

# Molecular Analysis of Bacterial Microbiota Associated with Oysters (*Crassostrea gigas* and *Crassostrea corteziensis*) in Different Growth Phases at Two Cultivation Sites

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Microbiota presumably plays an essential role in inhibiting pathogen colonization and in the maintenance of health in oysters, but limited data exist concerning their different growth phases and conditions. We analyzed the bacterial microbiota composition of two commercial oysters:

*Crassostrea gigas* and *Crassostrea corteziensis*. Differences in microbiota were assayed in three growth phases: post-larvae at the hatchery, juvenile, and adult at two grow-out cultivation sites.

Variations in the microbiota were assessed by PCR analysis of the 16S rRNA gene in DNA extracted from depurated oysters. Restriction fragment length polymorphism (RFLP) profiles were studied using Dice's similarity coefficient (Cs) and statistical principal component analysis (PCA).

The microbiota composition was determined by sequencing temperature gradient gel electrophoresis (TGGE) bands. The RFLP analysis of post-larvae revealed homology in the microbiota of both oyster species (Cs > 88 %). Dice and PCA analyses