

Insights into Genomic Variation within *Salmonella enterica*

Serrano PC¹, Perez LAM², Hernandez YE² and Nava GM^{2*}

¹Autonomous University of Mexico, Mexico City, Mexico

²Autonomous University of Queretaro, Mexico City, Mexico

*Corresponding author: Nava GM, Department of Research and Graduate Studies in Food Science, Faculty of Chemistry, Autonomous University of Queretaro, Mexico City, Mexico, Tel: +52-4424676817; E-mail: gerardomnava@gmail.com

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Editorial

Advances in molecular microbiology, comparative genomics and data mining have allowed us to uncover new insights into genome structure within bacterial species. To evolve, Bacteria gains and loses genes and other genomic sequences to adapt to specific ecological niches [1]. Thus, the intraspecies genomic variation found in numerous bacterial species has highlighted the need of analyzing genome composition to define bacterial species [1]. Fortunately, Whole-Genome Sequence Analysis (WGS) has uncovered the dynamic nature of genomic plasticity and the consequent extensive genetic diversity in Bacteria [2]. Currently, microbiological research has been focused on WGS within-species to identify molecular or virulence determinants. These studies could accelerate our understanding of bacterial pathogenesis and strains-specific traits of virulence; key factors in improving bacterial surveillance and development of antibacterial treatments or vaccines [3].

Herein, we investigate the genomic variation within *Salmonella enterica* as an example of the potential of comparative analysis of WGS to uncover intraspecies variation. A total of 1,604 *S. enterica* whole genomes were analyzed. This dataset comprised 38 different serotypes (Table 1) retrieved from the Integrated Microbial Genomes (IMG) system [4]. Serotypes with at least 3 genomes available were used for bioinformatics analyses. Intraspecies traits of genomic variation were assessed for each of the selected serotypes. Briefly, it was found that the genome size *S. enterica* serotypes varies considerably; for example, serotype Muenchen, in average, possess the largest genome size (5.00 Mbp) whereas Paratyphi possess the smallest (4.59 Mbp). Unexpectedly, a high variation in the genome size was observed in each serotype (Figure 1 and Table 1).

