Hybridization and morphological differences between the two closely related oyster taxa *Crassostrea angulata* and *C. gigas*

Frederico M. Batista [1, 2] Vera G. Fonseca [3], Radhouane Ben Hamadou [4], Nicolas Taris [3], Maria A. Henriques [2] and Pierre Boudry [3]

[1] Instituto Nacional de Investigação Agrária e das Pescas (INIAP/IPIMAR), CRIPSul, Av. 5 de Outubro, 8700-305 Olhão, Portugal.

[2] Instituto de Ciências Biomédicas Abel Salazar (ICBAS), Universidade do Porto, Largo Prof. Abel Salazar, 2, 4099-003 Porto, Portugal.

[3] Institut Français de Recherche pour l'Exploitation de la Mer (IFREMER), Laboratoire de Génétique et Pathologie (LGP), 17390 La Tremblade, France.

[4] Centro de Ciências do Mar (CCMAR), Universidade do Algarve, Campus de Gambelas, 8005-139 Faro, Portugal

Introduction

The Portuguese oyster *Crassostrea angulata* and the Pacific oyster *C. gigas* are two closely related taxa of high commercial value that sustained the European oyster production for several decades. Based on shell morphology, experimental hybridisation and allozyme studies several authors have considered these two taxa as being synonymous (1, 2, 3). More recently, clear genetic and phenotypic differences have been observed between them (4, 5, 6, 7). Since no major barriers to reproduction between *C. gigas* and *C. angulata* have been reported (2, 8), hybridization can be seen as a simple and efficient way to exploit putative heterotic effects and generate phenotypic and genetic novelty.

Material and Methods

Factorial crosses between *C. angulata* (from Sado estuary, Portugal) and *C. gigas* (from Seudre estuary, France) were done as shown in Fig. 1. Juveniles of the different progenies were reared in Cacela-Velha (Ria Formosa, Portugal) under usual farming conditions. Maternal origin of all groups was confirmed using a mitochondrial marker.

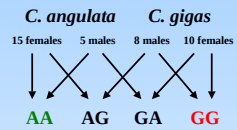


Fig. 1. Experimental crosses

The live weight and mortality was recorded monthly in all groups. At the end of the grow-out phase (268 days) the following shell measurements were obtained (with both valves fitted together): (i) height (H); (ii) length (L); and (iii) width (W). The measurements taken only on the right valve were: (i) height (RVH); (ii) length (LVH); (iv) length of the adductor muscle scar (MA(L)); (v) height of the adductor muscle scar (MA(H)).

Results and discussion

Abnormal high mortality occurred during the first months of the experimental period in the four genetic groups. The live weight of the oysters from all groups increased through time with the AA group growing slower than the AG, GA and GG groups that had a similar performance (Fig. 2). Significant differences in L/H, D/H, D/L, MA(L)/RVL, MA(H)/RVH and MA(H)/MA(L) were observed between AA and GG groups (Fig. 3; Mann Whitney U-test; $p < 0.001$). No significant differences were observed between reciprocal hybrids (AG and GA) for the same parameters. The results obtained also indicate that there is some overlap in canonical variates, but most individuals from AA and GG groups could be identified using the multivariate analysis (Fig. 4). The hybrids showed intermediate canonical variates and couldn't be differentiated from pure matings. Visual comparison of the 95 % confidence interval of the midparental mean with the GA hybrids mean for depth, indicate heterosis for this trait. Heterosis for depth may have resulted from the multiplication of characteristics showing additive effects. Nevertheless, no "useful" heterosis was observed since the amount by the F1 never exceeded significantly the better parent line for all traits analysed. No major maternal effects were observed for the different traits.

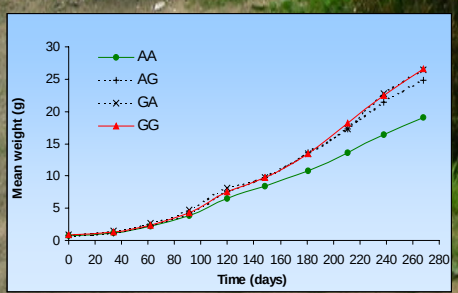


Fig. 2. Mean live weight during the grow-out period

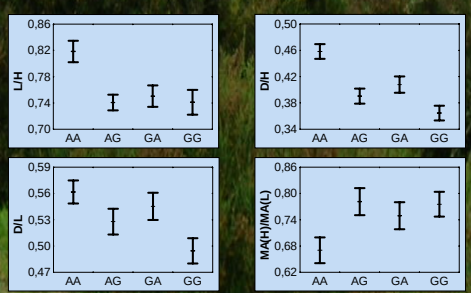


Fig. 3. Mean and 95 % confidence interval of L/H, D/H, D/L and MA(H)/MA(L)

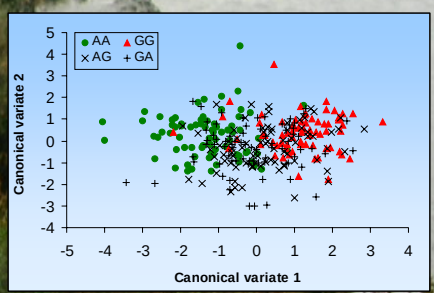
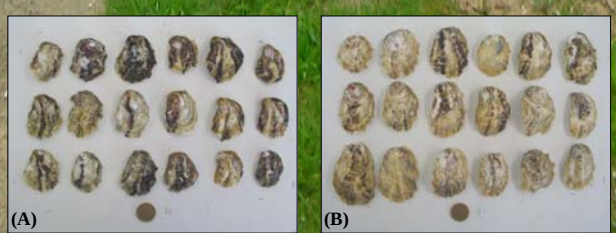


Fig. 4. First and second canonical variates of morphometric data from individuals from the different genetic groups



Right valve of (A) *C. angulata* and (B) *C. gigas* adults with the same age grown in identical conditions

References

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Background image: oyster bed in Sado estuary (Portugal)