

Corrigendum to “Genetic parameters for resistance to field mortality outbreaks and resistance to a pathogenic strain of *Vibrio splendidus* in *Mytilus edulis*, *Mytilus galloprovincialis* and natural hybrid” [Aquaculture, Volume 590]

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The authors regret that a few minor errors were found in the methodology and supplementary section of our published article. While these do not impact the fundamental conclusions of our study, they could lead to potential misinterpretations by readers. Below, we provide the necessary corrections.

Abstract

Original version:

The lowest heritability estimates were obtained for NH (0.21) and the highest for *M. galloprovincialis* (0.41), and the genetic correlation between AMM in MB and experimental infection was not significantly different from 0, suggesting that this *Vibrio* strain, is not the major cause of AMM outbreak observed in MB in 2018.

Correction:

The lowest heritability estimates were obtained for NH (0.15) and the highest for *M. galloprovincialis* (0.38), and the genetic correlation between AMM in MB and experimental infection was not significantly different from 0, suggesting that this *Vibrio* strain, is not the major cause of AMM outbreak observed in MB in 2018.

1. Introduction

Original version:

Recently, the bacteria *Francisella haliotidica* was identified in *Mytilus* spp. in Normandy and northern Brittany (France) but the authors didn't give any conclusive report on its role in AMM (Charles et al., 2020c).

Correction:

Recently, the bacteria *Francisella haliotidica* was identified in *Mytilus* spp. in Normandy and northern Brittany (France) but the authors didn't give any conclusive report on its role in AMM (Charles et al., 2020c).

2.1. Biological material

Original version:

In addition, species (*M. edulis*, *M. galloprovincialis*, and hybrid) of each population were confirmed using KASPTM array method, as all parents used to produce the families were sampled and genotyped (Supplementary Fig. S1 and Supplementary Table S1).

Correction:

In addition, species (*M. edulis*, *M. galloprovincialis*, and hybrid) of each population were confirmed using KASP™ array method (Semagn et al., 2014), as all parents used to produce the families were sampled and genotyped (Supplementary Fig. S1 and Supplementary Table S1).

Reference:

Semagn, K., Babu, R., Hearne, S., & Olsen, M. (2014). Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): Overview of the technology and its application in crop improvement. *Molecular Breeding*, 33, 1–14. <https://doi.org/10.1007/s11032-013-9917-x>

Table 1 We regret an incorrect spelling of sites in Table 1. Below are the necessary corrections:

DOI of original article: <https://doi.org/10.1016/j.aquaculture.2024.741034>.

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<https://doi.org/10.1016/j.aquaculture.2025.742456>

Moguéric should be written as Moguéric.

Ile Oléron should be written as Ile d'Oléron.

2.5. Statistical analysis

We regret an incorrect description of variance components in the statistical models. Below are the necessary corrections:

Original version:

σ_{α}^2 is a matrix of additive genetic variance.

Correction:

σ_{α}^2 is the additive genetic variance.

Original version:

σ_{ϵ}^2 is a matrix of the residual variance.

Correction:

σ_{ϵ}^2 is the residual variance.

Original version:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X & 0 \\ 0 & X \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z & 0 \\ 0 & Z \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \quad (\text{Model 3})$$

Equation 3 subscripts are missing for X and Z

Correction:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \quad (\text{Model 3})$$

The subscripts for Eq. 3 changed into X_1 and X_2 , and Z_1 and Z_2 .

The genetic correlation formulae have missed a square root and we have added in the corrected version.

Original version:

$$r_{xy} = \frac{\sigma_{ax,ay}}{\sigma_{ax}^2 \sigma_{ay}^2}$$

Corrected version:

$$r_{xy} = \frac{\sigma_{ax,ay}}{\sqrt{\sigma_{ax}^2 \sigma_{ay}^2}}$$

4.1.3. Genetic correlation between growing sites

Original version:

Genetic correlation between mortality recorded in MB and LF, was low and non significantly different from 0 across all mussel species (0.14), as well as for each species.

Corrected version:

Genetic correlation between mortality recorded in MB and LF, was low and non significantly different from 0 across all mussel species (0.14), as well as for each species.

