Pgp2 is an LD-Carboxypeptidase that Determines the Helical Cell Shape of *Campylobacter jejuni*

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Campylobacter jejuni is a primary cause of bacterial diarrhea worldwide. Helical shape of the bacterium aids in the successful host colonization by *C. jejuni.* Cell shape is maintained by the peptidoglycan (PG) structure in most bacteria, including *C. jejuni*. To achieve a helical morphology, modifications of both PG peptides and the glycan chains are important. Key shape-determining genes of *C. jejuni* have been identified as peptidoglycan peptidases. These enzymes include Pgp1, Pgp2, *cjj81176_1105*, and *cjj81176_1128*. Our goal is to provide a molecular perspective on the process of helical shape formation. Specifically, we study the activity regulation of Pgp2, which is an LD-carboxypeptidase (CPase) that cleaves the terminal D-Ala from the peptide stem of PG. A crystal structure of an N-terminal truncated Pgp2 construct covering residues Gln43 to Gln325 ($Pgp2^{43-325}$) was determined to a resolution of 1.6 Å. The structure consists of an N-terminal helix, an LD-CPase domain a C-terminal NTF2-like domain. InterPro database analysis revealed that the presence of both an LD-CPase domain and NTF2-like domain is unique among the superfamily. A sequence alignment of homologs carrying the same domain structure revealed two dominant patches of conserved residues on the protein surface. The first patch sits on the predicted cysteine CPase active site (His157, Gly158, and Cys176). The second one forms a pocket of charged (Lys307 and Glu324) and hydrophobic residues (Tyr233, Tyr237) in the NTF2-like domain. By using site-directed mutagenesis, peptidase activity analysis and *in vivo* complementation, we demonstrate that the conserved residues from both domains are important for Pgp2 activity regulation in generating helical cell shape.