

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



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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

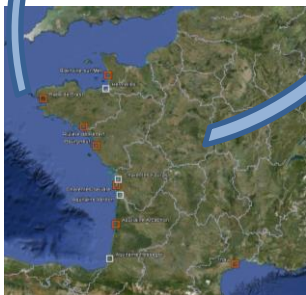
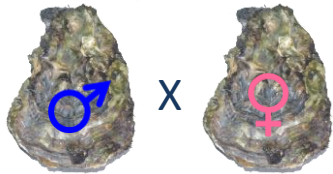
General protocol:

- 9 cohorts for the first generation
- 80 families per cohort



Experimental protocol per cohort

Reproduction of wild parents



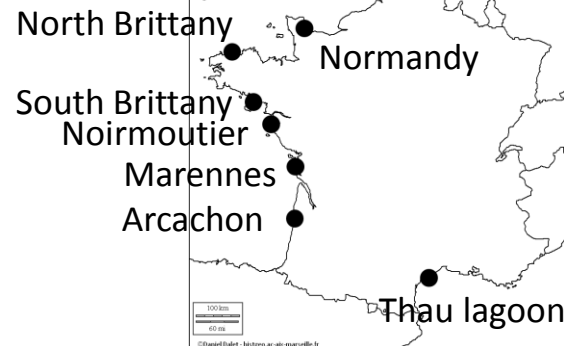
Hatchery/Nursery



Bagging project with Individual counting and bag weighting



1-3 bags per family with 300 spat in each



Sea shore challenge in 7 sites during summer 2013



Mortality

Final counting project



Bayesian binomial GLMM

- Model 1 : 3 independent intra cohort analysis

$$\text{logit}(Y) = \mu + \beta \cdot \text{initial weight} + \text{Site} + \text{Parental effect} + (\text{Site} * \text{Parental effect}) + \varepsilon$$

- Model 2 : 1 pooled data treatment with 18 Cohort x Site challenges considered as random effect

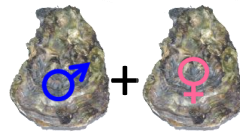
$$\text{logit}(Y) = \mu + \beta \cdot \text{initial weight} + \text{Challenge} + \text{Parental effect} + (\text{Challenge} * \text{Parental effect}) + \varepsilon$$



Burn-in: 150000 iterations

Parameter estimation: 4000 estimates sampled every 150 iterations

Parental effect



Sire + Dam



Family

Heritability

$$h^2 = \frac{2 \times (\sigma^2_{\text{Sire}} + \sigma^2_{\text{Dam}})}{\sigma^2_{\text{Total}}}$$

