

Prevalence, antimicrobial resistance, and distribution of *Shigella* among children under five in three sub-Saharan African countries in the Vaccine Impact on Diarrhea in Africa Study

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Background

- Shigellosis, caused by *Shigella*, is a leading cause of diarrheal morbidity and mortality worldwide.
- In the Global Enteric Multicenter Study (GEMS), *Shigella* was the second leading cause of moderate-to-severe diarrhea (MSD) in children aged less than 5 years and the most important bacterial pathogen in 12-23 and 24-59 month old children.
- A follow-up 36-month prospective, matched, case-control study called Vaccine Impact on Diarrhea in Africa (VIDA) assessed the impact of rotavirus vaccine introduction on moderate-to-severe diarrhea (MSD) in children <5 years in Kenya, Mali and The Gambia.
- Here, we describe the prevalence of *Shigella* and distribution of serogroups, serotypes and antimicrobial resistance (AMR) using standard microbiological culture during VIDA.

Methods

Enrollment: We enrolled 4840 MSD cases and 6213 healthy matched controls and collected stool and epidemiological data for all cases and controls. Cases were matched with controls by age, sex and proximity.

Molecular detection of *Shigella*: TaqMan Array Card (TAC) quantitative PCR was performed to detect *Shigella* directly from stool and to calculate the attributable fraction (AFe) for *Shigella*. AFe was calculated for each case with respect to age group, site and quantity of *Shigella* DNA detected in stool, and cases with an AFe ≥ 0.5 were considered to have *Shigella* attributable MSD.

Identification & Isolation: Conventional microbiological culture was used to identify and isolate *Shigella* from stool samples.

Antimicrobial resistance testing: Antimicrobial resistance was determined using the Kirby-Bauer disc diffusion method.

Results

Shigella detection: *Shigella* was detected in 355 (7.4%) MSD cases by conventional culture and in 1641 (34.2%) cases by TAC (using a cycle threshold less than 35 cutoff).

Table 1. Stool positivity by culture and TAC, and etiologic detection of *Shigella* among MSD cases and controls.

	All sites		The Gambia		Mali		Kenya	
	Cases (N=4804)	Controls (N=4803)	Cases (N=1665)	Controls (N=1665)	Cases (N=1601)	Controls (N=1600)	Cases (N=1538)	Controls (N=1538)
Stool culture	355 (7.4%)	72 (1.5%)	215 (12.9%)	42 (2.5%)	12 (0.7%)	5 (0.3%)	128 (8.3%)	25 (1.6%)
TAC Results								
Positive (Ct < 35)	1641 (34.2%)	1084 (22.6%)	770 (46.2%)	507 (30.5%)	438 (27.4%)	334 (20.9%)	433 (28.2%)	243 (15.8%)
Etiologic detection (AFe ≥ 0.5)	944 (19.7%)		515 (30.9%)		150 (9.4%)		279 (18.1%)	

