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The *Salmonella enterica* Pan-genome

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Abstract *Salmonella enterica* is divided into four subspecies containing a large number of different serovars, several of which are important zoonotic pathogens and some show a high degree of host specificity or host preference. We compare 45 sequenced *S. enterica* genomes that are publicly available (22 complete and 23 draft genome sequences). Of these, 35 were found to be of sufficiently good quality to allow a detailed analysis, along with two *Escherichia coli* strains (K-12 substr. DH10B and the avian pathogenic *E. coli* (APEC O1) strain). All genomes were subjected to standardized gene finding, and the core and pan-genome of *Salmonella* were estimated to be around 2,800 and 10,000 gene families, respectively. The constructed pan-genomic dendrograms suggest that gene

content is often, but not uniformly correlated to serotype. Any given *Salmonella* strain has a large stable core, whilst there is an abundance of accessory genes, including the *Salmonella* pathogenicity islands (SPIs), transposable elements, phages, and plasmid DNA. We visualize conservation in the genomes in relation to chromosomal location and DNA structural features and find that variation in gene content is localized in a selection of variable genomic regions or islands. These include the SPIs but also encompass phage insertion sites and transposable elements. The islands were typically well conserved in several, but not all, isolates—a difference which may have implications in, e.g., host specificity.

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Introduction

Salmonella are intracellular pathogens in cold-blooded as well as warm-blooded animals and important zoonotic agents. The genus *Salmonella* is currently divided into two species: *Salmonella enterica* and *Salmonella bongori*. *S. enterica* is further divided into six subspecies: *S. enterica* subsp. *enterica*, *S. enterica* subsp. *salamae*, *S. enterica* subsp. *arizonae*, *S. enterica* subsp. *diarizonae*, *S. enterica* subsp. *houtenae*, and *S. enterica* subsp. *indica*. To date, more than 2,500 different serovars have been characterized, with most (1,531) classified as part of the *Salmonella* subsp. *enterica* [1], which is the cause of more than 99% of the diseases in humans [1, 2]. The characterization is based on their surface antigens, where the O (somatic) antigens are part of the variable long chain lipopolysaccharide located on the outer membrane and the two H (flagellar) antigens are presented, when the two flagellar structures are expressed [1, 3].

S. enterica serovar Typhimurium and serovar Enteritidis are amongst the most common generalist pathogens, causing disease in a variety of animals [4, 5]. A smaller

proportion of the serovars is host-specific and cause severe diseases. *S. Typhi* and *Salmonella* Paratyphi are human-restricted, causing typhoid and paratyphoid fever respectively [6]. The bovine-adapted *Salmonella* Dublin and the porcine-adapted *Salmonella* Choleraesuis are occasionally seen in humans, causing severe disease [7–9]. Traditionally, animal models have successfully been employed to elucidate the pathogenicity of intestinal *Salmonella* [10, 11], but these methods have inherent limits. Many disease mechanisms in *Salmonella* are host-specific, most famously the enteroinvasive behavior of *S. Typhi* in human infections [12], or more recently the human-adapted behavior of strain *Salmonella* Typhimurium D23580 [13]. In these cases, comparative genomics represent an alternative approach [14]

Salmonella is closely related to *Escherichia coli*, but have an additional large number of virulence genes [15, 16]. Some of these virulence genes are located in genomic islands (GIs), which are large segments of DNA acquired by horizontal gene transfer. These GIs often display a different AT content than from the rest of the genome of *S. enterica* (which is ~48% AT) [15]. These are usually located near tRNA genes, which are believed to facilitate the integration of the GIs into the chromosome due to their high degree of conservation. Many *Salmonella*-specific GIs, *Salmonella* pathogenicity islands (SPIs) play a role in virulence and have been linked to influencing host specificity as well as the degree of invasiveness of the bacteria [17].

