Accessory Genome Dynamics and Structural Variation of Shigella from Persistent Infections



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INTRODUCTION **MATERIALS AND METHODS** Whole genome sequencing analysis of 57 pairs of Shigella Shigellosis caused mainly by Shigella flexneri and Shigella 176d 34d .636d isolates sampled from individuals at two time points (Table). sonnei is thought to be self-limiting, with short- to medium- term and serotype specific immunity provided. Working definitions of long-term carriage and re-infection 0 - 7 SNPs 10 – 1,462 SNPs associated pairs were established from previous SNP • Cases of men who have sex with men (MSM) associated analysis. shigellosis have been reported where Shigella of the same serotype were serially sampled from individuals between 1 to To investigate large-scale chromosomal structural changes, 1,862 days apart, possibly due to persistent carriage or Long-term carriage **Re-infection associated** 14 epidemic sub-lineage MSM-associated S. flexneri 3a reinfection with the same serotype. isolates serially sampled from 7 individuals (with sampling Carriage associated Re-infection associated Total pairs Serotype time ranging 9 to 911 days and using the same working Llara wa investigate the second represent dynamics of MCNA

	Here, we investigate the accessory genome dynamics of MSM-				
	associated S. flexneri and S. sonnei isolates serially sampled				
from individual patients at various days apart, to shed light on					
	the adaptation of these important pathogens during infection.				

definition of carriage (n=5) and re-infection (n=3) associated pairs) were PacBio and Illumina sequenced.

<i>S. flexneri</i> 2a	14	5	19
<i>S. flexneri</i> 3a	8	7	15
S. sonnei	15	8	23

RESULTS & DISCUSSION



- The average number of genes gained and lost between the pair class (i.e., carriage and reinfection) differed, but was not uniform across the three serotypes.
- S. sonnei reinfection-associated pairs demonstrated greater number of genes gained and lost than carriageassociated pairs, further supporting of a decreased genetic distance among carriage pairs compared to reinfection-associated pairs.
- Considerable differences in the number of accessory genes gained and lost in S. sonnei carriage-associated pairs, suggesting that a significant degree of within-host evolution might be occurring.

Number of genes lost (-) /gained (+)



- Majority of structural variations observed appeared to be artefactual, resulting from either prolonged storage or different DNA preparations/sequencing technologies.
- A prominent 166-kbp prophage region was exclusively absent in the PacBio-sequenced genomes may have resulted from their prolonged storage (relative to the Illumina preparations). Observation that this prophage region is lost in storage and retained in the clinical setting suggests that the region may have important functions involving infection and/or ecological interaction and thus warrants further investigation.
- A significantly lower proportion of genes involved in 3 key metabolic processes in the variable regions relative to the entire chromosome, suggests these may be functionally important for Shigella survival.
- Comparative enrichment of genes of unknown function in variable regions, highlighting yet again the limitations of our current understanding of the functional pathways of this important pathogen.





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