

# Development of a real-time PCR assay to investigate South African *Salmonella* Enteritidis clades

Sarah Gallichan
School of Pathology, Faculty of Health Science, University of Witwatersrand, Johannesburg, South Africa

*Salmonella* Enteritidis is the most commonly reported non-typhoidal *Salmonella* serovar, and is implicated in both gastroenteritis and invasive non-typhoidal disease. Whole-genome sequence comparison of *Salmonella* Enteritidis isolates from across the world identified four definitive clades: Outlier, Global, East African and West African. Three of these clades were implicated in epidemics: the Global Clade was linked to poultry-associated gastroenteritis, while the two African clades were related to invasive disease. Despite the recognition of different Salmonella Enteritidis clades, the distribution and epidemiology of these clades across Africa is poorly understood. To investigate this, we developed a sensitive real-time PCR assay that was capable of differentiating between the *Salmonella* Enteritidis clades. This assay was then used to investigate 618 *Salmonella* Enteritidis isolates originating from four South African provinces over a period of two years (2012 – 2013). Associations between particular clades and province of collection, antimicrobial resistance and HIV status were explored using statistical analysis. The majority of the South African isolates were classified within the Global Outlier clade (61.00%), with fewer classified within the Global clade (38.83%) and only one isolate classified within the West African Clade (0.16%). Of note, were the isolates within the Global clade, which were strongly associated with ciprofloxacin resistance (15.42%, OR: 7.45, CI: 3.526 – 15.751) and invasive disease (58.33%, OR: 1.57, CI: 1.13 – 2.17) in humans. Thus, we have highlighted the importance of monitoring Salmonella Enteritidis clades in sub-Saharan Africa in order to gain a better understanding of the distribution and epidemiology. The development of a sensitive real-time PCR assay provides a cost-effective alternative to whole-genome sequencing for use in resource limited settings.

## Biography

Sarah Gallichan recently completed her Masters of Science in Medicine and will graduate in June 2020. Concurrent with her Masters degree, she completed an internship at the National Institute for Communicable Diseases (NICD), Johannesburg, South Africa. She was awarded the *Best Scientific Presentation* award for her presentation of her Masters project at the NICD Scientific Meeting in 2019.

## Presenting author details

Full name: Sarah Gallichan
Contact number: +27 83 291 0805
Linked In account: https://www.linkedin.com/in/sarah-gallichan-52b90810a/
Session name/ number: Medical Microbiology
Category: (Oral presentation/ Poster presentation)