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Genomic approach to the search for enzymes for triterpene glycoside transformation

Key words: bacterial genomes, triterpene glycosides, biotransformation

Triterpene glycosides, known as holothurins (or saponins), are the main bioactive metabolites of sea cucumbers (class Holothuroidea) with a wide range of biological activities that allows to consider them as very promising anticancer, antifungal, antiprotozoal and antiviral therapeutic agents [2]. Many holothurins are sulfated or acetylated triterpene glycosides having two parts: aglycone and glycone. Cytotoxic activity could be affected by the side chain position and number of monosaccharide units and sulfate groups [1].

Microbial transformation of holothurins has provided novel low toxicity derivatives with an enhanced bioactivity that are potentially useful for pharmacological studies. Based on the structure of triterpene glycosides, the following classes of bacterial enzymes are of interest for bioconversion: glycoside hydrolases and glycosyltransferases, sulfatases and sulfotransferases, monooxygenases and oxidoreductases.

The genomes of representative marine *Flavobacteriaceae* (*Mesonia*, *Vitellibacter*, *Zobellia*, and *Formosa*) have been analyzed to understand the occurrence and diversity of genes involved in bioconversion/degradation of glycosides. The family members reveal a huge potential for degradation of (poly)saccharides including sulfated ones. We performed in silico search for genes encoding members of GH1, 3, 4, 109, GT1, 4, and GMC oxidoreductase families. The genome survey showed that glycoside hydrolases, particularly beta-glucosidases of GH1 and GH3, and GMC oxidoreductases from *Zobellia*, and *Formosa* might be good candidates to hydrolyze carbohydrate moieties from triterpene glycosides. The gene sequences were subjected to an analysis of their gene duplication/reduction and evolutionary relationships.

Thus, genome analysis revealed a huge potential for glycoside degradation/bioconversion.

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