Heritability and GxE interactions of disease resistance to summer spat mortalities in Pacific oyster *Crassostrea gigas* using Bayesian model

Enez F., Puyo S., Boudry P., Lapègue S., Gonzalez-Araya R., Guémené D., Chapuis H., Haffray P.

\(^a\) SYSAAF, Rennes, France  
\(^b\) Unité Physiologie Fonctionnelle des Organismes Marins, Ifremer, Plouzané, France  
\(^c\) SG2M-LGPM, Ifremer, La Tremblade, France  
\(^d\) CNC, Paris, France
Mortality problems affecting oyster production

Spat summer mortality syndrome (20 %) since at least 1975 due to OsHV-1 virus

Intermediate to high heritability (Dégremont et al., 2005 ; $h^2 = 0.27-0.68$)

A new µ var herpes virus variant increased mortality to 90 % in 2008

Aim of the study:
Estimation of genetic parameters and GxE interactions in separated-family rearing with the new virus variant

General protocol:
• 9 cohorts for the first generation
• 80 families per cohort
Experimental protocol per cohort

Reproduction of wild parents

Hatchery/Nursery

Bagging project with Individual counting and bag weighting

1-3 bags per family with 300 spats in each

Sea shore challenge in 7 sites during summer 2013

Mortality

Syndicat des Sélectionneurs Avicoles et Aquacoles Français
Bayesian binominal GLMM

Model 1: 3 independent intra cohort analysis
\[ \text{logit}(Y) = \mu + \beta \cdot \text{initial weight} + \text{Site} + \text{Parental effect} + (\text{Site} \times \text{Parental effect}) + \epsilon \]

Model 2: 1 pooled data treatment with 18 Cohort x Site challenges considered as random effect
\[ \text{logit}(Y) = \mu + \beta \cdot \text{initial weight} + \text{Challenge} + \text{Parental effect} + (\text{Challenge} \times \text{Parental effect}) + \epsilon \]

Burn-in: 150000 iterations
Parameter estimation: 4000 estimates sampled every 150 iterations

Parental effect
\[ h^2 = \frac{2 \times (\sigma^2_{\text{Sire}} + \sigma^2_{\text{Dam}})}{\sigma^2_{\text{Total}}} \]

Heritability
\[ h^2 = \frac{2 \times \sigma^2_{\text{Family}}}{\sigma^2_{\text{Total}}} \]

\[ \rho_{\text{Site1} ; \text{Site2}} = \frac{\sigma_{\text{Family}} (\text{Site1} ; \text{Site2})}{\sigma_{\text{Family}} (\text{Site1}) \times \sigma_{\text{Family}} (\text{Site2})} \]
Only 3 cohorts successfully produced (170 families)

<table>
<thead>
<tr>
<th>Cohort</th>
<th>Production</th>
<th>Sea transfert</th>
<th>Family number</th>
<th>Challenge sites</th>
<th>Individual weight at sea transfert</th>
<th>Final survival</th>
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<tbody>
<tr>
<td>C4</td>
<td>September 2012</td>
<td>Early April 2013</td>
<td>50</td>
<td>7</td>
<td>0.09 g ± 0.02</td>
<td>12.6% ± 10.9</td>
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<td></td>
<td></td>
<td>End of June 2013</td>
<td>17</td>
<td>2</td>
<td>0.64 g ± 0.29</td>
<td>15.1% ± 9.7</td>
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<td>C5</td>
<td>February 2013</td>
<td>End of June 2013</td>
<td>54</td>
<td>7</td>
<td>0.49 g ± 0.20</td>
<td>3.7% ± 4.6</td>
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<td>C6</td>
<td>April 2013</td>
<td>End of July 2013</td>
<td>49</td>
<td>2</td>
<td>0.55 g ± 0.10</td>
<td>70.7% ± 26.7</td>
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</tbody>
</table>
Heritability of survival between sites and cohorts

Sire-dam model

Family model

Site

Heritability

Normandy (NY) N. Brittany (NB) S. Brittany (SB) Noirmoutier (NO) Marennec (MA) Arcachon (AB) Thau (TL) All sites
Heritability of survival with all challenges

18 challenges (cohort x site) considered as random effect (Model 2)

Heritability density of probability distribution.
Genetic correlations between sites

### Cohort 4

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<thead>
<tr>
<th></th>
<th>AB</th>
<th>MA</th>
<th>NO</th>
<th>SB</th>
<th>NB</th>
<th>NY</th>
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<tbody>
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<td>TL</td>
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<td>0.19</td>
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<tr>
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<tr>
<td>NB</td>
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<tr>
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<td>0.90</td>
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### Cohort 5

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<th>NY</th>
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<tbody>
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<td>TL</td>
<td>0.16</td>
<td>0.66</td>
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<td>0.81</td>
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<tr>
<td>AB</td>
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<td>0.36</td>
<td>0.89</td>
<td>0.74</td>
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<tr>
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### Cohort 6

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- Generally high to very high genetic correlations...
- No site repetition between cohorts → limited Genotype x Site interaction
- **High stability of families ranking between sites** *(Wilcoxon signed-rank test ; α=0.05)*
Conclusion

• **Intermediate heritability** (0.26) lower than realized heritability estimated by mass selection (Dégremont et al., 2015 ; $h^2 = 0.34-0.63$)

• **Limits of the protocol:**
  - Non optimal mating design
  - Initial mortality information at hatchery were not available
  - Very high within-family bag effect
  - Uncertainty about the pathogen agent
  - High mortality rate $\downarrow h^2$ and $\uparrow$ error in estimation (verified by simulation)

• **Limited GxE interaction** ➡ Genetic progress should benefit to the whole French industry
Thank you for your attention
Heritability error according to survival rates

Simulation

Survie

Biais h2

Survie
Model Estimation

Sire-dam model: \[ Y = \text{site} + \text{weight} + \text{Sire} + (\text{Sire} \times \text{site}) + \text{Dam} + (\text{Dam} \times \text{site}) + (\text{Sire} \times \text{Dam}) + \varepsilon \]

Significant fixed effects estimated by « glmer » function (R)

Site

Increase individual weight

- Better survival than mean
- Survival not different than mean
- Lower survival than mean
- Not tested