

Response to divergent selection for resistance to summer mortality in Pacific oyster spat: genetic parameters and correlated responses with subsequent survival and growth.

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Introduction

- ➤ To date, the main contribution of genetics to the improvement of Pacific oyster is the production triploids. This is even more significant since the development of tetraploid oysters, allowing the production of "natural" triploids (i.e. 2n x 4n).
- ➤ Oysters are good candidates for selective breeding (Gosling, 2003), as confirmed by the programs currently initiated in USA, Australia and New Zeland.
- Knowledge about heritability and genetic correlations between traits of aquacultural interest is essential to establish selective breeding programs
- ➤ In bivalves, most of the available heritability estimates concern growth related traits. Quantitative genetic studies on survival traits are far less common.



Main objectives of this study:

- Determine if the variation observed for survival of spat over the summer period is heritable
- If yes, is it possible to select oysters to improve/decrease their survival?
- Is spat survival (negatively) correlated with other traits, such as growth or survival at later stages?



2000-2005: 4 successive generations

- > Determine if the variation observed for survival of spat over the summer period is heritable
 - ❖ G1 (2001): estimation of genetic parameters for spat survival and growth
- > If yes, is it possible to select oysters to improve/decrease their survival?
 - ❖ G2 (2002): response one generation of divergent selection: 'R' & 'S' oysters
 - ❖ G3 et G4 (2003-2005) : repeatability of this response

> Is spat survival correlated with other traits, such as growth or survival at later stages?

| | 2001 | 2002 | 2003 | 2004 | 2005 |
|----|------|------|------|------|------|
| G1 | × | × | | | |
| G2 | | × | × | | |
| G3 | | | × | × | |
| G4 | | | | × | × |

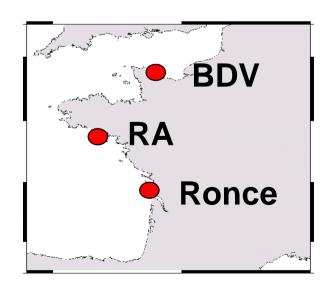
(× first summer; × second summer)



Studied material:

- Bi-parental (G1) and multi-parental (G2-G4) progenies
- inbred and outbred progenies
- Diploids / triploids
- High selected 'R' / control / low selected 'S'

3 study sites:



