Crystal Structure of a Glu-tRNA^{Gln} Amidotransferase at 2.7Å

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Aminoacyl-tRNA plays an important role in protein biosynthesis. The aminoacylation of tRNA is performed with 20 amino acids and the corresponding aminoacyl-tRNA synthetases (aaRSs), and aaRSs catalyze the formation of 20 aminoacyl-tRNAs in a direct amino-acylation pathway in most organisms. However, an indirect pathway is present in organisms that lack Gln-tRNA synthetase. To synthesis Gln-tRNA^{Gln} in the organisms, non-discriminating Glu-tRNA synthetase charges glutamic acid on both tRNA^{Glu} and tRNA^{Gln}, and then the mischaged Glu-tRNA^{Gln} is transamidated to Gln-tRNA^{Gln} by Glu-tRNA^{Gln} amidotransferase (Glu-AdT).[1]

Glu-AdT forms a heterotrimer composed of A, B, and C subunit (encoded by the *gatCAB* operon) in some of eubacteria and eukaryotic organelles, while archaea has a heterodimeric Glu-AdT composed of D and E subunit (encoded by the *gatD* and *gatE* genes)[2]. The detailed mechanism of the enzymes has not been clear yet, because the three-dimensional structures of the enzymes is still unknown.

We have determined the crystal structure of GatCAB complex from Gram-positive eubacteria at 2.7 Å resolution, and will discuss the moleculer mechanism of this enzymatic reaction.

[1] Alan W. *et al.*, *Proc. Natl. Acad. Sci USA*, 1997, **94**, 11819. [2] Tumbula D.L. *et al*., *Nature*, 2000, **407**, 106.

Keywords: tRNA, aminoacyl tRNA synthetase, amidotransferase