Feb 13th, 11:30 AM - 12:30 PM

Oral Concurrent Session III: Biological Sciences III: Microbiology

Dayle Daines
Old Dominion University

Daines, Dayle, "Oral Concurrent Session III: Biological Sciences III: Microbiology" (2016). *Undergraduate Research Symposium*. 14.
http://digitalcommons.odu.edu/undergradsymposium/2016/MasterSchedule/14

11:30 AM -12:30 PM (ROOM 1310)

Biological Sciences III: Microbiology

Chair: Dayle Daines, Department of Biological Sciences

Characterization of a toxin-antitoxin locus in *Acinetobacter baumannii*

Michaela Frost (Mentor: Dr. Dayle Daines)

Toxin-antitoxin (TA) systems are mechanisms of survival in many species of bacteria. In nontypeable *Haemophilus influenzae* (NTHi), the type II TA gene pair vapBC-1 encodes the VapB-1 antitoxin protein and the VapC-1 ribonuclease toxin. This locus contributes significantly to NTH's survival and virulence during infection. Orthologues of vapBC-1 are present in the Gram-negative bacillus *Acinetobacter baumannii*, a causative agent of nosocomial infections. In this study, we hypothesized that protein homologues of VapB-1 and VapC-1 in *A. baumannii* would interact similarly as those in NTHi. We also investigated whether the VapCAb toxin protein had ribonuclease activity and led to growth arrest.

Analyzing phylogenetic relationships of bacterial strains in Mycobacterium marinum using ortholog clustering

Dillion Matthews (Mentor: Dr. David Gauthier)

Mycobacterium marinum is a species of bacteria known for its ability to cause fish and zoonotic infections in aquaculture. Phylogenetic analysis of 32 strains of *Mycobacterium marinum* revealed a clade organization based on host. The strains that were isolated from a broad range of hosts, including humans, fish, and amphibians, formed clade I; those isolated entirely from fish grouped together in clade II. Within clade II, a subgrouping of strains infecting solely hybrid striped bass was termed the KST-clade. The evolutionary paths of these clades were analyzed and compared through ortholog clustering. Each clade's core genome was defined as the genes present in every strain of a particular grouping. These cores were compared to the entire collection of genes in all 32 strains to determine the presence of genes exclusive to each clade. No such genes were found in clade I, but clade I and KST groupings possessed 7 and 13 respectively. Of these genes, almost all code for functions that have yet to be determined. Further investigation is necessary to determine whether these hypothetical proteins actually play a role in the selection for fish or striped bass hosts in these groupings.

Examining Positive Selection in *Mycobacterium marinum* genomes

Miranda Ryan (Mentor: Dr. David Gauthier)

Mycobacterium marinum, infects multiple poikilothermic and endothermic species, and can produce zoonotic infections. Comparative analyses of *M. marinum* isolates revealed two apparent clades, clade I, a mix of human, fish and reptile/amphibian isolates, and clade II, comprised almost exclusively of fish isolates. A sub-clade of clade II, the KST clade, is composed of strains isolated exclusively from hybrid striped bass. To analyze clade II and the KST clade, rates of nonsynonymous to synonymous mutations (dN/dS) were calculated. Analysis of results from dN/dS analyses may reveal virulence and host selection of isolates characteristic to specific *M. marinum* clades.