Field trials



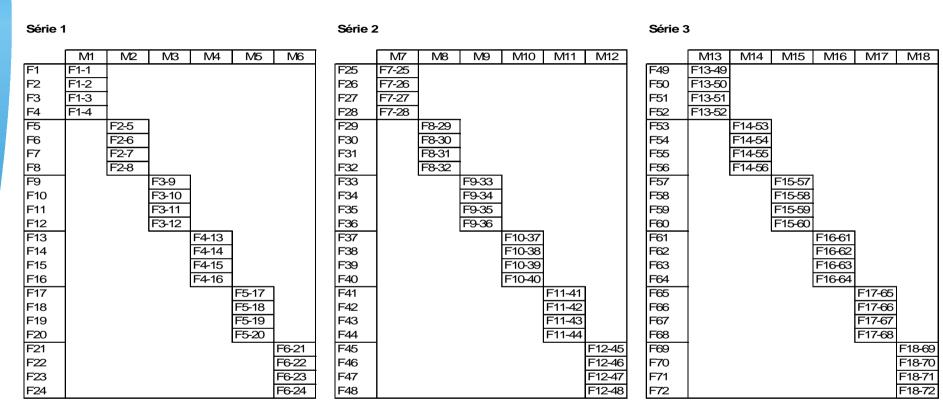


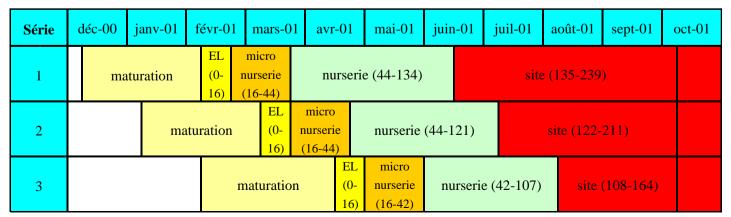
Lab trials





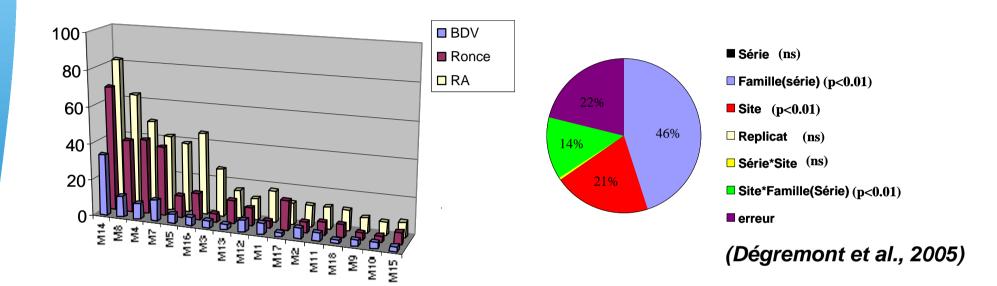
Genetic basis of spat survival over the summer period







Genetic basis of spat survival over the summer period



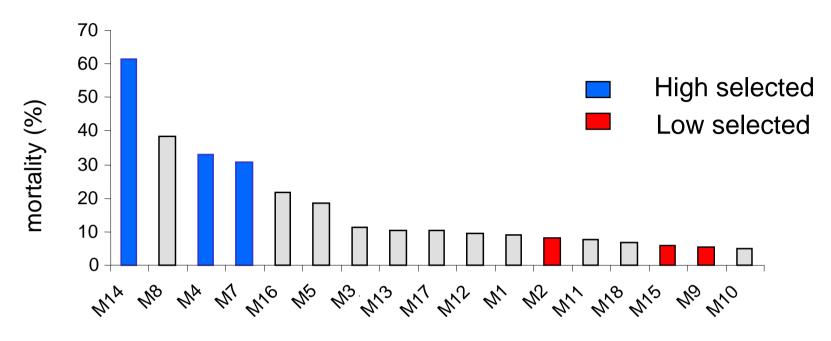
Heritability estimates (± standard error):

Ronce: 1.05 ± 0.44*
 RA: 0.86 ± 0.38*
 BDV: 0.46 ± 0.20**

➤ All sites together: 0.83 ± 0.40*



Divergent selection



Best and worst family selected within each G1 set

Within and among family crosses generating inbred and outbred 'R' or 'S' progenies



- > 2002
- **> 2003**
- **> 2004/2005**
- **G2S, G2cS**
- G3S, G3cS, G3c²S, G3S3n
- G4S, G4cS, G4S3n



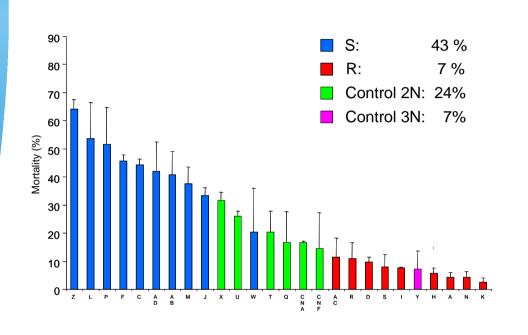
G2R, G2cR

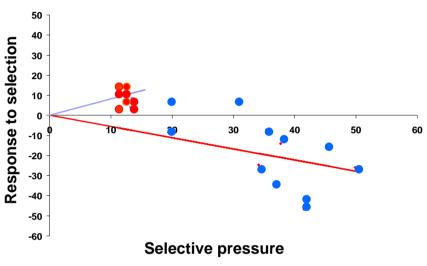
G3R, **G3cR**, **G3c²R**, **G3R3n**

G4R, G4cR, G4R3n



Response to divergent selection





Realized heritability (± standard error):

