Final Project Report

Title: Lateral Gene Transfer and the History of Bacterial Genomes
Project ID: 0007062
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A. Specific Aims

The aims of this research were to elucidate the role and extent of lateral transfer in the differentiation of bacterial strains and species, and to assess the impact of gene transfer on the evolution of bacterial genomes. The ultimate goal of the project is to examine the dynamics of a core set of protein-coding genes (*i.e.*, those that are distributed universally among Bacteria) by developing conserved primers that would allow their amplification and sequencing in *any* bacterial taxa. In addition, we adopted a bioinformatic approach to elucidate the extent of lateral gene transfer in sequenced genome.

B. Summary Narrative

Over the funded period, we completed virtually all of our original aims and goals as well as understanding several bioinformatic analyses on newly available microbial genomes. In short, we: (1) assessed the degree of lateral gene transfer affecting the full set of orthologs present in completely sequenced bacterial genomes; (2) investigated the rates of transfer among genes having sporadic distributions among sequenced genomes; (3) elucidated the origins of new genes in bacterial genomes; (4) analyzed previously published claims of large-scale lateral gene transfer among divergent bacterial lineages; (5) developed universally conserved primers pairs for obtaining sequence information from virtually any bacterial genome; (6) developed resources, available at the RDP website, for analyzing these universally distributed sequences, (7) appraised the amount of genetic variation and the phylogenetic relationships among strains within several bacterial species from diverse sources worldwide, and (8) assessed the diversity of environmental samples with conserved protein sequences and compared this to the 16S rDNA diversity within the same samples.

C. Publications

The following manuscripts stemmed from this support since the previous progress report. I have included electronic copies of those already published as attachments. There still two more manuscripts that will be submitted within a couple of months.

- Lerat, E., V. Daubin, H. Ochman and N.A. Moran (2005) Evolutionary origins of genomic repertoires in bacteria. *PLoS Biology* 3: 807-814.
- Ochman, H., E. Lerat, E. and V. Daubin (2005) Examining bacterial species under the specter of gene transfer and exchange. *Proc. Natl. Acad. Sci. USA* 102: 6595-6569.
- Wirth, T., Falush, D., Lan, R., Colles, F., Mensa, P., Wieler, L.H., Karch, H., Reeves, P., Maiden, M.C.J., Ochman, H. and M. Achtman (2005) Sex and virulence in *Escherichia coli*: an evolutionary perspective. *PLoS Genetics*, submitted

- Daubin, V. and H. Ochman (2004) Bacterial genomes as new gene homes: The genealogy of ORFans in *E. coli*. *Genome Research* 14: 1036-1042.
- Daubin, V. and H. Ochman (2004) Recognizing lateral gene transfer by quartet mapping. *Molec. Biol. Evol.* 21: 48-51.
- Daubin, V. and H. Ochman (2004) Start-up entities in the evolution of new genes. *Curr. Opin. Genet. Devel.* 14: 616-619.
- Santos, S.R. and H. Ochman (2004) Identification and phylogenetic sorting of bacterial lineages using universally conserved genes and proteins. *Environ. Microbiol.* 6: 754-759.
- Daubin, V., N.A. Moran, and H. Ochman (2003) Phylogenetics and the cohesion of bacterial genomes. *Science* 301: 829-832.

Also note that there has been no project-generated resource or inventions and patents stemming from support over the project period.