Much research has been invested in order to identify *Salmonella*-specific genes and to determine genes specific to the different serovars. The *S. Typhi* and *S. Paratyphi A* serovars are both adapted to the same host and cause enteric fever in humans. This study shows that they are highly homologous at the protein level. A comparison of their evolutionary relatedness has suggested that they have evolved the ability to cause human-specific systemic disease by different paths. *S. Paratyphi A* is less diverse in terms of the proteins encoded in the genome, and contains fewer pseudogenes, which indicates that it has evolved more recently than *S. Typhi* [18]. When the complete genome sequence of *S. Typhi* CT18 was published, 204 pseudogenes were annotated, out of a genome of 4,599 genes [19]. This total was increased later, when the second *Paratyphi A* genome (strain AKU_12601) was sequenced and through comparative genomics revealed several additional pseudogenes in *S. Typhi*. Further, the two strains shared 66 pseudogenes, revealing that many of these have appeared from adaption to the same niche [6]. Some of these genes have been shown to relate to virulence and gastroenteritis, leading to the hypothesis that the original function of many of these pseudogenes was to cause gastroenteritis or infection in other hosts [18].

This work represents a data-driven approach towards elucidating the differences as well as similarities between fully sequenced *Salmonella* genomes. As the number of fully sequenced genomes available for analysis increases, so will the possibility to differentiate at greater detail between phenotypic characteristic such as host-specificity and the degree of invasiveness. At the time of writing (late 2010) we found 45 fully sequenced *Salmonella* genomes publicly available covering 21 serotypes within *Salmonella* subsp. *enterica* and representing, to our knowledge, the total sum of public genomes. Of these, 22 were complete, and 23 were draft sequences (consisting of many pieces or “contigs” and often with incomplete gene annotation). This study compares the sequences having the highest quality, which corresponds to 35 *Salmonella* genomes. We estimated both the sizes of the pan- and core genomes, as well as illustrated the spatial distribution of core and non-core genes across the chromosome. From these data, we describe several variable gene islands in specific locations on the chromosome including, but not limited to, the SPIs [20]. It follows that some of these unnamed gene islands are likely to play a role in *Salmonella* virulence and/or host specificity, even if others may be a little more than inactive remnants of phage inserts.

Materials and Methods

Genomes and Gene Annotations

All available genome sequences of *S. enterica* from NCBI as of 1 July, 2010, were downloaded and used in this work [21], and are shown in Table 1, which also contains accession numbers and references to the sequencing centers. This list includes 18 fully sequenced and 23 almost completed genomes of *S. enterica* which we supplemented with another four genomes from the Sanger Center [22]. In addition, two *E. coli* genomes were also downloaded and used for comparison. All genomes were subjected to de novo gene finding using two previously published gene finders: EasyGene [23, 24] and Prodigal [25] with the Prodigal annotation software providing the optimal foundation for comparisons (see Supplemental Data). Both gene finders were run using default settings.

16S rRNA Phylogeny

Two phylogenetic trees were constructed based on 16S rRNA: one tree included 21 enteric strains and the other tree included only *Salmonella* strains. In both cases, the sequences were identified using RNAmmer [26] with a length between 1,400 and 1,700 nt and an RNAmmer score above 1,700. When several 16S rRNAs from the same

Table 1 General properties of the *S. enterica* and *E. coli* genomes used in this study