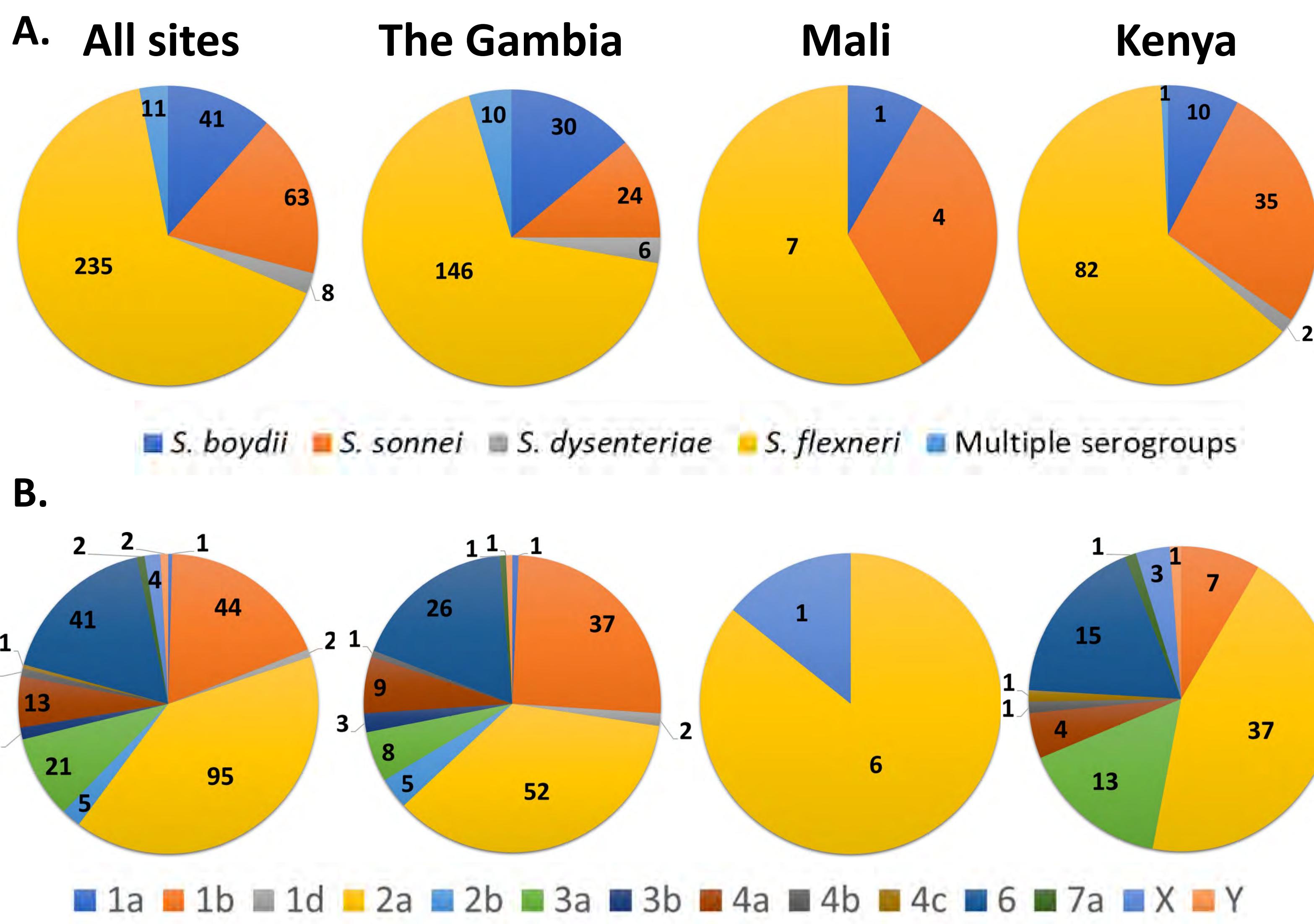


Figure 1. Distribution of A) *S. flexneri*, *S. sonnei*, *S. boydii* and *S. dysenteriae*; and B) *S. flexneri* serotypes isolated from MSD cases in the VIDA study.

Table 2. Antimicrobial resistance of *Shigella* isolates from MSD cases in the VIDA study.

Antibiotic	All sites (N=342)	The Gambia (N=202)	Mali (N=11)	Kenya (N=129)
Ampicillin	164 (48.0%)	83 (41.1%)	6 (54.5%)	75 (58.1%)
Ceftriaxone	1 (0.3%)	1 (0.5%)	0 (0%)	0 (0%)
Nalidixic Acid	4 (1.2%)	0 (0%)	2 (18.2%)	2 (1.6%)
Sulfamethoxazole	322 (94.2%)	187 (92.6%)	9 (81.8%)	126 (97.7%)
Ciprofloxacin	0 (0%)	0 (0%)	0 (0%)	0 (0%)

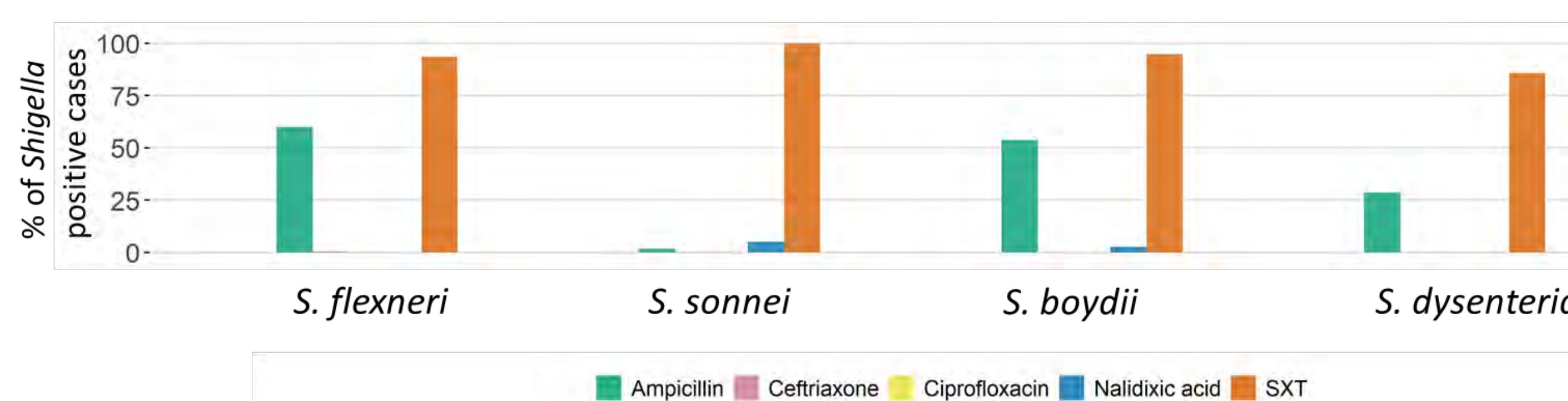


Figure 2. Antimicrobial resistance by serogroup.

Conclusion

Shigella continues to be a major pathogen causing MSD among children under five years in sub-Saharan Africa. A high burden of *Shigella*-associated diarrhea was seen among the three African sites. Preventive strategies focusing on *Shigella* could further reduce the burden of under-five diarrhea.

Acknowledgments

We wish to thank all the clinical, field, epidemiological and lab staff of all the VIDA sites and the Center for Vaccine Development and Global Health, University of Maryland School of Medicine, Baltimore. We also thank the study participants and their care givers for participating in the study. The VIDA study was funded by the Bill & Melinda Gates Foundation.