Genomic characterization of Tenacibaculum maritimum O-antigen gene cluster and development of a multiplex PCR-based serotyping scheme

Pierre Lopez[1], Sébastien Bridel[2], Denis Saulnier[1], Rarahu David[1], Beatriz Magariños[3], Beatriz S. Torres[3], Jean François Bernardet[2], and Eric Duchaud[2]

[1]Institut Louis Malarde
[2]Institut National de Recherche pour l'Agriculture l'Alimentation et l'Environnement Centre Ile-de-France Jouy-en-Josas Antony
[3]Universidade de Santiago de Compostela

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Abstract

Tenacibaculum maritimum is a devastating bacterial pathogen affecting a large variety of marine fish species. It is responsible for significant economic losses in aquaculture farms worldwide. Different typing methods have been proposed to analyze bacterial diversity and population structure. Serological heterogeneity has been observed and up to four different serotypes have been described so far. However, the underlying molecular factors remain unknown. By combining conventional serotyping and genome-wide association study, we identified the genomic loci likely involved in the O-antigen biosynthesis. This finding allowed the development of a robust multiplex PCR-based serotyping scheme able to detect subgroups within each serotype and therefore performs better than conventional serotyping. This scheme was successfully applied to a large number of isolates from worldwide origin and retrieved from a large variety of fish species. No obvious correlations were observed between the mPCR-based serotype and the host species or the geographic origin of the isolates. Strikingly, the distribution of mPCR-based serotypes does not follow the core-genome phylogeny. Nevertheless, this simple and cost-effective mPCR-based serotyping method could be useful for different applications such as population structure analysis, disease surveillance, vaccine formulation and efficacy follow-up.

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