Ronce: 0.64 ± 0.09 *
 RA: 0.65 ± 0.08 *
 BDV: 0.82 ± 0.24 **

Is this response to selection repeatable over years?

| | | Ronce | | RA | | BDV | | | |
|----------------|------------------|---------------|----------------------|---------------|------------|------------|--|--|--|
| | | R t | S | R t | S | R t S | | | |
| | G2 | 5 = | 8 < 33 | 7 < 2 | 24 < 43 | 7 = 6 < 19 | | | |
| Outbreed | G3 | 27 < 4 | 17 < <mark>72</mark> | | | | | | |
| progenies | G4 | 18 < 5 | 57 < 70 | | | | | | |
| | G2c | 4 = | 4 < 43 | | | | | | |
| Inbred | G3c | 30 = 2 | 4 < 60 | | | | | | |
| progenies | G3c ² | 34 < 6 | 1 < 73 | | | | | | |
| | G4c | 8 < 2 | 4 < 42 | | | | | | |
| - Triploids | G3 3n | | | 35 < 5 | 0 < 58 | | | | |
| | G4 3n | | | 5 = 4 | = 9 | | | | |

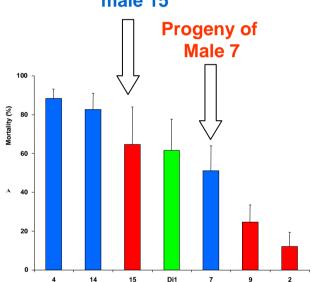
- ➤ When mortality in controls were above 10%, survival of R progenies was always significantly higher than those of the control progenies
- Mortality of S progenies were always higher than in the control progenies (and of than in the R progenies).



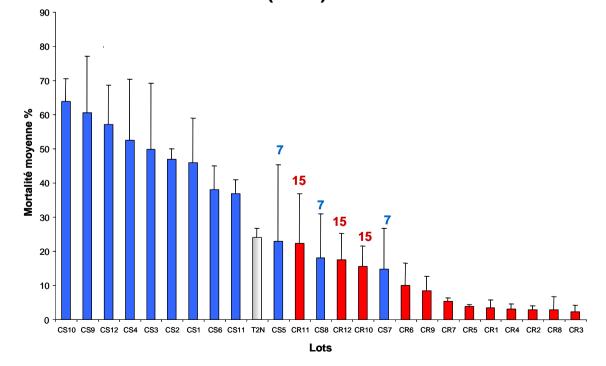
Is this response to selection repeatable over years?

Mean mortality per male in the third generation of inbreeding tested in Ronce (2003)

Progeny of male 15



Mean mortality in the forth generation of inbreeding tested in Ronce (2004)





What about survival during the second summer?

| - | | | Ronce | | RA | | | BDV | | |
|--------------------------------------|--------------|--------|-------|---|----|---|-----------|-----|---|----|
| _ | | | R | S | R | | S | R | | S |
| | G1 | 6 mo. | 4 | | 7 | < | 52 | 3 | < | 15 |
| | G1 | 18 mo. | 5 | | 8 | = | 7 | 24 | | |
| 2 successive |) | | | | | | | | | |
| summers in | G2 | 6 mo. | | | 6 | < | 48 | | | |
| the fields | G2 | 18 mo. | | | 6 | = | 7 | | | |
| | G3 | 6 mo. | | | 38 | < | 83 | 2 | < | 6 |
| | G3 | 18 mo. | | | 7 | = | 8 | 20 | < | 42 |
| 1 st summer | G1 | 18 mo. | | | 4 | < | 14 | | | |
| in nursery 2 nd summer | G2 | 18 mo. | | | 6 | < | 14 | | | |
| In the field | G3 | 18 mo. | | | 22 | = | 27 | 12 | < | 33 |

