s8a.m3.o5 **tRNA^{Arg} recognition by yeast Arginyl-tRNA synthetase: crystal structure of the yeast arginyl-tRNA synthetase–yeast tRNA^{Arg} complex at 2.2 Å.** B. Delagoutte, D. Moras and J. Cavarelli. *UPR 9004 Biologie et Génomique Structurale, Institut de Génétique et de Biologie Moléculaire et Cellulaire, CNRS/INSERM/ULP, BP 163, 67404 Illkirch Cedex, France. Correspondence e-mail: cava@igbmc.u-strasbg.fr*

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Aminoacyl-tRNA synthetases (aaRS) are a family of enzymes essential for gene expression. Extensive progress in understanding the structure-function relationship of this heterogenous family of RNA-binding proteins has been made during the last decade. Aminoacyl-tRNA synthetases now constitute the best text-book example of multi-domain proteins including insertion and terminal functional modules appended to one of the two class-specific active site. However, each new structure of aaRS, either in the free state or engaged in complexes with the other partners of the aminoacylation reaction, leads to unexpected results, which always refine our comprehension of the structure-function relationships and molecular recognition principles. Moreover, complete sequencing of several archaeal genomes led to the discovery of novel pathways and enzymes for the synthesis of several aminoacyl-tRNAs. Phylogenetic analysis of the 20 aaRSs also revealed a complex evolutionary. In this context, structures are essential to gain structural insights from sequences block alignments and therefore to decipher the relationships among function, evolution and sequences. The structures of nearly all class-II aaRSs and several class-I aaRSs have been determined by X-ray crystallography either in the free state or engaged in complexes with the small substrates of the aminoacylation reaction (ATP, amino acid, Mg^{2+} ions). However, for class-I aaRS, our present understanding of the second step of the aminoacylation reaction, which implies specific tRNA recognition, is essentially based on two crystal structures (GlnRS and IleRS).

We will present the crystal structure of two complexes involving Arginyl-tRNA synthetase from yeast *Saccharomyces cerevisae* (yArgRS) and the yeast second major tRNA^{Arg} (tRNA^{ArgICG}) isoacceptor.

Crystal form I containing yArgRS, tRNA^{Arg} and L-arginine (L-Arg) has been solved at 2.2Å resolution and refined to a crystallographic R-factor of 19.0% (R-free 23.3%). This crystal form presents the highest resolution obtained for an active form of an aaRS-tRNA complex. The crystal structure of yArgRS with (L-Arg) bound to the active site has already been described. Crystal form II, a binary complex containing yArgRS and tRNA^{Arg}, has been solved at 2.9Å resolution and refined to a crystallographic R-factor of 19.3% (R-free 24.0%). Therefore, one can now visualize at the atomic level the molecular features involved in specific tRNA^{Arg} recognition and the conformational changes which occur upon substrates binding. A complete description of the structures will be presented highlighting novel molecular mechanisms involved in specific RNA recognition by proteins.

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