



Real-Time Use of Whole Genome Sequencing to Help Solve Foodborne and Zoonotic Disease Outbreaks

Full Day Session

Whole genome sequencing (WGS) of pathogens such as *Listeria monocytogenes*, Shiga toxin-producing *E. coli* (STEC), and *Salmonella enterica* are having a major impact on how foodborne and zoonotic outbreaks are being investigated in the US. As federal, state, and local capacity to sequence these organisms increases, knowledge of how to interpret and apply WGS data during urgent public health responses will become an essential skill for epidemiologists. This workshop will focus on understanding the basic science behind whole genome sequencing techniques, interpreting WGS data on the genetic relatedness of pathogens, and using this data to inform investigational decisions. The session will include a combination of presentations and practical exercises, including real world examples of the use of WGS in foodborne and zoonotic disease outbreaks.

Time	Topic	Speaker
8:00 – 8:15	Welcome	Matt Wise (CDC)
8:15 – 10:00	Basics of Analysis Overview Tree Interpretation Group Activity	Heather Carleton (CDC)
10:00 – 10:30	Break	
10:30 – 12:00	Foodborne WGS Implementation: State Examples <ul style="list-style-type: none"> • Case studies • Discussion • Panel 	Carlota Medus (MN), Beth Melius (WA), Lisha Constantine-Renna (TN), Jane Yackley (TN) Moderator: Kirk Smith (MN)
12:00 – 1:30	Lunch	
1:30 – 3:00	Use of WGS in Multistate Investigations Foodborne outbreaks: <ul style="list-style-type: none"> • <i>E. coli</i> O121 and O26 in flour case study Outbreaks linked to animal contact: <ul style="list-style-type: none"> • <i>S. Heidelberg</i> in WI • <i>S. enteritidis</i> in MN • Turtles from overseas 	Matt Wise (CDC), Megin Nichols (CDC)
3:00 – 3:30	Break	
3:30 – 4:00	Epi-Lab Integration/Communication Tips	Amy Woron (HI)
4:00 – 4:45	Future of WGS and Closing Remarks	Matt Wise (CDC), Carlota Medus (MN), Heather Carleton (CDC)