- ➢ In Ronce and RA, most mortality occurred during the first summer and survival of R and S progenies were similar in their second summer
- In BDV, mortality was higher in the second summer, and survival of R progenies was higher that in S progenies



What about survival in the lab?

| | | Nb. tested progenies | | Mortality | | | | | Correlation with | | |
|------------------|----|----------------------|-----------|-----------|---------|-----------|---|-----------|--------------------------|--|--|
| | | R | S | R | control | | | S | mortality in the field | | |
| G2 | L1 | 9 | 9 | 28 | < | 38 | < | 53 | r = 0.43 (p=0.06) RA | | |
| G2 | L2 | 6 | 5 | 18 | < | 44 | = | 49 | r = 0.58 (p=0.02) RA | | |
| G2 | L3 | 11 | 11 | 26 | = | 25 | < | 53 | r = 0.63 (p < 0.01) RA | | |
| | | | | | | | | | r = 0.47 (p=0.01) Ronce | | |
| G2c | L4 | 10 | 8 | 18 | < | 35 | < | 58 | r = 0.94 (p<0.001) Ronce | | |
| G3 | L5 | 12 | 12 | 31 | < | 52 | = | 53 | r = 0.85 (p<0.001) RA | | |
| G3c ² | L6 | 12 | 11 | 45 | < | 68 | < | 76 | r = 0.84 (p<0.001) Ronce | | |
| G3c | L7 | 12 | 12 | 14 | = | 36 | < | 44 | r = 0.94 (p<0.001) Ronce | | |
| G4c | L8 | 3 | 3 | 7 | = | 8 | = | 8 | ns | | |

- ➤ In most cases, survival of R progenies was higher than those of the control progenies
- ➢ In most cases, mortality of S progenies was higher than those of the control progenies (and tos of R progenies).
- In most cases, data in the field and in the lab were well correlated



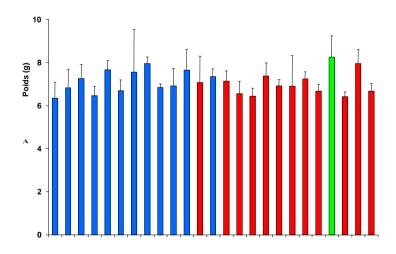
What about growth?

> G1 : estimates of genetic correlation between growth and survival

❖ Ronce: 0.24 ± 0.11*
 ❖ RA: - 0.01 ± 0.09 ns
 ❖ BDV: 0.17 ± 0.11 ns

❖ All sites together : - 0.17 ± 0.14 ns

➤ G2, G3, G4 : no significant difference in growth between R et S progenies
 eg. G3c² in Ronce





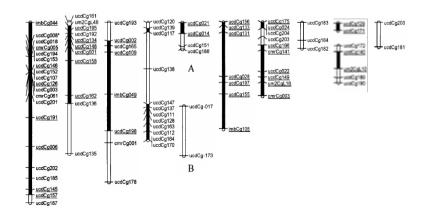
Main conclusions:

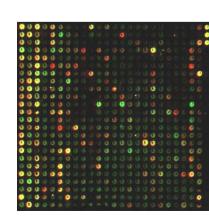
- ❖ ≈ 50% of the observed variability for spat survival is between families (Dégremont et al., 2005; Evans & Langdon, in press).
- Heritability of spat survival is high (Dégremont et al., submitted) and this trait can efficiently be selected for.
- ❖ Among the different hypothesis that could explain the mainteance of additive variance for survival, the existence of a trade-off between reproduction and survival is favored (Ernande et al. 2004)
- ❖ Physiological differences observed between R and S progenies (under laboratory and field conditions) and better survival of triploids support this hypothesis.



Current research and projects:

- **❖QTL** mapping of resistance to summer mortality
- Production and progeny testing of 'R' and 'S' tetraploid oysters
- Establishment of a full-scale breeding program together with the industry
- ❖ Functional genomics of 'R' and 'S' lines





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