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Crystallography of YloQ, a GTPase of unknown function essential for *Bacillus subtilis* viability

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1. Introduction

The genome of *Bacillus subtilis* contains around 4100 genes, of which some 270 have either been shown to be or predicted to be essential (Kunst *et al.*, 1997; Kobayashi *et al.*, 2003). Out of this group of genes, 11 have unknown roles in the physiology of the cell. YloQ, a polypeptide of 298 residues, is one such protein. Although it has not been possible to generate strains harbouring deletions in *yloQ*, low-level expression of this gene (together with the downstream genes *yloR* and *yloX*) is associated with morphological changes in which the cells have a more spherical shape (E. Madec & S. J. Séror, unpublished results). YloQ contains motifs characteristic of a GTP-binding site, including the G1 (Walker A), G3 (Walker B) and G4 signature sequences. The order in which these motifs appear in the sequence of YloQ indicates a circular permutation of a classical GTPase, the G1–G3–G4 motifs appearing in the order G4–G1–G3. Another protein that exhibits this permutation is YjeQ from *Escherichia coli*, the function of which is also unknown (Leipe *et al.*, 2002; Daigle *et al.*, 2002). It has been confirmed that YloQ is a GTP-binding protein with a low intrinsic GTPase activity that is abolished by a mutation in the Walker A motif (Cladière *et al.*, in preparation). YloQ, like YjeQ, also possesses a putative zinc-binding site as deduced from the presence of a Cys-X₄-Cys-X-His-X₅-Cys motif towards its C-terminus.

To provide a structural description of this curious GTPase, we have overexpressed, purified and crystallized YloQ from *B. subtilis* and collected preliminary diffraction data from these crystals. It is hoped that combined with biochemical and genetic analyses, the structure of YloQ will define the essential function of this protein and illuminate its contribution to cell physiology.

2. Expression and purification

YloQ was produced as an N-terminally hexahistidine-tagged protein from *E. coli* DH5α harbouring pOMG201, a pBAD plasmid derivative in which expression of the recombinant protein is driven by the arabinose-inducible pBAD promoter. Cells were grown in LB medium supplemented with ampicillin at 310 K to OD₆₀₀ = 1.5. Expression of recombinant His₅-YloQ was induced by the addition of arabinose to a final concentration of 0.05%. Cells were subsequently lysed, the cell extract loaded onto a nickel-chelation column equilibrated with 20 mM imidazole and the Histagged YloQ was eluted with a 20–300 mM imidazole gradient. The wild-type protein, which was >90% pure, was identified by its size and its GTPase activity, whereas the matching peak fraction from cells overexpressing a catalytic site mutation in YloQ was completely inactive (Cladière *et al.*, in preparation).

Column fractions were analysed by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS–PAGE) and those containing YloQ were identified and pooled. The YloQ sample was concentrated by ultrafiltration in an Amicon cell and loaded onto a Superdex S200 (120 ml, Pharmacia) gel-filtration column equilibrated with 30 mM HEPES buffer pH 7.5, 100 mM NaCl. The gel-filtration profiles suggest that YloQ is present as a mixture of monomers and dimers, a conclusion that was confirmed by analytical ultracentrifugation analysis (Cladière *et al.*, in preparation). This two-step purification procedure yielded 65 mg of pure (~97% as judged by SDS–PAGE) His₅-tagged YloQ suitable for crystallization trials from 21 of culture grown in a fermentor. YloQ was concentrated to 15–25 mg ml⁻¹ in 30 mM HEPES pH 7.5, 100 mM NaCl and stored as frozen aliquots at 193 K.
3. Crystallization

Crystallization experiments with His-tagged YloQ were set up at 291 K using the hanging-drop vapour-diffusion method exploiting a variety of screening kits (Brzozowski & Walton, 2001; Jancarik & Kim, 1991). Initial crystals of YloQ appeared from CSS-I condition No. 6 and CSS-II condition No. 6. The conditions were refined by varying the PEG concentrations and sizes until small single crystals (0.2 × 0.2 × 0.1 mm) were obtained from hanging drops consisting of 1 μl of 10–15 mg ml⁻¹ protein and an equal volume of either (a) 0.1 M HEPES pH 7.5, 0.2 M calcium acetate and 10–14% polyethylene glycol 5000 or (b) 0.1 M HEPES pH 7.5, 0.8 M sodium formate and 22% polyethylene glycol 2000 (Fig. 1). These crystals were grown with potted protein containing the monomer and dimer fractions following gel-filteration chromatography. Curiously, attempts to grow crystals from the separate monomer and dimer fractions have so far been unsuccessful. Crystals of YloQ have also been grown in the presence of the non-hydrolysable GTP analogue GTPγS. These crystals grew under the same conditions as those of the native protein; however, they have a different needle-like morphology, perhaps indicating that the nucleotide is bound. As yet these crystals are unsuitable for X-ray analysis.

4. Data collection

A single crystal grown under condition (a) above was transferred into a solution of mother liquor supplemented with 25% glycerol and flash-cooled in liquid N₂. The crystal was exposed to synchrotron radiation on beamline BM14 at the ESRF, Grenoble (λ = 0.9184 Å) and diffraction data were recorded on a MAR three-dimensional CCD detector. A complete three-dimensional data set extending to 2.5 Å spacing was recorded in 360 exposures with a 0.5° oscillation. The exposure time was 25 s and the total data acquisition time was 2.5 h. The data were processed using DENZO, SCALEPACK and TRUNCATE (Otwonowski & Minor, 1999; Collaborative Computational Project, Number 4, 1994). The crystals belong to space group P4₁2₁2₁ with unit-cell parameters a = b = 47.9, c = 274.2 Å, and have a mosaicity of 0.5°. If there is assumed to be a single YloQ protomer in the asymmetric unit, the solvent content is 46.3% and the Matthews coefficient is 2.3 Å³ Da⁻¹. 220,313 observations of 11,898 reflections in the resolution range 25–2.5 Å were measured (286 observations of 83 reflections were rejected during scaling). The mean overall redundancy is 6.1 (5.4); figures in parentheses represent the highest resolution shell (2.59–2.50 Å). The data are 99.9% (99.7%) complete with an overall Rmerge (on intensities) of 0.091 (0.268); the mean I/σ(I) is 12.9 (5.5) and the percentage of reflections for which I/σ(I) > 3 is 85.2 (66.8). A subsequent resolution test suggested that the crystals diffract to 2.2 Å spacing.

5. Discussion

Crystals of YloQ suitable for structure determination have been grown and efforts are currently under way to determine suitable phases for this purpose. Attempts to determine the structure of YloQ by molecular replacement using the coordinates of the Era (Chen et al., 1999) translation factor and GTPase (the two proteins have 37 identical and 63 conserved residues over ~300 residues) as a search model have proved unsuccessful and ab initio phases are sought. We are therefore (i) preparing SeMet-substituted YloQ for crystallization and (ii) screening for conventional derivative.

References


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