machinery of all known types of archaeal disrupted tRNAs. Possible evolutionary scenarios of tRNA gene (6) and possible translocations of the archaeal tRNA introns during their evolution will be discussed.

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Disrupted tRNA gene diversity and possible evolutionary scenarios

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Recently, various types of unusual tRNAs have been discovered in the genomes of Archaea and primitive Eukaryotes; multiple-intron-containing tRNAs that possess more than one introns; split tRNAs that are produced from two pieces of RNAs transcribed from separate genes; tri-split tRNAs that are produced from three separate genes; and permuted tRNA in which its 5' and 3' halves are encoded within a permuted orientation in a single gene. All these disrupted tRNAs can form mature contiguous tRNA and be aminoacylated after processing via cis- or trans-splicing. The discovery of such tRNA disruptions has raised a question of when—and why—these complex tRNA processing pathways have emerged though the evolution of life. Many previous reports have noted that tRNA genes contain a single intron at the anticodon loop region, a

feature which is common throughout all three domains of life, suggesting an ancient trait of the Last Universal Common Ancestor (LUCA). In this context, these unique tRNA disruptions recently found only in Archaea and primitive Eukaryotes provide a new insight into the origin and evolution of tRNA genes, encouraging further investigation in this research field. Here we summarize the phylogeny, structure and processing machinery of all known types of disrupted tRNAs and discuss possible evolutionary scenarios of tRNA gene.

Oct. 17 (Sat.) 10:40-11:20

Structure of the bacterial flagellum and its evolutionary relation to other biological molecular machines

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Gram-negative bacteria swim by rotating helical filamentous organelle called the flagellum. The flagellum rotates at a speed of 200 to 300 Hz driven by a reversible rotary motor embedded in the cell membrane at the base of the filament. The motor utilizes electrochemical potential gradient of proton across the cytoplasmic membrane for rotation. The flagellum is a huge molecular assembly made of 20 to 30 thousands of subunits of about 30 different proteins. The structural components can be divided into two classes, the basal body rings and the tubular axial structure. The basal body rings form the rotary motor with the stator complex composed of cytoplasmic membrane proteins. The torque is generated by the rotor-stator interactions coupled with proton flow through the channel formed within the stator. Since the axial structure of the flagellum extends from the cytoplasmic membrane, its component proteins must be exported from the cytoplasm. The protein subunits are translocate d into the central channel of the growing flagellum by the flagellar type III protein export apparatus, and then travel through the channel to the growing end for their self-assembly.

Structural and genetic studies have demonstrated that the flagellar system resembles to the bacterial injectisome, which is a molecular machine to inject virulence proteins directly into host cells for their infection. Moreover, our recent structural studies revealed that an outstanding similarity between the flagellar export apparatus and F0F1-ATP synthase. In my talk, I will present an overview of current understanding of the structure and function of the bacterial flagellum, and discuss the evolutionary relation between the flagellum and other biological macromolecular assemblies.