Organism ^a (publication reference)	Genome Size	Contigs	Quality Score	Accession	PID	Genes	Specificity	Serogroup (O antigen)
<i>S. Paratyphi A</i> str. AKU_12601 [6]	4.58 MB	1	1	FM200053	30943	4,351	Human-restricted	O:2
<i>S. Paratyphi A</i> str. ATCC 9150 [18]	4.59 MB	1	1	CP000026	13086	4,348	Human-restricted	O:2
<i>S. 4,[5],12:i:-</i> str. CVM23701 [45]	4.90 MB ^b	113	3	ABAO000000000	19465	4,694	Ubiquitous	O:4
<i>S. Agona</i> str. SL483	4.84 MB	2	1	CP001138	20063	4,508	Ubiquitous	O:4
<i>S. Heidelberg</i> str. SL476	4.89 MB	3	1	CP001120	20045	4,680	Ubiquitous	O:4
<i>S. Heidelberg</i> str. SL486	4.73 MB ^b	48	3	ABEL000000000	20065	4,432	Ubiquitous	O:4
<i>S. Paratyphi B</i> str. SPB7	4.86 MB	1	1	CP000886	27803	4,555	Ubiquitous	O:4
<i>S. Saintpaul</i> str. SARA23	4.72 MB ^b	2	1	ABAM000000000	19461	4,350	Ubiquitous	O:4
<i>S. Saintpaul</i> str. SARA29	4.93 MB ^b	182	5	ABAN000000000	19463	4,757	Ubiquitous	O:4
<i>S. Schwarzengrund</i> str. CVM19633	4.71 MB	3	1	CP001127	19459	4,551	Ubiquitous	O:4
<i>S. Schwarzengrund</i> str. SL480	4.76 MB ^b	67	3	ABEJ000000000	20071	4,547	Ubiquitous	O:4
<i>S. Typhimurium</i> str. 140288 [72]	4.76 MB	2	1	CP001363	33067	4,653	Ubiquitous	O:4
<i>S. Typhimurium</i> str. D23580 [13]	4.88 MB	1	1	FN424405	40625	4,804	Ubiquitous	O:4
<i>S. Typhimurium</i> str. DT104	4.93 MB	2	1	–	–	4,752	Ubiquitous	O:4
<i>S. Typhimurium</i> str. LT2 [4]	4.86 MB	2	1	AE006468	241	4,635	Ubiquitous	O:4
<i>S. Typhimurium</i> str. SL1344	4.88 MB	4	1	–	–	4,774	Ubiquitous	O:4
<i>S. Choleraesuis</i> str. SC-B67 [69]	4.76 MB	3	1	AE017220	9618	4,792	Porcine-adapted	O:7
<i>S. Paratyphi C</i> str. RKS4594 [52]	4.83 MB	2	1	CP000857	20993	4,690	Ubiquitous	O:7
<i>S. Tennessee</i> str. CDC07-0191	4.79 MB ^b	94	3	ACBF000000000	30831	4,546	Ubiquitous	O:7
<i>S. Virchow</i> str. SL491	4.88 MB ^b	5	2	ABFH000000000	20595	4,596	Ubiquitous	O:7
<i>S. Hadar</i> str. RI_05P066	4.79 MB ^b	50	3	ABFG000000000	20593	4,487	Ubiquitous	O:8
<i>S. Hadar</i> str. 18 Bela Nagy	4.79 MB	3	1	–	–	4,448	Ubiquitous	O:8
<i>S. Kentucky</i> str. CDC 191	4.70 MB ^b	53	3	ABEJ000000000	20069	4,383	Ubiquitous	O:8
<i>S. Kentucky</i> str. CVM29188 [70]	4.79 MB ^b	4	2	ABAK000000000	19457	4,745	Ubiquitous	O:8
<i>S. Newport</i> str. SL317	4.95 MB ^b	63	3	ABEW000000000	20047	4,720	Ubiquitous	O:8
<i>S. Newport</i> str. SL254	4.83 MB	3	1	CP001113	18747	4,710	Ubiquitous	O:8
<i>S. Dublin</i> str. CT_02021853	4.84 MB	2	1	CP001144	19467	4,682	Bovine adapted	O:9
<i>S. Enteritidis</i> str. P125109 [5]	4.69 MB	1	1	AM933172	30687	4,363	Ubiquitous	O:9
<i>S. Gallinarum</i> str. 28791	4.66 MB	1	1	AM933173	30689	4,466	Avian restricted	O:9
<i>S. Javiana</i> str. GA_MM04041433	4.55 MB ^b	19	4	ABEH000000000	20049	4,221	Ubiquitous	O:9
<i>S. Typhi</i> str. CT18 [19]	4.81 MB	3	1	AL513382	236	5,065	Human-restricted	O:9
<i>S. Typhi</i> str. Ty2 [58]	4.79 MB	1	1	AE014613	371	4,632	Human-restricted	O:9
<i>S. Typhi</i> str. J185 ^c	4.74 MB ^b	1065	6	CAAW000000000	28303	5,626 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. M223 ^c	5.02 MB ^b	3024	6	CAAX000000000	28305	7,442 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. E98-0664 ^c	4.71 MB ^b	3939	6	CAAU000000000	28299	7,759 ^d	Human-restricted	O:9

Table 1 (continued)

