**Background**

- Non-typhoidal *Salmonella* (NTS), an etiologic agent of gastroenteritis, is a risk factor for morbidity and mortality in young children.
- The two most common serovars that cause gastroenteritis worldwide are *S. Typhimurium* and *S. Enteritidis*.
- Additionally, variants of these two serovars, such as *S. Typhimurium* sequence type (ST) 313, also cause invasive disease in infants in sub-Saharan Africa.
- The Vaccine Impact on Diarrhea in Africa (VIDA) study evaluated the impact and effectiveness of rotavirus vaccine introduction and its effect on etiological agents of moderate-to-severe diarrhea (MSD) in children <5 years of age at study sites in The Gambia, Mali, and Kenya. Children were grouped in 3 age cohorts: 0-11, 12-23 and 24-59 months.

**Objective**

To evaluate the serovars, antimicrobial resistance (AMR) and genotypes of *Salmonella* isolated from stools of children < 5 years old with moderate-to-severe diarrhea (MSD) or matched community controls at sites in The Gambia, Mali and Kenya during VIDA (2015-2018) and compare data to isolates from the Global Enteric Multicenter Study (GEMS; 2007-2010) and the follow-up study GEMS1a (2011).

**Methods**

- Identified *Salmonella* spp. using standard microbiological and biochemical tests.
- Identified serovars using agglutination and typing antisera.
- Determined antimicrobial sensitivity using the Kirby-Bauer disk diffusion method.

**Summary findings**

- NTS isolated from stools of MSD cases and healthy controls
- Shifts in the proportion of NTS serovars from GEMS to VIDA
- MDR *S. Typhimurium* were isolated in Kenyan stools; 98% were ST313 the genotype associated with invasive NTS disease in sub-Saharan Africa.

**Results**

- 191 NTS isolates were recovered from stools
- 44.7% were from The Gambia, 1.1% were from Mali and 54.2% from Kenya

**S. Typhimurium genotypes**

- Of 7 *S. Typhimurium* isolates:
  - 5 ST313 – all MDR
  - 2 ST36 – pan-susceptible to antibiotics

**Temporal shifts in NTS serovars**

- During VIDA, the most common serovars were serogroup B (18.4%), serogroup C2-C3 (12.3%), serogroup F (11.7%), and serogroup G (11.2%)
- *S. Typhimurium* reduced from 38.2% in GEMS to 5.0% in VIDA
- *S. Enteritidis* increased from 6.3% in GEMS to 9.5% in VIDA

**AMR in The Gambia and Kenya from GEMS to VIDA**

- Isolates were pan-susceptible to ciprofloxacin
- Ceftriaxone resistance emerged during GEMS1a
- High rates of AMR in Kenya