Editorial

Evolutionary Mechanisms of Microbial Genomes

Hiromi Nishida,¹ Shinji Kondo,² Hideaki Nojiri,³ Ken-ichi Noma,⁴ and Kenro Oshima⁵

¹ Agricultural Bioinformatics Research Unit, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo 113-8657, Japan

² Laboratory for Cellular Systems Modeling, RIKEN Research Center for Allergy and Immunology, Kanagawa 230-0045, Japan

³ Laboratory of Environmental Biochemistry, Biotechnology Research Center, The University of Tokyo, Tokyo 113-8657, Japan

⁴ Gene Expression and Regulation Program, The Wistar Institute, Philadelphia, PA 19104, USA

⁵ Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo 113-8657, Japan

Correspondence should be addressed to Hiromi Nishida, hnishida@iu.a.u-tokyo.ac.jp

Received 3 April 2011; Accepted 3 April 2011

Copyright © 2011 Hiromi Nishida et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Sequencing of more than 1,600 microbial genomes has been complete, and rigorous studies are underway to reveal the mechanisms of evolution which gave rise to the great variety in combination of gene functions encoded on these genomes. Although comparative genomics based on orthologous genes has elucidated a great deal of the phylogenetic relationship among the sequenced genomes, the mechanisms which have shaped the current states of the microbial genomes remain elusive. Particularly, the contribution of external forces such as horizontal gene transfer and pressure from environmental factors to genome evolution has yet to be investigated. This special issue presents six, three, and two papers related, respectively, to bacterial, fungal, and viral evolutionary mechanisms.

Among the six papers regarding bacterial evolution, H. Nishida and C. -S. Yun in “*Phylogenetic and guanine-cytosine content analysis of *Symbiobacterium thermophilum* genes*” reported a mechanism of the *Symbiobacterium* genome which increased GC content of horizontally transferred genes and thereby maintained the genome with high GC content. K. Oshima et al. in “*Unique evolution of *Symbiobacterium thermophilum* suggested from gene content and orthologous protein sequence comparisons*” performed phylogenetic analyses of more than 50 *Clostridia* by comparing gene content and orthologous protein sequence and demonstrated that these two phylogenetic relationships are topologically different, strongly suggesting that each *Clostridia* has a species-specific gene content likely due to frequent genetic exchanges or gene losses which have occurred during evolution.

H. -Y. Dou et al. in “*Prevalence of *Mycobacterium tuberculosis* in Taiwan: a model for strain evolution linked to population migration*” presented an association study of distinct *Mycobacterium tuberculosis* strains prevalent in Taiwan with historical migrations of different ethnic populations based on a comparison of the tandem repeat sequences as genetic markers. T. Takeda et al. in “*Distribution of genes encoding nucleoid-associated protein homologs in plasmids*” reported biases associated with certain bacterial plasmids, that is, increase of nucleoid-associated protein genes in large bacterial plasmids and low GC content of plasmids encoding (histone-like nucleoid structuring protein) H-NS. V. Pérez-Brocal et al. in “*New insights on the evolutionary history of aphids and their primary endosymbiont *Buchnera aphidicola**” presented a study which supports the hypotheses of divergence of *Buchnera aphidicola* from their host lineages during an early Cretaceous period by demonstrating a closer relationship of a subfamily Eriosomatinae with Lachninae than with Aphidinae. A. Moreno-Letelier et al. in “*Parallel evolution and horizontal gene transfer of the *pst* operon in Firmicutes from oligotrophic environments*” demonstrated that the phosphate transport system gene operon of Firmicutes has two highly divergent clades which do not correlate either with the type of habitat or with a phylogenetic congruence and proposed parallel evolution of this gene after horizontal gene transfer events.

Of the three papers dealing with fungal evolution, R. T. Morris and G. Drouin in “*Ectopic gene conversions in the genome of ten hemiascomycete yeast species*” found that

ectopic gene conversions in the genome of ten hemiascomycetes tend to occur more frequently between closely linked genes and proposed that the mechanisms responsible for the loss of introns in *Saccharomyces cerevisiae* were also involved in the 3'-end gene conversion bias observed among the paralogs. E. van Zijl de Jong et al. in "Sequence analysis of SSR-flanking regions identifies genome affinities between pasture grass fungal endophyte taxa" demonstrated that some asexual *Neotyphodium* species arose following interspecies hybridization between sexual *Epichloe* ancestors and characterized *Neotyphodium* isolates based on sequence analysis of genomic regions flanking simple sequence repeats. N. Khaldi and K. H. Wolfe in "Evolutionary origins of the fumonisin secondary metabolite gene cluster in *Fusarium verticillioides* and *Aspergillus niger*" compared the fumonisin secondary metabolite gene cluster and proposed that the gene cluster was horizontally transferred to *Aspergillus niger* from a Sordariomycete.

As for the two papers of viral evolution, K. Tang and X. Wu in "Computational analysis suggests that *Lyssavirus* glycoprotein gene plays a minor role in viral adaptation" found no significant evidence of positive selection on any site of the *Lyssavirus* glycoprotein-coding gene (except for AY987478) and proposed that the glycoprotein gene has been under purifying selection and that the evolution of this gene may not play a significant role in *Lyssavirus* adaptation. S. A. B. Miele et al. in "*Baculovirus: molecular insights on their diversity and conservation*" reported an evidence which supports the current division of the *Baculoviridae* into four genera, *Alpha*-, *Beta*-, *Gamma*-, and *Deltabaculovirus* based on comparative studies of 57 genome sequences from baculoviruses.

In closing this introduction to the special issue, we would like to express our full appreciation to all the authors and reviewers for their enormous efforts that have made the timely completion of our assignment successful. We sincerely hope that this special issue will stimulate further the investigation of evolutionary mechanisms of microbial genomes.

Hiromi Nishida
Shinji Kondo
Hideaki Nojiri
Ken-ichi Noma
Kenro Oshima