Organism ^a (publication reference)	Genome Size	Contigs	Quality Score	Accession	PID	Genes	Specificity	Serogroup (O antigen)
<i>S. Typhi</i> str. E98-2068 ^c	4.76 MB ^b	3682	6	CAAV000000000	28301	7,637 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. E98-3139 ^c	4.60 MB ^b	415	5	CAAZ000000000	28309	5,051	Human-restricted	O:9
<i>S. Typhi</i> str. 404ty ^c	4.68 MB ^b	6441	6	CAAQ000000000	28289	10,055 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. AG3 ^c	4.75 MB ^b	7336	6	CAAY000000000	28307	10,675 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. E00-7866 ^c	4.76 MB ^b	1445	6	CAAR000000000	28291	5,749 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. E01-6750 ^c	4.58 MB ^b	4564	6	CAAS000000000	28293	8,315 ^d	Human-restricted	O:9
<i>S. Typhi</i> str. E02-1180 ^c	4.71 MB ^b	422	5	CAAT000000000	28295	5,097	Human-restricted	O:9
<i>S. Weltevreden</i> str. HI_N05-537	5.05 MB ^b	81	3	ABFF000000000	20591	4,784	Ubiquitous	O:9
<i>S. arizonae</i> 62:z4,z23:- str. RSK2980	4.60 MB	1	1	CP0000880	13030	4,278	Ubiquitous	O:3,10
<i>S. bongori</i> str. NCTC_12419	4.79 MB	1	1	–	–	4,049	Ubiquitous	
<i>E. coli</i> str. K-12 substr. DH10B [71]	4.69 MB	1	1	CP0000948	20079	4,398	Ubiquitous	
<i>E. coli</i> APEC O1 [73]	5.08 MB	3	1	CP0000468	16718	5,259	Ubiquitous	

PID project ID

^aData for organisms is collected from NCBI.^bNote that draft genomes may contain plasmid DNA^cStrains not used in this study because of bad quality score and high number of contigs.^dGene counts are included here for completeness sake even though poor genome quality leads to spurious gene prediction

