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Screening of a genomic library of
Pseudoalteromonas tunicata for the
identification of genes involved in the
production of bioactive compounds

Candidato

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Abstract

The genus *Pseudoalteromonas* contains numerous marine species which synthesize biologically active molecules. Many *Pseudoalteromonas* species have been demonstrated to produce an array of low and high molecular weight compounds with antimicrobial, anti-fouling, algicidal, neurotoxic and various pharmaceutically relevant activities.

P. tunicata is the most studied species within the genus, live associated with the surfaces of eukaryotic algae and tunicate, and is a known producer of several bioactive compounds with directed activity towards organisms including bacteria, fungi, invertebrate larvae, diatoms, algal spores and protozoa.

The aim of this study is the identification of gene(s) involved in the synthesis of bioactive compounds in the marine bacterium *P. tunicata*.

The nematode *Caenorhabditis elegans* was used in this study as an infections model organism for screening bioactive compounds produced by *P. tunicata*. This was achieved by the development of a genomic library screening allowing for the identification of genes encoding for compounds acting against the model organism *C. elegans*.

Three positive clones with anti-nematode activity were found out: the fosmid DNA was extracted and sequenced, matching with genes of the *P. tunicata* D2 genome, the genes for the anti-nematode activity were found out, a gene encoding for a unknown protein was also found out to be involved in the nematode killing.