Supplementary file:

In our original supplementary file, phenotypic correlations were presented for all mussel families combined. However, as significant differences were observed among species, this approach may misrepresent true correlations at the species level. To address this, we have now provided species-specific phenotypic correlations to ensure a more accurate representation of the data.

3.4.2. Genetic correlations

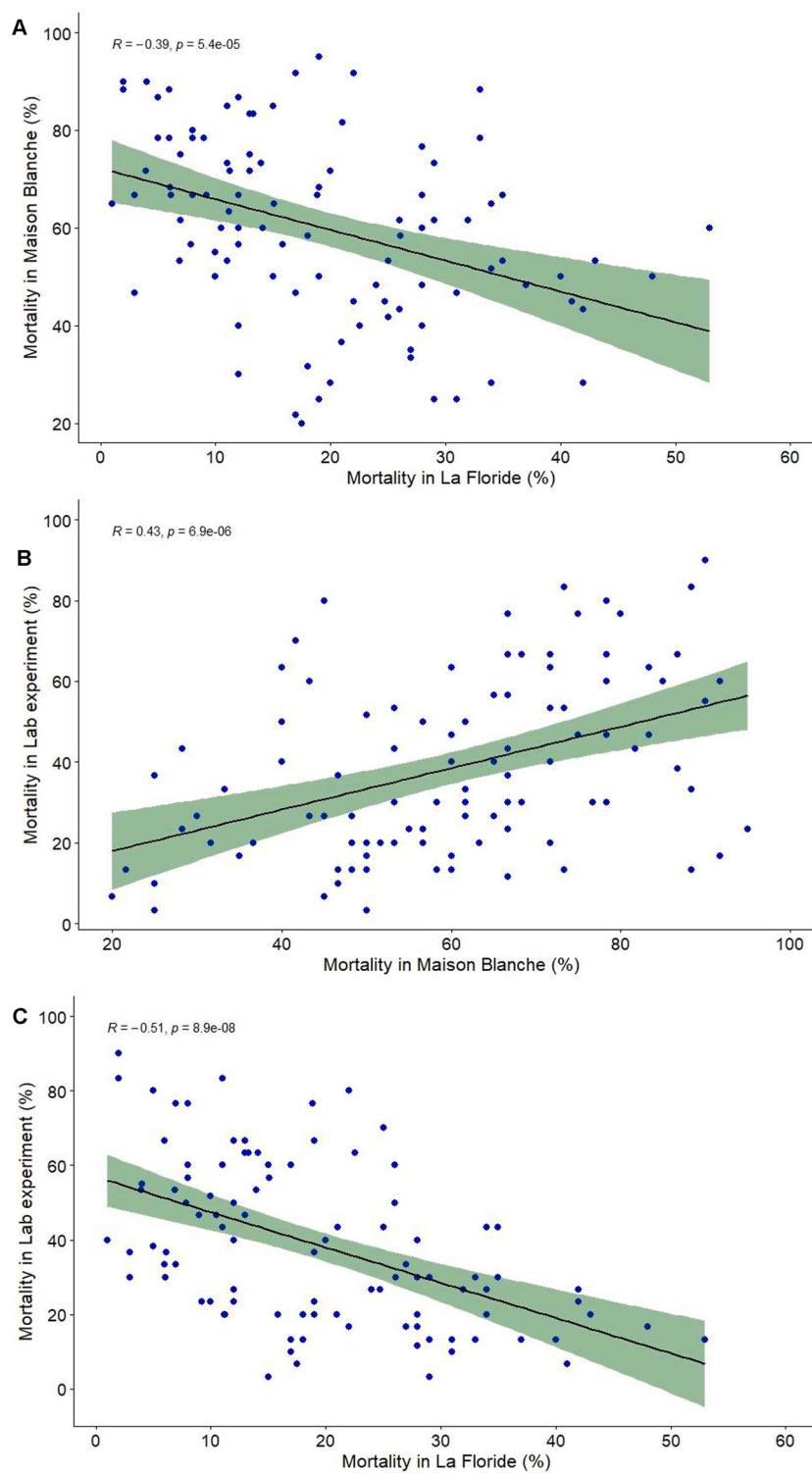
Original version:

The phenotypic correlation between sites and experimental infection across species is illustrated in Supplementary Fig. S4.

