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Introduction

Summer mortality has been reported in the Pacific oyster, *Crassostrea gigas*, for many years and in several countries (1,2,3,4). The phenomenon affects both adults and juveniles (2,4) and its causes are complex. Others studies have shown that genetic variability exists in sensitivity to summer mortality (5,6). The French project "Morest", coordinated by IFREMER, aims to better understand the causes of the summer mortality in juvenile oysters by a multidisciplinary approach. Within this program, environmental, physiological, pathological and genetic putative factors are studied. A multi-site field experiment was designed to assess to what extent genetic variability exists for survival in French populations of *C. gigas* and to determine whether selective breeding could improve this trait.

Material and Methods

Three sets of bi-parental families were bred in the IFREMER hatchery in La Tremblade (France) following a nested half-sib crossing design (7). After a conditioning period, each sire was mated with four different dams, producing six half-sib families (HSF) and twenty-four full-sib families (FSF). This was repeated 3 times, in February, March and April 2001, producing 3 successive sets of families. During the summer period, 17 HSF including 44 FSF were placed in three sites along French coasts (Ronce-Perquis = Ronce, Rivière d 'Auray = RA and Baie des Veys = BDV) and reared following usual practices. In October 2001, survival, growth and yield were recorded for all families in all sites. In March 2002, 3 "good" HSF and 3 "bad" HSF were selected for their survival performances to perform a divergent selection ("DS"). Survival of the DS was recorded during the summer period in the 3 sites according to the same protocol as in 2001, and DS was also monitored in several laboratory experiments. Survival was analysed by logistic regression using the GENMOD procedure in the SAS® software package. The ASREML program was used to determine variance components of survival and to estimate heritability of this trait in the first generation. For the second generation, realized heritability was determined by the regression between the offsprings and parents.
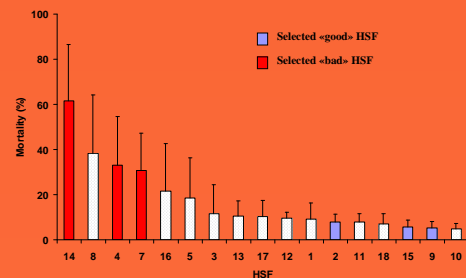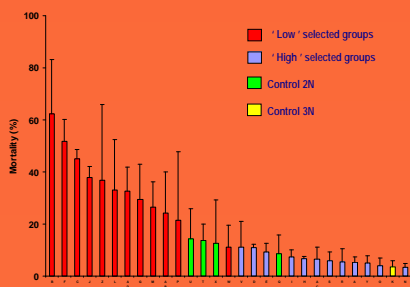
Results
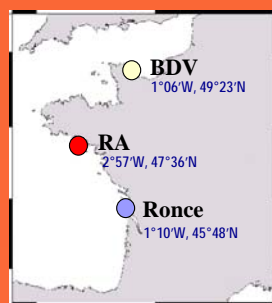
**Figure 1** : Map showing locations of the 3 sites along the French Coast.
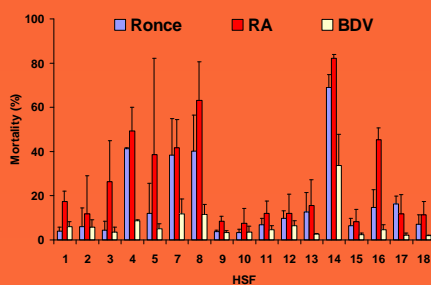
Figure 2 : Mortality rates in the field (average and standard deviation of the FSF) of the 17 HSF in the 3 sites in October 2001 (First generation).

Figure 3 : Mortality rates in the field (average and standard deviation at the 3 sites) of the 17 HSF in October 2001 (First generation).

