Crystal structure of a MarR family protein from the psychrophilic bacterium Paenisporosarcina sp. TG-14 in complex with a lipid-like molecule

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MarR family proteins regulate the transcription of multiple antibiotic-resistance genes and are widely found in bacteria and archaea [1, 2]. Recently, a new MarR family gene was identified by genome analysis of the psychrophilic bacterium Paenisporosarcina sp. TG-14, which was isolated from sediment-laden basal ice in Antarctica [3]. In this study, the crystal structure of the MarR protein from Paenisporosarcina sp. TG-14 (Pa MarR) was determined at 1.6 Å resolution. In the crystal structure, a novel lipid-type compound (palmitic acid) was found in a deep cavity, which was assumed to be an effector-binding site (Fig. 1). Comparative structural analysis of homologous MarR family proteins from a mesophile and a hyperthermophile showed that the DNA-binding domain of PaMarR exhibited relatively high mobility, with a disordered region between the β1 and β2 strands [4]. In addition, structural comparison with other homologous complex structures suggests that this structure constitutes a conformer transformed by palmitic acid. Biochemical analysis also demonstrated that PaMarR binds to cognate DNA, where PaMarR is known to recognize two putative binding sites depending on its molar concentration, indicating that PaMarR binds to its cognate DNA in a stoichiometric manner. The present study provides structural information on the cold-adaptive MarR protein with an aliphatic compound as its putative effector, extending the scope of MarR family protein research [5].

![Figure 1. A novel lipid-type effector bound in PaMarR](image-url)

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