



EvoLunch

Evolution of the secondary replicons in bacterial genomes

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Genomes of bacteria had been thought to consist of a single chromosome, possibly including some smaller, nonessential, circular plasmids. However, multi-chromosomal genome organization was recently observed in many plant symbionts and plant, animal, and human pathogens. In these genomes the gene distribution among the chromosomes is not random showing that, multipartite structure of genomes is shaped by selection forces. A majority of genes necessary for the basic life processes are usually located on the primary (and the largest) chromosome. Other chromosomes are smaller and mainly composed of genes with functions associated with adaptation to specific, diverse niches. We reconstructed the evolutionary history of the genes forming the pan-genome of genus *Vibrio* including gene gains, losses, and intra-genome translocations. We demonstrate that the secondary replicon of *Vibrio* evolved from a plasmid by acquiring essential genes from the primary chromosome. We also demonstrate that the secondary replicon faster accumulates horizontally transferred genes. These results allow us to formulate the adaptive advantage of multi-partite genome structure.

Wednesday, October 23, 2019 12:30pm - 01:30pm

IST Austria Campus I22 Lakeside View (I22.01)



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