COLLEGE OF AGRICULTURE & LIFE SCIENCES
Soil, Water and
Environmental Science

SWES Colloquium Series 2017-2018

Department of Soil, Water and Environmental Science

Comparative microbial genomics: Applying next generation sequencing as a critical food safety tool and beyond

Next generation sequencing (NGS) has arisen as a powerful tool to address many food safety issues on a much deeper level than previously possible. Using Pacific Biosciences (PacBio) single molecule real time (SMRT) sequencing technology the first complete genomes of enterohemorrhagic *Escherichia coli* O145:H28 were generated. Comparative genomic analysis revealed that unlike the other non-O157 “big six” serotypes, O145 evolved along a similar lineage as O157:H7 and shares many similar genetic traits. Additionally, epigenomic analysis of curli variants of the O145 strains suggested a critical role for DNA methylation in regulating the expression of curli in *E. coli*. Whole genome sequencing (WGS) is rapidly becoming the gold standard for source tracking by public health officials during a foodborne outbreak, but we currently lack standardized parameters such as the number of single nucleotide polymorphisms (SNPs) to utilize to effectively include or eliminate strains from an outbreak investigation. Using NGS, we conducted a retrospective study on the relationship of 18 environmental, food, and clinical *Salmonella* Typhimurium strains isolated across the United States between 2002 and 2011; all the strains were originally considered identical by the poor resolution of classic subtyping methods such as PFGE, MLST, and MLVA. The study revealed a previously unknown multistate outbreak from an unknown source, and also determined ≤ 5 SNPs would effectively include epidemiologically linked *S.* Typhimurium strains during an outbreak investigation. However, the longer an outbreak occurs the more SNPs needed to include appropriate strains during the investigation. Beyond food safety tools, we also used NGS to sequence 28 cocci-shaped *Sporosarcina* strains with very diverse spatial isolation. Cocci-shaped *Sporosarcina* strains are currently one of the very few known cocci-shaped spore-forming bacteria, and also belong in a genus where all other species are rod-shaped. Comparative genomics of core genes, accessory genes or spore-related genes consistently resulted in the 28 strains being divided into eight clades. Therefore, comparative genomics supports the identification of several novel species of cocci-shaped *Sporosarcina*. Hence, we used NGS to determine evolutionary lineages, determine gene expression regulators, strengthen epidemiological investigations, and identify novel bacterial species.

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Monday, April 2, 2018 -- 3:00pm

Marley 230

Light refreshments served in courtyard at 2:45

School of Earth and Environmental Sciences