.* 20g
- ○Sent to four ongrowing sites (A, B, C, D) chosen with contrasted situations:
  - site A: sea cages in tropical waters (20-28°C),
  - site B: on-shore tanks with constant temperature (22°C) well water
  - site C: on-shore tanks and natural temperature sea water (15-27°C)
  - site D: tidal earthen ponds with natural temperature (13-25°C).
- ○ Fish were individually weighed at 20 and 200g
- ○ Thermal growth coefficient (TGC) was calculated for each fish

Genotyping with 7 microsatellites➔ 98.9% fish with known family and population origin (6024 fish in total).
Data analysis with mixed models with site, sex, sire and dam populations as fixed effects, and sire and dam as random effects using SAS-Mixed. GxE interactions evaluated considering TGC in each environment as a separate trait using VCE6 with an animal model, with sex, sire and dam populations as fixed effects. With such a model, a low genetic correlation between sites is indicative of a high GxE interaction

Results and Discussion

At the population level

At the sire population level, there was a significant GxE interaction between site A and the other three (P<0.01 – figure 3).

In site A: **NEM=SEM > SAT> WEM=NAT**

In sites B,C,D: **SAT=NEM>NAT>SEM=WEM**

Populations differences moderate (8% TGC between best and worst)

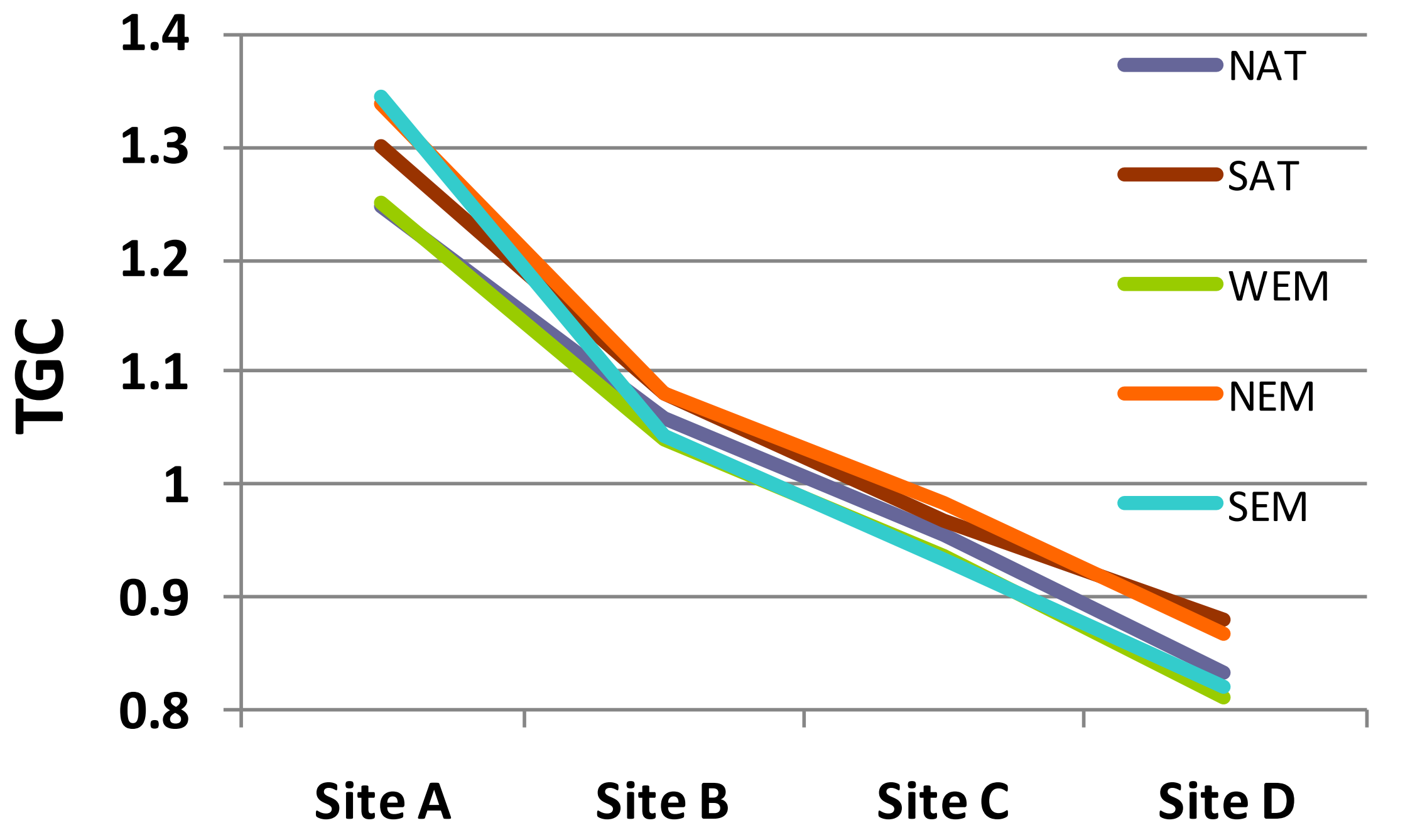

***Figure 3:** Mean thermal growth coefficient (TGC) of the offspring of the 5 sire populations in the 4 ongrowing sites*

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

***Table 1**. Heritabilities of TGC (in bold on the diagonal) in each rearing site and genetic correlations for TGC between sites (± SE). The difference in mean rearing temperature between sites is given in italics*

At the family level

High heritability of TGC (Table 1)

➔good prospects to select for growth rate

Moderate genetic correlations, indicative of significant GxE (family re-ranking)

Higher for sites with small differences in rearing temperatures (Mantel test, P<0.05).

Conclusion

GxE interaction for growth in seabass is larger when the difference in rearing temperature between sites increases. Breeding for faster growth then has to be done at a temperature close to that 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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