$$h^2 = \frac{2 \times \sigma^2_{\text{Family}}}{\sigma^2_{\text{Total}}}$$

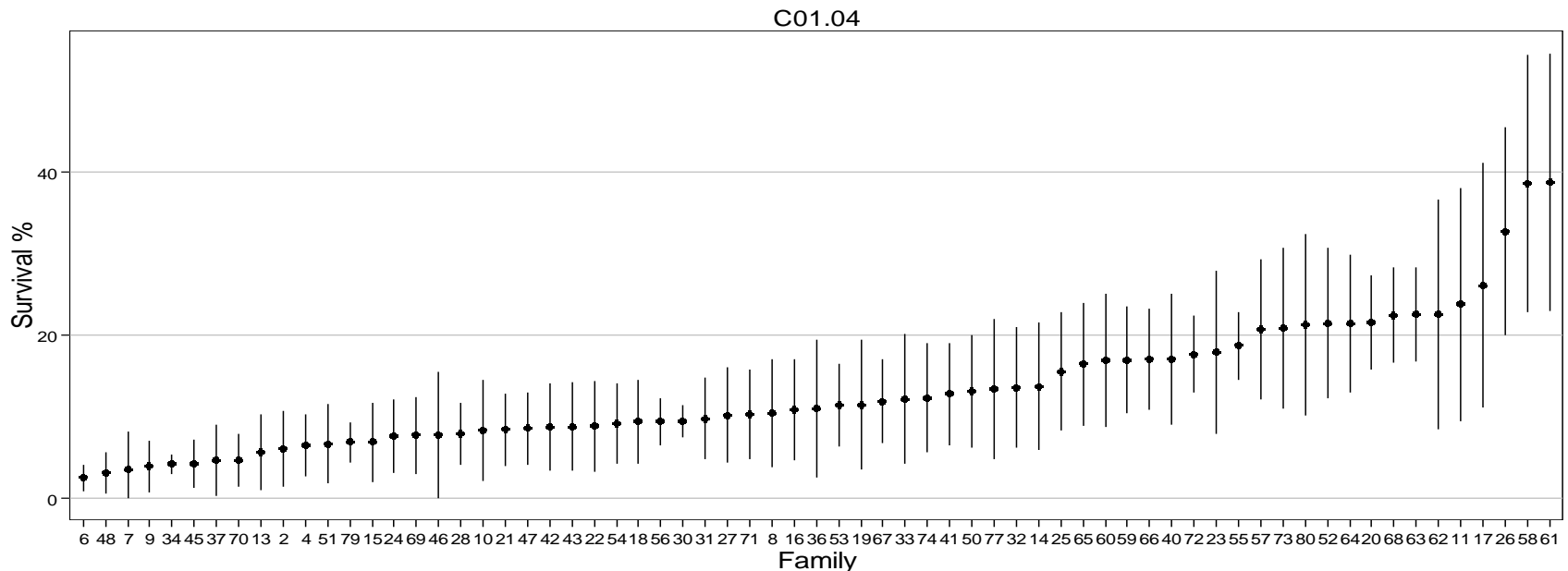
GxE interaction

X

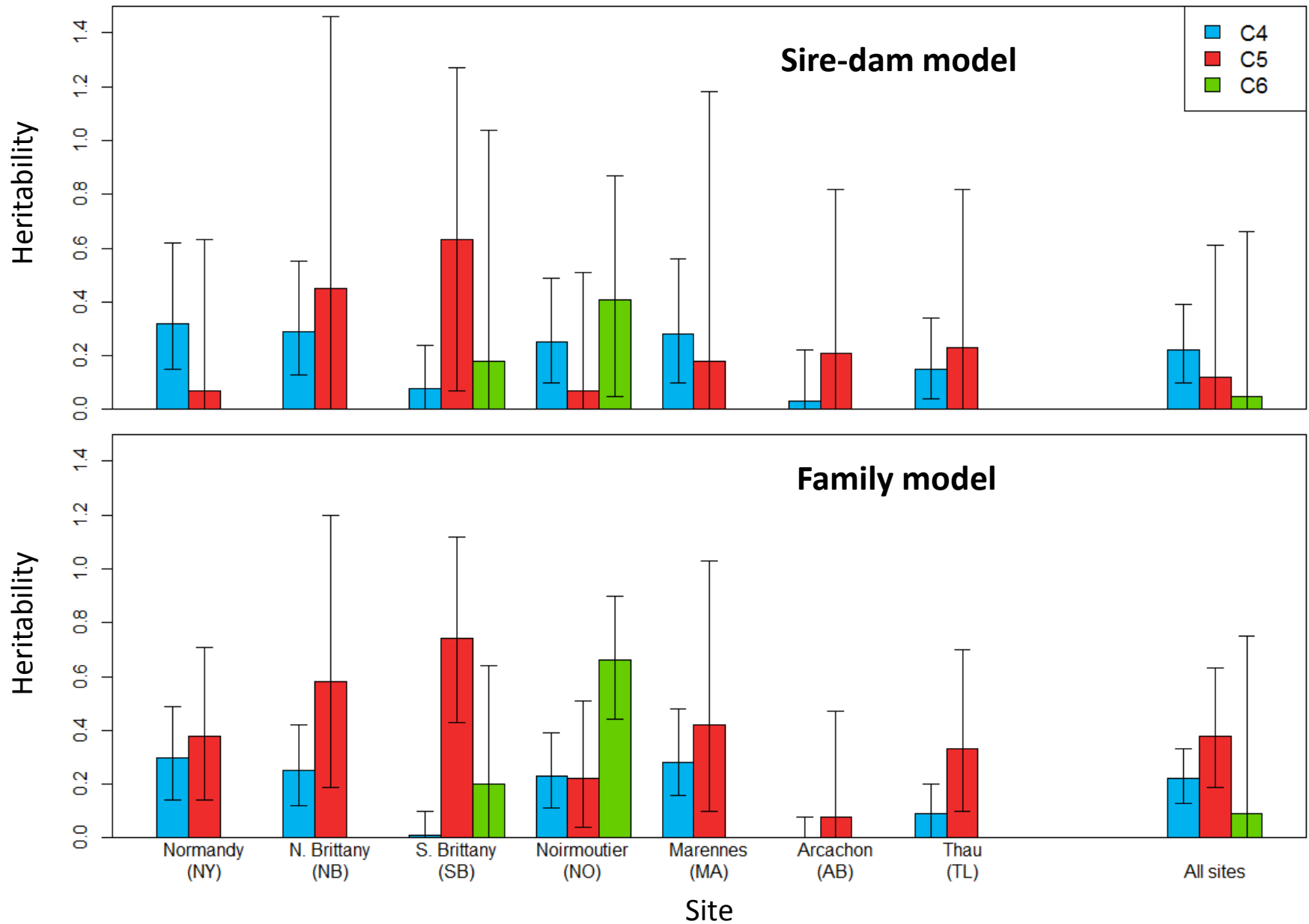
$$\rho_{\text{Site1 ; Site2}} = \frac{\sigma_{\text{Family}}(\text{Site1 ; Site2})}{\sigma_{\text{Family}}(\text{Site1}) \times \sigma_{\text{Family}}(\text{Site2})}$$

