Module 3 Microbial Species Concepts

Evidence worksheet\_05 “Extensive mosaic structure”

Part 1: **Learning objectives:**

* Evaluate the concept of microbial species based on environmental surveys and cultivation studies.
* Explain the relationship between microdiversity, genomic diversity and metabolic potential
* Comment on the forces mediating divergence and cohesion in natural microbial communities

**General Questions:**

• *What were the main questions being asked?*

How different are these 3 genomes beyond their 16S sequences?

• *What were the primary methodological approaches used?*

Random clones sequenced with dye terminator chemistry (Automated Sanger) on 3700 machines. Assembled with SEQMANII (CFT073 strain)

Annotated online in a multiuser interface – MAGPIE

Predicted proteins, based on ORF, were searched on BLAST.

7 coverage

• *Summarize the main results or findings.*

Similar backbone (VGT) in all 3 strains but have many gene islands that are different in each strain. These islands were acquired by horizontal gene transfer.

CFT073 doesn’t have type III secretion system or phage/plasmid encoded virulence genes that are common in O157:H7

All three strains have a pilus gene similar to salmonella enterica but amino acid sequence identity is only 53-81%. This means that there are probably different selective pressures on different strains.

• *Do new questions arise from the results?*

Do other microbial species have this large of a variance in gene presence between strains?

Is this variance more common in pathogenic strains?

Is 16S a reasonable way to classify microbial species, if 3 strains that match to the same species based on 16S, only share 39% of their genes.

• *Were there any specific challenges or advantages in understanding the paper (e.g. did the authors provide sufficient background information to understand experimental logic, were methods explained adequately, were any specific assumptions made, were conclusions justified based on the evidence, were the figures or tables useful and easy to understand)?*

The techniques for data processing were not very clear. Combined with a very brief introduction it made it difficult to follow the connections they were making between their new sequence data and outside sources.

Part 2: **Learning objectives:**

* Comment on the creative tension between gene loss, duplication and acquisition as it relates to microbial genome evolution
* Identify common molecular signatures used to infer genomic identity and cohesion
* Differentiate between mobile elements and different modes of gene transfer

Based on your reading and discussion notes, explain the meaning and content of the following figure derived from the comparative genomic analysis of three *E. coli* genomes by Welch et al. Remember that CFT073 is a uropathogenic strain and that EDL933 is an enterohemorrhagic strain. Explain how this study relates to your understanding of ecotype diversity. Provide a definition of ecotype in the context of the human body. Explain why certain subsets of genes in CFT073 provide adaptive traits under your ecological model and speculate on their mode of vertical descent or gene transfer.

The X axis is position along the genome, minus island insertion distances. Each vertical deviation is the size of a gene island at that location, and which strain it is present in is shown by direction. An ecotype is a specific version of a species of a microbe that is adapted to a certain niche habitat. In the context of the human body this could be life in the mouth vs life in the gut. The two strains of E. coli here, CFT073 and EDL933, have acquired and retained gene islands that help them survive in the urinary tract or intestinal tract, respectively. Some islands are in both strains. These likely contain genes that are useful just for life in the human body, regardless of specific microenvironment. Islands that are only in one strain were likely acquired from other strains or species through horizontal gene transfer. Islands that are present in both strains could be the result of horizontal gene transfer between them, horizontal gene transfer with a third party by both of them, or inherited vertically from a common ancestor.