From the genome to structure and function: treasure hunting in the genome of the heterotrophic marine bacteria Zobellia galactanivorans

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The recent availability of genomic data on heterotrophic marine bacteria emphasizes the crucial role that microbes play in the global carbon cycle. However, the massive presence of proteins of unknown function hampers our understanding of the detailed mechanisms by which this carbon cycle is fine-tuned. Moreover, genome data from marine organisms are essentially annotated at the light of the biochemical knowledge accumulated on bacteria and fungi decomposing terrestrial plants. But marine algal polysaccharides clearly differ from their terrestrial counterparts (Kloareg and Quatrano, 1988) and their associated enzymes usually constitute novel protein families, as described in the Carbohydrate-Active enZyme (CAZy) database (http://www.cazy.org). We actually have applied a knowledge-based strategy for the structural and biochemical characterization of candidate 'hypothetical conserved proteins' to identify new enzyme functions, missing in the metabolic pathways by which marine polysaccharides are degraded in the marine environment. With this aim, our group is developing *Zobellia galactanivorans* as a model marine bacterium for the bioconversion of algal polysaccharides. This marine flavobacterium has been isolated from the red alga *Delesseria sanguinea* (Barbeyron et al., 2001) and extensively studied for its capacity to degrade agars and carrageenans (see for review, Michel et al., 2006). In collaboration with the Max Planck Institute for Marine Microbiology (Bremen, Germany) and the Genoscope (Evry, France), we have recently sequenced the complete genome of *Z. galactanivorans*, confirming that this marine bacterium display a huge potential for the degradation of algal polysaccharides (Barbeyron et al., in preparation). To characterize new glycoside hydrolases in *Zobellia* genome, we have developed different strategies to identify and select relevant target-proteins. Phylogenic approaches can be used to detect new subfamily within polyspecific GH families, as exemplified by the discovery of the first porphyranases in the family GH16 (Hehemann et al., 2010). Another example concerns the complete characterization of a new family of glycoside hydrolases typical of coastal environment, using a combination of comparative genomic approaches, activity screening and crystallographic methods.

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