

Comparative genomic and phenotypic characterization of invasive non-typhoidal *Salmonella* isolates from Siaya, Kenya

Abstract

Non-typhoidal *Salmonella* (NTS) is a major global health concern that often causes bloodstream infections in areas of the world affected by malnutrition and comorbidities such as HIV and malaria. Developing a strategy to control the emergence and spread of highly invasive and antimicrobial resistant NTS isolates requires a comprehensive analysis of epidemiological factors and molecular pathogenesis. Here, we characterize 11 NTS isolates that caused bloodstream infections in pediatric patients in Siaya, Kenya from 2003–2010. Nine isolates were identified as *S. Typhimurium* sequence type 313 while the other two were *S. Enteritidis*. Comprehensive genotypic and phenotypic analyses were performed to compare these isolates to those previously identified in sub-Saharan Africa. We identified a *S. Typhimurium* isolate referred to as UGA14 that displayed novel plasmid, pseudogene and resistance features as compared to other isolates reported from Africa. Notably, UGA14 is able to ferment both lactose and sucrose due to the acquisition of insertion elements on the pKST313 plasmid. These findings show for the first time the co-evolution of plasmid-mediated lactose and sucrose metabolism along with cephalosporin resistance in NTS further elucidating the evolutionary mechanisms of invasive NTS phenotypes. These results further support the use of combined genomic and phenotypic approaches to detect and characterize atypical NTS isolates in order to advance biosurveillance efforts that inform countermeasures aimed at controlling invasive and antimicrobial resistant NTS.

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