

Detection of transposons modifying genome background in probiotics

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The study of probiotic microorganisms is very interesting in the aquaculture field. Administration of live microorganisms in adequate amounts confers some benefits to the host (Kechagia et al. 2013). Even if *Shewanella putrefaciens* include pathogens and saprophytic strains related to fish spoilage and fish infection (Esteve, Merchán, and Alcaide 2016). The Pdp11 strain of *Shewanella putrefaciens* has been proved to provide beneficial effects in *Sparus aurata* (Chabrilón et al. 2005) and *Solea senegalensis* (Rodrigáñez et al. 2008). Studies focused on Pdp11 could shed light on the origin of this probiotic character.

We have designed a bioinformatic workflow to detect transposons in the newly sequenced Pdp11 genome (Tapia-Paniagua et al, in press). Their presence interrupting genes account for a contribution to its probiotic character due to the loss of virulence or the gain of probiotic effect. The workflow was developed in Ruby programming language and provides: the genomic localisation of known transposons, host coding regions disrupted by complete transposons or their repeated insertion sequences, and transposons and coding regions disrupted identifiers, to establish the putative functions of Pdp11 that could be affected by the transposons disruption.

These results would support new possible hypothesis about the Pdp11 probiotic character since 14 coding regions related to *S. putrefaciens* were disrupted by transposons, 4 of which are directly involved in pathogenic mechanisms.

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