

Structural studies on cold adaptation of a psychrophilic cellulase

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Pseudoalteromonas haloplanktis is a psychrophilic gram negative bacterium isolated in Antarctica, living on organic remains of algae. It ensures the conversion of cellulose into an immediate nutritive form by biodegrading the biopolymer highly constitutive of algae. To understand the mechanisms of cold adaptation of its enzymatic components, we have studied the structural properties of an endoglucanase, Cel5G, using the complementary methods X-ray crystallography and small angle X-ray scattering. The structure of the catalytic core module of the family 5 endoglucanase, Cel5G has been determined to 1.4 Å resolution in its native form and to 1.6 Å in the cellobiose-bound form. The catalytic module of Cel5G presents the $(\beta/\alpha)_8$ barrel structure typical of the glycoside hydrolase families clan GH-A and the structural comparison of Cel5G with the mesophilic *Erwinia chrysanthemi* Cel5A reveals details leading to higher flexibility and thermolability. Small angle X-ray scattering has been used to analyse the dimensions, shape and conformation of the entire protein and mutants and especially of the linker between the catalytic module and the cellulose binding module. The results show that the linker is highly flexible and unstructured. Loops formed at the base by disulfide bridges, presumably add constraints to enable the most extended conformations. This unusually long and extended structure is a new factor of cold adaptation in the psychrophilic cellulase, allowing steric optimization of substrate accessibility.

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