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**Regulation of Nitrogen Metabolism in *Bacillus subtilis*: X-ray Crystal Structure of Glutamine Synthetase.**

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In *Bacillus subtilis*, the dodecameric ammonia ligase, glutamine synthetase (GS), catalyzes the reaction of ammonia and glutamate in the presence of ATP to produce glutamine and ADP. The ADP product is further processed into AMP and ATP by adenylate kinase. A second function of GS is to sense nitrogen levels via feedback inhibition primarily by glutamine and AMP. GS from *B. subtilis* is regulated principally at the transcriptional level by two similar MerR-like proteins, GlnR and TnrA. GlnR represses the transcription of *glnA* (GS), urease, and TnrA during excess nitrogen conditions. Conversely, TnrA transcriptionally represses GS during nitrogen poor conditions and activates the *nrg*, *ure*, and *nas* operons, which initiate nitrogen scavenging. However, during nitrogen excess conditions, feedback inhibited GS represses TnrA via a protein/protein interaction. To begin to understand the structural basis of nitrogen metabolism regulation in *B. subtilis*, we have crystallized GS in its apo form along with soaking apo crystals with glutamine and AMP. The protein crystallizes in space group P2<sub>1</sub> with unit cell dimensions of 133.5 Å x 144.5 Å x 174.5 Å and  $\beta = 91.5^\circ$ . Assuming 12 subunits per asymmetric unit (mw = 600 kDa), the Matthews coefficient is 2.8 Å<sup>3</sup> Da<sup>-1</sup> with a solvent content of 55.7%. Intensity data have been collected (100°K) to 2.62 Å at ALS (8.2.1) for the apo form ( $I/\sigma I = 2.0$ ,  $R_{\text{sym}} = 0.077$ ) and to 2.55 Å at SSRL (BL-9.1) for glutamine/AMP soaked form ( $I/\sigma I = 2.3$ ,  $R_{\text{sym}} = 0.050$ ) crystals. Structure determination of both forms of GS by molecular replacement (employing EPMR) is underway utilizing a dodecamer of the *Mycobacterium tuberculosis* GS (38% identity) as a search model. These structures will begin to provide insight into the structural mechanisms by which TnrA and GS regulate each other.