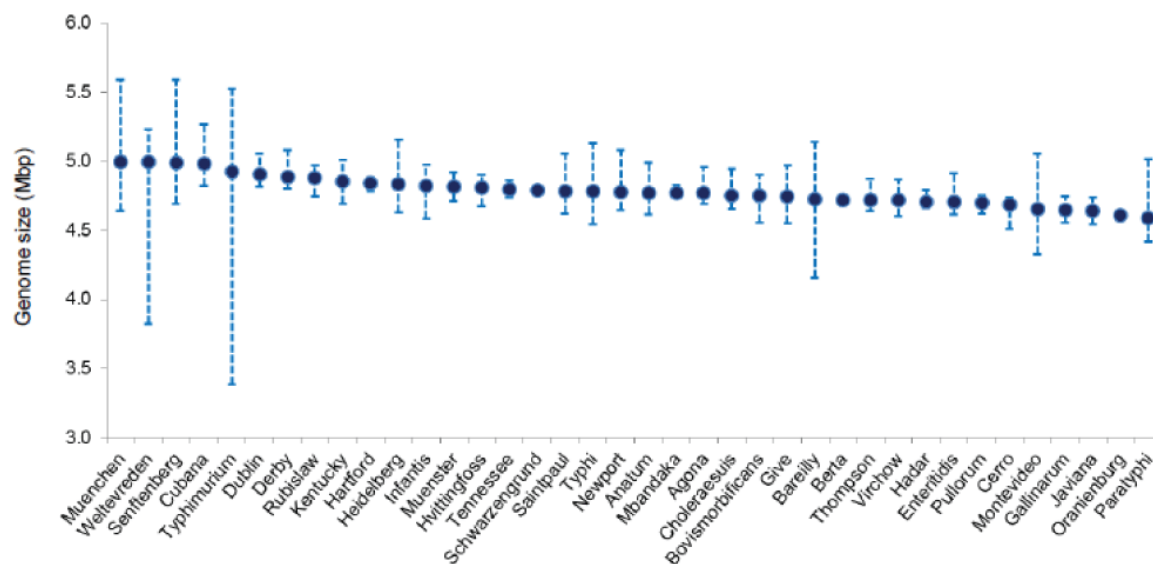


Figure 1: Genome size comparisons between different serotypes of *Salmonella enterica*. Whole-genomes (n=1,604) covering at least 38 serovars were analyzed. Genomes were obtained from the Integrated Microbial Genomes (IMG) system. Mean values of genome size are presented. Blue dashed lines depict the range between the smallest and largest genome size for each serotype.

Serotypes Typhimurium, Weltevreden, Bareilly, Muenchen, Senftenberg, Montevideo, Paratyphi, Typhi and Heidelberg showed the highest variation (difference between the smallest and the largest chromosome) in genome size. This variation corresponds to differences in genome size ranging between 0.53-2.14 Mbp. These

numbers represents from 10% to 43% extra genome. Such differences in genome size have been observed between different bacterial species and genera [5]; thus, it is possible to contemplate the need for reviewing the “bacterial species concept” in *S. enterica*.

Together, these analyses reveal that the gain and loss of genes is an important mechanism used by *S. enterica* to adapt to different niches. The intra-species genomic variation reported here highlights the need for deeper WGS to uncover the extent of the genomic plasticity of this pathogen. Understanding genome diversity will help us to understand the dynamics of bacterial-host interactions.

Serotype	Genome size (Mbp)				
	Number	Mean	Smallest	Largest	Difference
Muenchen	6	5.00	4.64	5.59	0.95
Weltevreden	119	4.99	3.83	5.23	1.40
Senftenberg	14	4.99	4.69	5.59	0.90
Cubana	5	4.98	4.82	5.27	0.44
Typhimurium	457	4.93	3.39	5.53	2.14
Dublin	6	4.91	4.81	5.06	0.24
Derby	4	4.88	4.81	5.08	0.27
Rubislaw	3	4.88	4.74	4.97	0.23
Kentucky	15	4.85	4.70	5.01	0.31
Hartford	3	4.84	4.78	4.88	0.10
Heidelberg	105	4.83	4.63	5.16	0.53
Infantis	10	4.82	4.58	4.98	0.39
Muenster	4	4.82	4.71	4.92	0.21
Hvittingfoss	3	4.81	4.67	4.90	0.23
Tennessee	9	4.79	4.74	4.86	0.13
Schwarzengrund	3	4.79	4.76	4.82	0.06
Saintpaul	6	4.78	4.62	5.05	0.43
Typhi	88	4.78	4.54	5.13	0.59
Newport	68	4.78	4.65	5.08	0.44
Anatum	15	4.77	4.62	4.99	0.37
Mbandaka	3	4.77	4.74	4.83	0.08

Agona	112	4.77	4.69	4.96	0.26
Choleraesuis	4	4.75	4.66	4.94	0.29
Bovismorbificans	29	4.75	4.56	4.90	0.35
Give	3	4.74	4.55	4.97	0.42
Bareilly	105	4.73	4.16	5.14	0.98
Berta	3	4.72	4.72	4.73	0.01
Thompson	6	4.72	4.65	4.88	0.23
Virchow	3	4.72	4.60	4.87	0.27
Hadar	7	4.71	4.66	4.79	0.13
Enteritidis	134	4.70	4.62	4.91	0.29
Pullorum	5	4.70	4.62	4.75	0.13
Cerro	20	4.69	4.52	4.74	0.22
Montevideo	57	4.65	4.32	5.05	0.73
Gallinarum	6	4.65	4.56	4.75	0.19
Javiana	5	4.64	4.55	4.74	0.19
Oranienburg	3	4.61	4.60	4.63	0.02
Paratyphi	156	4.59	4.42	5.02	0.60

Table 1: Genome size variation between different *Salmonella enterica* serotypes.

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