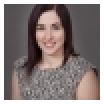
Genome sequencing reveals diversification of virulence factor content and possible host adaptation in distinct subpopulations of Salmonella enterica [1]

Submitted by Lorraine Doralys Rodriguez-River... [2] on 5 May 2014 - 4:27pm

 [2]

Title	Genome sequencing reveals diversification of virulence factor content and possible host adaptation in distinct subpopulations of Salmonella enterica
Publication Type	Journal Article
Year of Publication	2011
Authors	Bakker, HC den [3], Switt, AIMoreno [4], Govoni, G [5], Cummings, CA [6], Ranieri, ML [7], Degoricija, L [8], Hoelzer, K [9], Rodriguez-Rivera, LD [10], Brown, S [11], Bolchacova, E [12], Furtado, MR [13], Wiedmann, M [14]
Journal	BMC Genomics
Volume	12
Issue	1
Pagination	425 - 425
Date Published	2011///
ISBN Number	ISSN~~1471-2164

Abstract	ABSTRACT: BACKGROUND: Divergence of bacterial populations into distinct subpopulations is often the result of ecological isolation. While some studies have suggested the existence of Salmonella enterica subsp. enterica subclades, evidence for these subdivisions has been ambiguous. Here we used a comparative genomics approach to define the population structure of Salmonella enterica subsp. enterica, and identify clade-specific genes that may be the result of ecological specialization. RESULTS: Multi-locus sequence analysis (MLSA) and single nucleotide polymorphisms (SNPs) data for 16 newly sequenced and 30 publicly available genomes showed an unambiguous subdivision of S. enterica subsp. enterica into at least two subpopulations, which we refer to as clade A and clade B. Clade B strains contain several clade-specific genes or operons, including a betaglucuronidase operon, a S-fimbrial operon, and cell surface related genes, which strongly suggests niche specialization of this subpopulation. An additional set of 123 isolates was assigned to clades A and B by using qPCR assays targeting subpopulation-specific SNPs and genes of interest. Among 98 serovars examined, approximately 20% belonged to clade B. All clade B isolates contained two pathogenicity related genomic islands, SPI-18 and a cytolethal distending toxin islet; a combination of these two islands was previously thought to be exclusive to serovars Typhi and Paratyphi A. Presence of beta-glucuronidase in clade B isolates specifically suggests an adaptation of this clade to the vertebrate gastrointestinal environment. CONCLUSIONS: S. enterica subsp. enterica consists of at least two subpopulations that differ specifically in genes involved in host and tissue tropism, utilization of host specific carbon and nitrogen sources and are therefore likely to differ in ecology and transmission characteristics.

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