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### **Fieldhouse Fellowship Research Update**

By incorporating the full sequence of 20 genomes on a single DNA microarray, we conducted, to our knowledge, the first pan-genomic analysis of *Listeria monocytogenes*, an important food-borne pathogen of serious public health concern.

Major milestones achieved so far include:

On the bioinformatic side of the proposal, we developed a data analysis pipeline and a comparative genomic database that enabled information extraction and interpretation from large volumes of data generated from this study. These achievements along with our previously published pan-genome microarray design algorithm (PanArray) provide the complete bioinformatic framework for our proposed fast genotyping/comparative genomic analysis method.

On the biology side, we explored the intraspecific genetic diversity of *Listeria monocytogenes* including a rare and understudied genetic lineage of this species. We identified unique protein-coding genes and regulatory RNAs in the predominant disease-causing lineages, as they may relate to ecological fitness, host niche adaptation and pathogenicity. We estimated the core and pan-genome that define the *Listeria monocytogene* species. We also reconstructed the evolutionary phylogeny of this species based on pan-genome characteristics. These results show that our pan-genomic approach is highly efficient and robust in exploring the genomic diversity in bacterial species; information gained from such study would be extremely valuable for us to better understand the intraspecific variations in virulence, ecology, epidemiology and evolution of microbial pathogens.

Due to this work, I was invited to deliver an oral presentation at 17<sup>th</sup> International Symposium on Problems of Listeriosis (ISOPOL XVII) this May in Porto, Portugal. ISOPOL is the most prominent international conference dedicated to *Listeria* research, which only takes place once every three or four years. The manuscript of this work has been submitted to *BMC Genomics* and is currently being reviewed. Part of this work was also presented at the 110<sup>th</sup> General Meeting of the American Society for Microbiology this June in San Diego, CA.