Poster Section: Surveillance and Diagnostics, with an Update on Rapid Diagnostics

Section Chair: David Hillyard, MD

Poster Title: Website Development for the Advancement of Influenza Primer and Probe Design

Michael E. Bose, Jiang Fan, MD, Andrew Patzer, Jack Littrell, Andrea J. Kraft, Kelly J. Henrickson, MD

Children's Hospital of Wisconsin

The 1997 Hong Kong avian influenza epizootic and the return of H5N1 in 2003 have led to an increased investment by the United States (NIH, CDC, USDA) and countries around the world in the areas of influenza vaccines, therapeutics, and diagnostics. A result of these efforts is a significant increase in the amount of genomic data for influenza (TIGR, etc) that is now greater than 44,000 nt sequences and growing by hundreds weekly. Each year, considerable resources in many laboratories are spent on primer and probe design to improve influenza diagnostics. The NIH has funded improved bioinformatics for a number of agents, including influenza (www.biohealthbase.org), but that website does not greatly facilitate primer and probe design. To solve this problem, we have created an automatically updating database, containing all accessible nucleotide sequences of influenza A, B, and C, which will be integrated into a website that allows all 44,000+ sequences to be searched with a variety of criteria, including gene segment, year, species, geographic location, and subtype. The website quickly aligns the sequences and displays the consensus sequence with the percent conservation at each position and the percentage of sequences contributing to every base pair decision. Additionally, the consensus sequences are BLASTed against a database of published primers and probes and displayed with the output aligned below the sequence. We believe this website will significantly advance the development of diagnostic assays for influenza, decrease expenditures in resources around the world, and allow for rapid response as new influenza strains emerge.