Only 3 cohorts successfully produced (170 families)

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

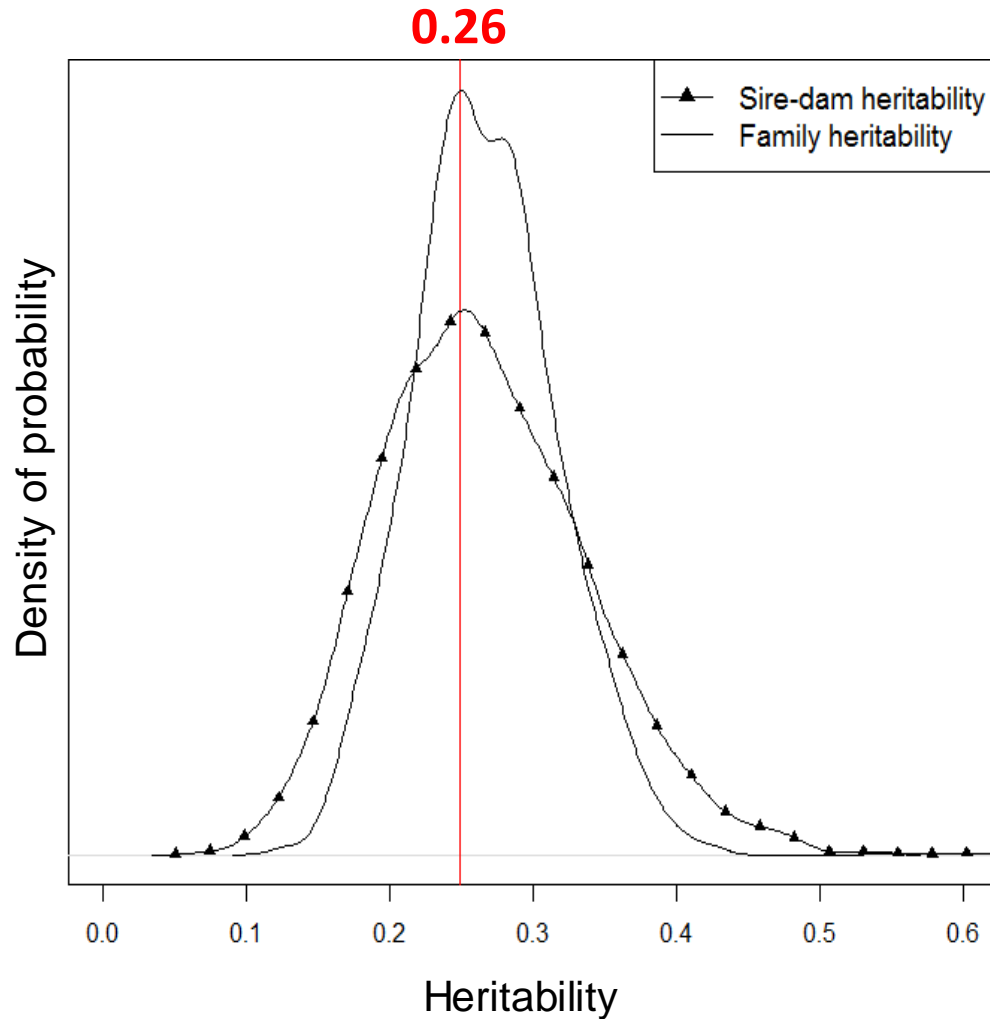


Heritability of survival between sites and cohorts



Heritability of survival with all challenges

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



Genetic correlations between sites

Cohort 4

	AB	MA	NO	SB	NB	NY
TL	0.55	1	0.19	0.25	-0.50	0.90
AB		1	0.99	0.97	0.92	1
NO			0.99	0.98	0.90	1
SB				0.99	0.95	1
NB					0.94	1
NY						0.90

Cohort 5

	AB	MA	NO	SB	NB	NY
TL	0.16	0.66	0.90	0.81	0.91	0.63
AB		0.98	0.36	0.89	0.74	0.86
NO			0.55	0.99	0.87	0.99
SB				0.54	0.91	0.22
NB					0.92	0.95
NY						0.69


Cohort 6

	MA
NO	0.97

- 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 ; $\alpha=0.05$)



