

Legends of Supplementary Material

Microbiota composition and evenness predict survival rate of oysters confronted to Pacific Oyster Mortality Syndrome

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Legends of supplementary figures

Supplementary Figure 1. Rarefaction analyses of species richness for oyster microbiota. (n=83).

Supplementary Figure 2. Heatmap of bacterial genera that were significantly different between resistant and susceptible oyster families in the controlled condition (hatchery). Only bacterial genera with a frequency above 4% in at least one sample are shown. Frequencies above and below 4% are displayed in red and blue, respectively (n=41).

Supplementary Figure 3. Heatmap of bacterial genera that were significantly different between resistant and susceptible oyster families in the infectious condition (field). Only bacterial genera with a frequency above 4% in at least one sample are shown. Frequencies above and below 4% are displayed in red and blue, respectively (n=39).

Legends of supplementary tables

Supplementary Table 1. Number of sequences and OTUs.

Supplementary Table 2. OTU annotations and abundances in the 83 oyster microbiota.

Supplementary Table 3. Metadata and alpha diversity indices.

Supplementary Table 4. Significant bacterial genera. For *DESeq* columns, *resistant* and *susceptible* indicate if abundances of each bacterial genus were higher in resistant or susceptible oyster families, respectively. NS: not significant. NT: not tested (absent from the dataset).

Supplementary Table 5. Significant bacterial families. For *DESeq* columns, *resistant* and *susceptible* indicate if abundances of each bacterial family were higher in resistant or susceptible oyster families, respectively. NS: not significant. NT: not tested (absent from the dataset).