The Ribosomal Protein Cluster Organization In Asgard Archaea – An Analysis

Madhan R. Tirumalai^{1,1}, George E. Fox^{1,1}, Raghavan V. Sivaraman Jr^{2,3}, Layla A. Kutty^{4,5}, and Eric L. Song^{4,4}

¹University of Houston ²Harvard Medical School, Wyss Institute Boston MA, USA ³Harvard Medical School ⁴University of Texas at Austin, Austin, TX, USA ⁵University of Texas at Austin

November 30, 2022

Abstract

Introduction: It has been proposed that the recently discovered superphylum of Asgard archaea may represent a historical link/bridge between the Archaea and Eukarya. The arrangement of genes in genomes is a window to understand how organisms are related. In particular, the translation machinery and the genes that encode the same have a long evolutionary history. In order to gain further insight into the evolutionary position of the Asgard archaea, the genome order of ribosomal protein coding genes was analyzed. The Asgard archaea were compared with non-Asgard archaeal and bacterial genomes. Results: A core of co-occurring 15 genes belonging to the segment of the S10 and spc cluster (which are characterized and established as operons in Bacteria), was identified as conserved in gene order, arrangement and genome location in Asgard archaea, non-Asgard archaea and Bacteria. This core occurs as a complete set in the genomes of Lokiarchaeota MK-D1 (Candidatus Prometheoarchaeum syntrophicum), and Candidatus Odinarchaeota archaeon LCB_4. The genome assemblies of the other Asgard genomes are incomplete and occur in multiple contigs (>50) and hence this cluster is found in sections across contigs, with a section often either ending or beginning a contig. The cluster organization is indicative of co-occurrence, if the genome was complete. A second smaller cluster comprising the homologs of the most conserved genes of the bacterial S10 operon/cluster namely, uS10uL3-uL4-uL23-uL2 occurs independently on the Asgard genomes, separate from the rest, a feature shared by many non-Asgard archaea as well. Other clusters. A new cluster L7ae-infB was identified to co-occur with the minor S24e-S27ae cluster in the two complete Asgard genomes. The L7ae-infB cluster co-occurs with the S24e-S27ae cluster in some (non-Asgard) Crenarchaeota (Desulfurococcacea) and Euryarchaeota (Methanobacteriaceae), while it co-occurs with the (Alpha operon) L18e cluster in some (non-Asgard) Euryarchaeota (Halobacteriaceae). Overall, the organization of the most universal and highly conserved S10 and spc cluster in Asgard archaea resembles that of the non-Asgard Thaumarchaeota and the DPANN group. References: Wang J et al (2009) Archaea, 2(4), 241–251. Da Cunha V et al (2017) Plos Genetics 13(6), e1006810. Bowman J. C. et al. (2020) Chem Rev, 120(11), 4848-4878.

The Ribosomal Protein Cluster Organization In Asgard Archaea - An Analysis

Madhan R. Tirumalai¹, Raghavan V. Sivaraman Jr², Layla A. Kutty³, Eric L. Song³ and George E. Fox^{1*},

¹Biology and Biochemistry, University of Houston, Houston, TX 77204-6934, USA

² Harvard Medical School, Wyss Institute Boston MA, USA

³ University of Texas at Austin, Austin, TX, USA

*For correspondence: *fox@uh.edu*.

Introduction: It has been proposed that the recently discovered superphylum of *Asgard* archaea may represent a historical link/bridge between the *Archaea* and *Eukarya*. The arrangement of genes in genomes is a window to understand how organisms are related. In particular, the translation machinery and the genes that encode the same have a long evolutionary history. In order to gain further insight into the evolutionary position of the *Asgard* archaea, the genome order of ribosomal protein coding genes was analyzed. The *Asgard* archaea were compared with non-*Asgard* archaeal and bacterial genomes.

Results: A core of co-occurring 15 genes belonging to the segment of the *S10* and *spc* cluster (which are characterized and established as operons in *Bacteria*), was identified as conserved in gene order, arrangement and genome location in *Asgard archaea*, non-*Asgard archaea* and *Bacteria*. This core occurs as a complete set in the genomes of *Lokiarchaeota* MK-D1 (Candidatus *Prometheoarchaeum syntrophicum*), and Candidatus *Odinarchaeota* archaeon LCB_4. The genome assemblies of the other *Asgard* genomes are incomplete and occur in multiple contigs (>50) and hence this cluster is found in sections across contigs, with a section often either ending or beginning a contig. The cluster organization is indicative of co-occurrence, if the genome was complete. A second smaller cluster comprising the homologs of the most conserved genes of the bacterial *S10* operon/cluster namely, *uS10-uL3-uL4uL23-uL2* occurs independently on the *Asgard* genomes, separate from the rest, a feature shared by many non-*Asgard* archaea as well.

Other clusters. A new cluster L7ae-infB was identified to co-occur with the minor S24e-S27ae cluster in the two complete Asgard genomes. The L7ae-infB cluster co-occurs with the S24e-S27ae cluster in some (non-Asgard) Crenarchaeota (Desulfurococcacea) and Euryarchaeota (Methanobacteriaceae), while it co-occurs with the (Alpha operon) L18e cluster in some (non-Asgard) Euryarchaeota (Halobacteriaceae).

Overall, the organization of the most universal and highly conserved *S10* and *spc* cluster in *Asgard* archaea resembles that of the non-*Asgard Thaumarchaeota* and the *DPANN* group.

References:

Wang J et al (2009) Archaea, 2(4), 241–251.

- Da Cunha V et al (2017) Plos Genetics 13(6), e1006810.
- Bowman J. C. et al. (2020) *Chem Rev*, 120(11), 4848-4878.