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 (INIA/PIPMAR), 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), hybridisation can be seen as a simple and efficient way to exploit putative heterotic effects and generate phenotypic and genetic novelty.

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 hybrid mean for depth, indicate heterosis for this trait. Heterosis for depth may have resulted from the 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), hybridisation can be seen as a simple and efficient way to exploit putative heterotic effects and generate phenotypic and genetic novelty.

References