Figure 4 : Mortality rates in the field (average and standard deviation of the 3 sites) of the DS batches and hatchery controls in October 2002.
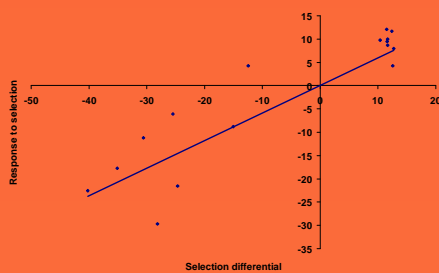
Figure 5 : Regression (slope = 0,59 ± 0,29) of offspring on parent for survival of juvenile *C. gigas* in the field.
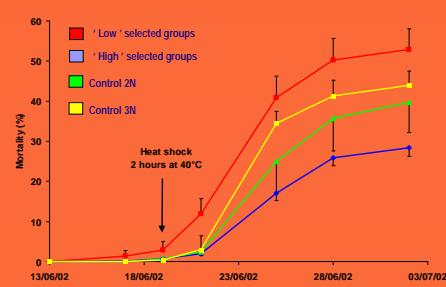
Figure 6 : Evolution of mortality (average and standard error) in laboratory of the DS groups and hatchery controls.

Conclusions

▨ **First generation**: Our results show that some of the half-sib families exhibit high levels of mortality in all sites (figure 2), clearly indicating a genetic basis for survival. Heritability estimate of survival was very high with a value of 0.81 ± 0.29.

▨ **DS in the field**: Significant differences in survival were found between the offspring of the "high" and "low" selected groups in the field (figure 4). Realized heritability of survival was 0.77 ± 0.23 for the high group, 0.56 ± 0.30 for the low group and 0,59 ± 0,29 for the 2 selected groups (figure 5). The DS confirms the G1 results with a positive response to selection, and the strong heritability for survival indicates that selective breeding programs could efficiently improve survival of juvenile oysters.

▨ **DS in the laboratory** : This environment allows us to observe significant differences of survival between the 2 selected groups over less than 2 weeks (figure 6). This experiment also shows that it is possible to obtain a positive response to selection for 3 month old oysters in the laboratory.

References

(1) Koganezawa, A., 1975. Present status of studies on the mass mortality of cultured oysters in Japan and its prevention. In: *Proceedings of the Third U.S.-Japan Meeting on Aquaculture.* Tokyo, Japan, October 15-16, 1974, pp 29-34.
(2) Glude, J.B., 1975. A summary report of Pacific coast oyster mortality investigations 1965-1972. *In : Proceedings of the Third U.S.-Japan Meeting on Aquaculture.* Tokyo, Japan, October 15-16, 1974, pp 1-28.
(3) Goulletquer, P., Soletchnik, P., Le Moine, O., Razet, D., Geairon, P., Faury, N. & Taillade, S., 1998. Summer mortality of the Pacific cupped oyster *Crassostrea gigas* in the Bay of Marennes-Oléron (France). *Cons. int. Explor. Mer, CM 1998 / CC 14 :* 20 p.
(4) Cheney, D.P., MacDonald, B.F & Elston, R.A., 2000. Summer mortality of Pacific oysters, *Crassostrea gigas* (Thunberg) : Initial findings on multiple environmental stressors in Puget Sound, Washington, 1998. *J. Shellfish Res., 19 : 353-359.*
(5) Beattie, J., Chew, K. & Hershberger, W., 1980. Differential survival of selected strains of Pacific Oysters (*Crassostrea gigas*) during summer mortality. *Proc. Nat. Shellfish. Ass.,* 70 : 184-189.
(6) Hershberger, W.K., Perdue, J.A. & Beattie, J.H., 1984. Genetic selection and systematic breeding in Pacific oyster culture. *Aquaculture,* 39 : 237-245.
(7) Ernande B, Clobert J, McCombie H, Boudry P (2003). Genetic polymorphism and trade-offs in the early life-history strategy of the Pacific oyster, *Crassostrea gigas* (Thunberg, 1795): A quantitative genetics study. Journal of Evolutionnary Biology 16 : 399-141.

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