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**Insights into genetic basis of virulence in *Salmonella* Dublin****Manal Mohammed**  
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**S**almonellosis is one of the most common foodborne diseases worldwide that causes a huge burden of morbidity and mortality in humans. Although non-typhoidal *Salmonella* serovars including *Salmonella* Dublin are associated primarily with self-limiting gastrointestinal illness they have adapted to cause invasive disease and systemic illness in humans particularly children, elderly and immunocompromised people. *Salmonella enterica* serovar Dublin is a zoonotic infection that can be transmitted from cattle to humans through consumption of contaminated milk and milk products. Outbreaks of human infections by *Salmonella* Dublin have been reported in several countries including high-income countries. The genetic basis of virulence and invasiveness of *Salmonella* Dublin is not well characterized. We apply next generation sequencing and associated bioinformatics analyses tools to characterize the invasome of *Salmonella* Dublin that enable the bacteria to cause systemic illness in humans. We identified several virulence factors that enable the bacteria to cause

invasive disease in humans however, no genomic markers were detected that differentiate among invasive and non-invasive isolates suggesting that host factors and immune response play a significant role in the disease outcome. There is no vaccine against non-typhoidal *Salmonella* however our understanding of the molecular basis of virulence in invasive *Salmonella* Dublin will provide insights into the development of an effective vaccine through identification of novel virulence-attenuated strains with a potential for use as vaccine candidates for high-risk groups.

**Speaker Biography**

Manal Mohammed is a lecturer in Medical Microbiology at University of Westminster, UK. She did her PhD at University of Liverpool, UK where she studied the molecular evolution of incurable Japanese encephalitis virus associated with high morbidity and mortality in humans. Her research is focused on application of next generation sequencing technologies and associated bioinformatics analyses tools in investigating the molecular basis of virulence of non-typhoidal salmonellosis in humans and understanding the complex dynamics of bacteria-phage interaction aiming to develop phage therapy as an alternative to antibiotics.

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