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



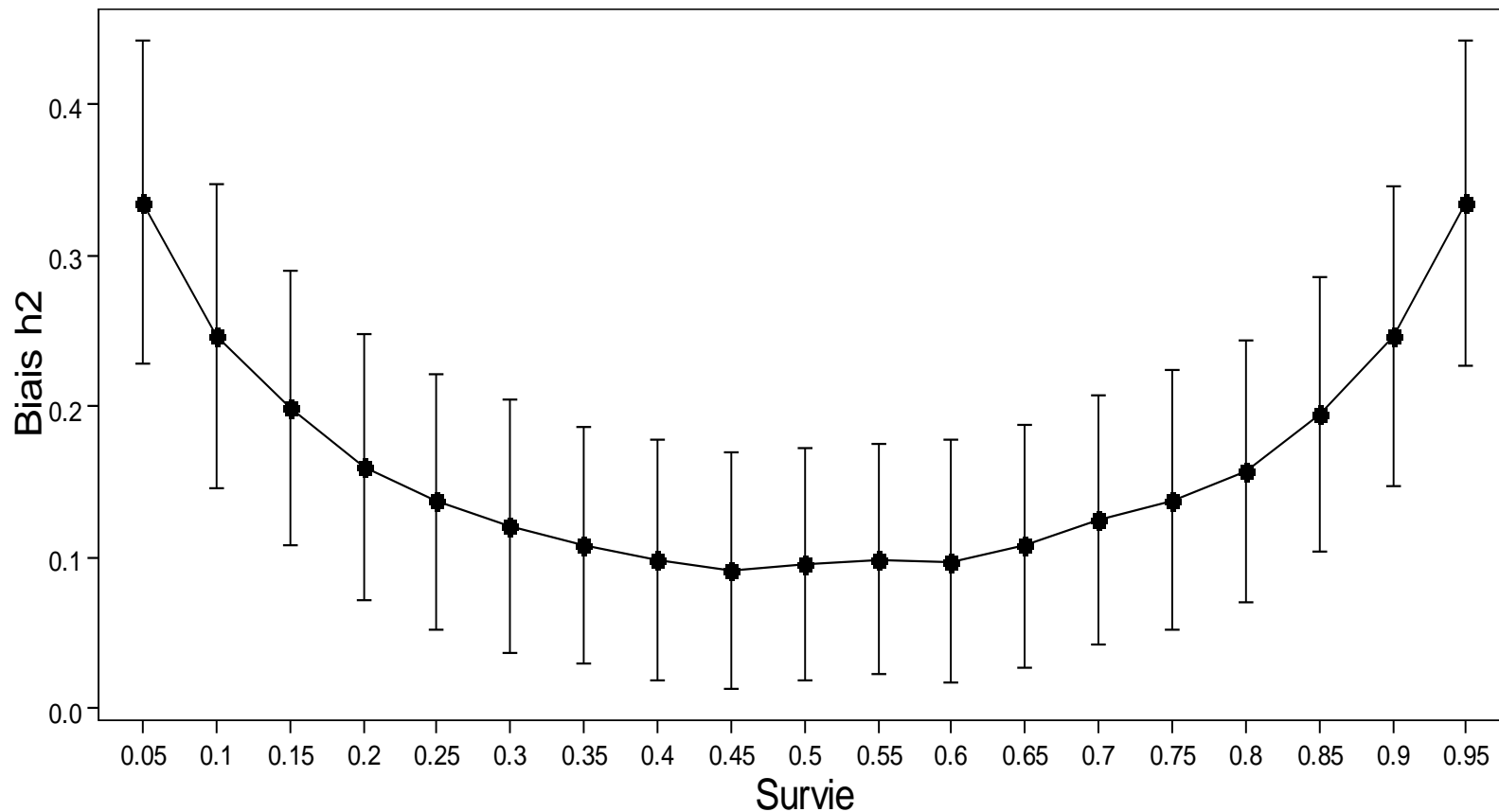


Thank you for your attention

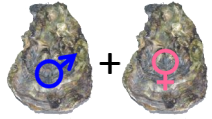


Heritability error according to survival rates

Simulation

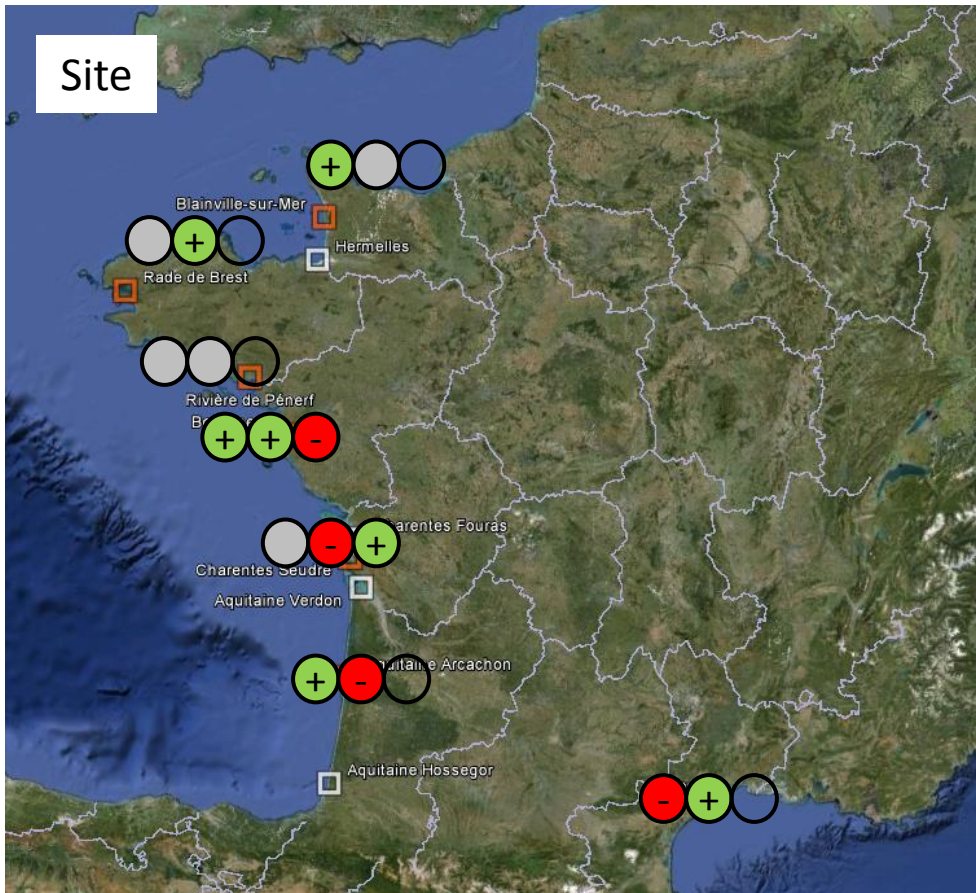


Model Estimation



Sire-dam model : $Y = site + weight + Sire + (Sire * site) + Dam + (Dam * site) + (Sire * Dam) + \varepsilon$

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



Increase individual weight C4 C5 C6
+ + -

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