Revised version:

The phenotypic correlation between sites and experimental infection among species is illustrated in Supplementary Fig. S4.

Original Figure:

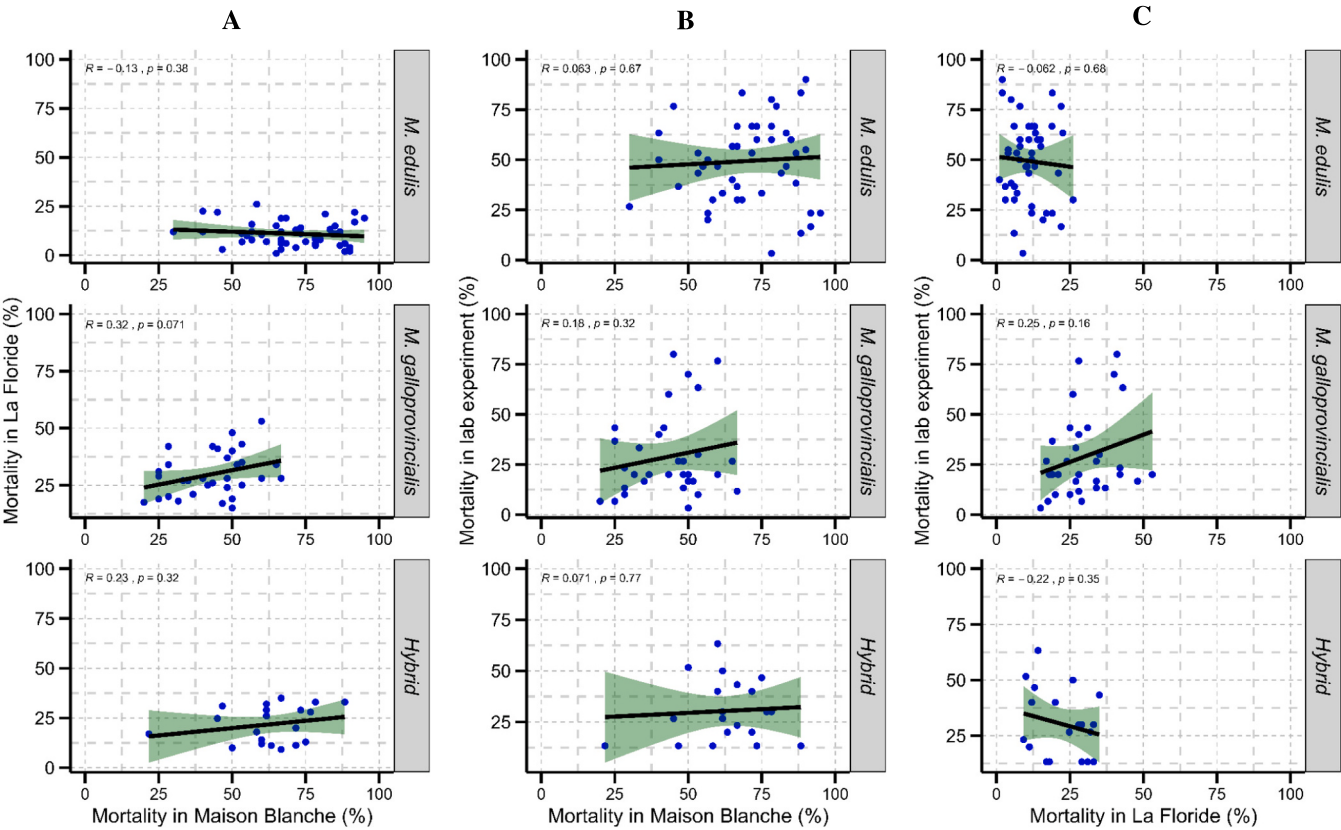


Supplementary Figure S4: Phenotypic correlation for mortality between the testing sites; La Floride vs Maison Blanche (A), Maison Blanche vs experimental infection (B) and La Floride vs experimental

infection (C)

The revised figure is added below:

Supplementary Figure S4: Phenotypic correlations for mortality



across testing sites among species: (A) Maison Blanche vs La Floride, (B) Maison Blanche vs experimental infection, and (C) La Floride vs

experimental infection. The authors would like to apologise for any inconvenience caused.