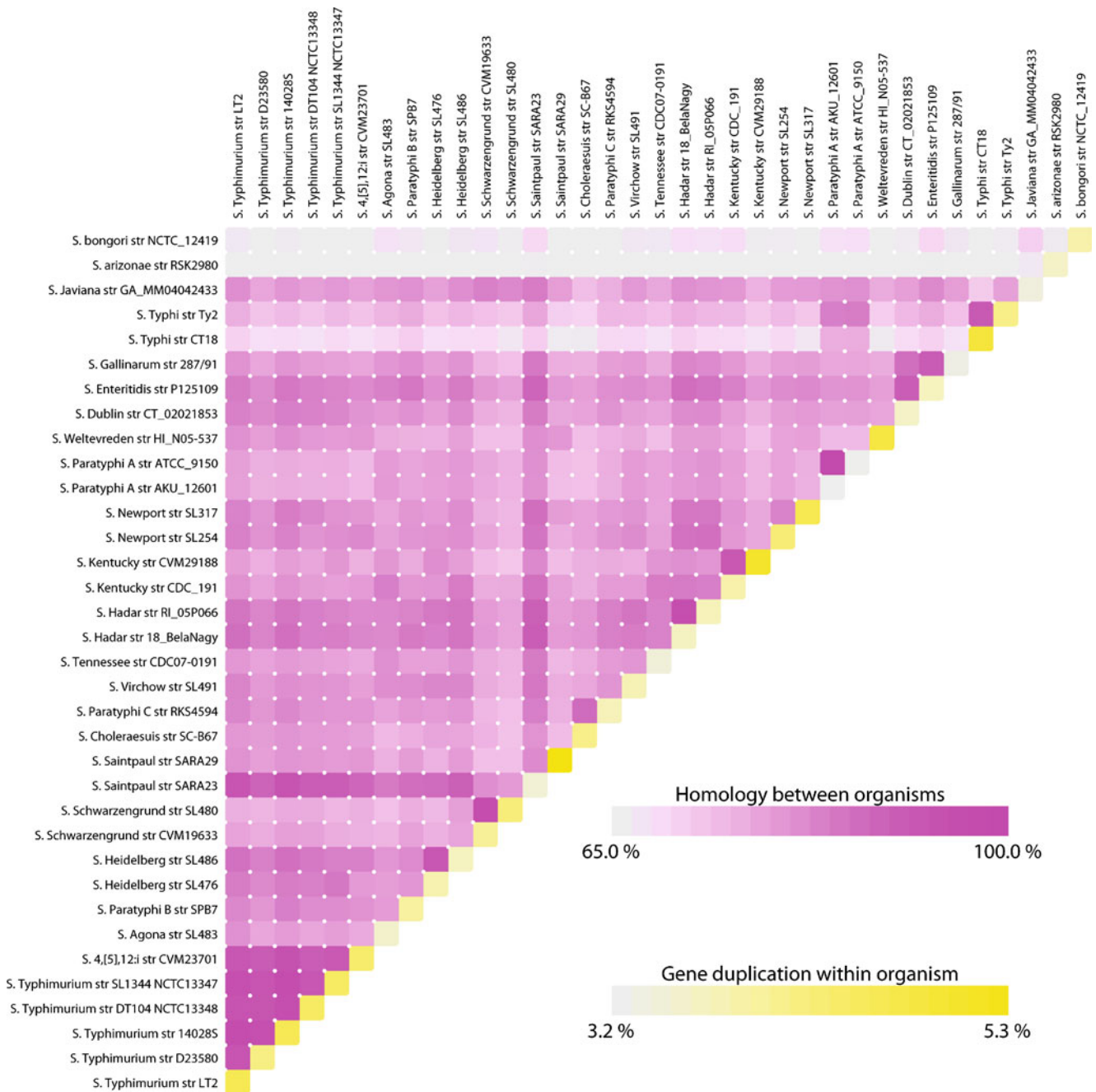


Figure 1 BLAST Matrix of 35 *S. enterica* genomes. The figure shows the number of gene families found in common between the *Salmonella* strains and the degree of gene duplication within each by

pairwise all-against-all BLAST comparisons at the amino acid level. A higher resolution version is available in the [Supplemental Section](#) with additional data viewable under zoom

strain met the criteria, the closest match to the first 16S rRNA in *S. Typhimurium* LT2, *rssH*, was selected. While 16S rRNA was already annotated in many of the genomes analyzed, then because each genome contains several 16S rRNA, using this approach eliminates any arbitrary bias from having to select one by hand. The ClustalX [27] program was used to align the 16S rRNA sequences and subsequently in constructing a tree using the bootstrap neighborhood-joining method with 1,000 trials. The tree

was visualized by using NJplot [28]. It was not possible to find 16S rRNA sequences obeying the aforementioned quality criteria for all 45 sequenced *Salmonella* genomes.

Definition of Gene Families

To identify and process homology within and across genomes, all genes were assigned into unique gene families based on sequence similarity. The genes were translated

into amino acid sequences and aligned all-against-all using BLASTP [29], and any two genes were considered a gene pair if the alignment could meet “the 50/50 rule”; at least 50% of the length of the longest sequence was continuously aligned under default gap penalties, and more than 50% of the aligned sequences must be reported identical. Since each member of a pair can be a member of other pairs as well, all gene pairs sharing members were subsequently combined into one gene family. Each gene will then exclusively belong to one gene family [30]. This is the same method used previously to describe the core and pan-genome of *Vibrio*, *E. coli*, and *Bacteroides* [31–33].

BLAST Matrix

All proteomes were compared with BLASTP using “the 50/50 rule” to categorize genes into gene families. The BLAST matrix shows the comparison of each proteome to another. The percentages show the amount of proteins shared between two proteomes along with the corresponding

fraction showing the number of gene families present in both genomes over the total amount of gene families in the two strains [34].

Pan- and Core genome Plot

The pan- and core genome plot is a simple illustration of the distribution of gene families defined above, as more and more genomes are considered. It is the result of applying a basic set theory, each genome being a set of gene family, some of which are also found in other genomes. In this context, the pan-genome becomes the union of the genomes under consideration, while the core genome is the intersection of those genomes. Thus, the total number of gene families is shown for the leftmost genome. Then, moving to the right, more genomes are considered, and any gene families not previously encountered are added to the pan-genome (the union), while the core genome is reduced to only those gene families shared by every genome analyzed at this point (the intersection). The last point defines the

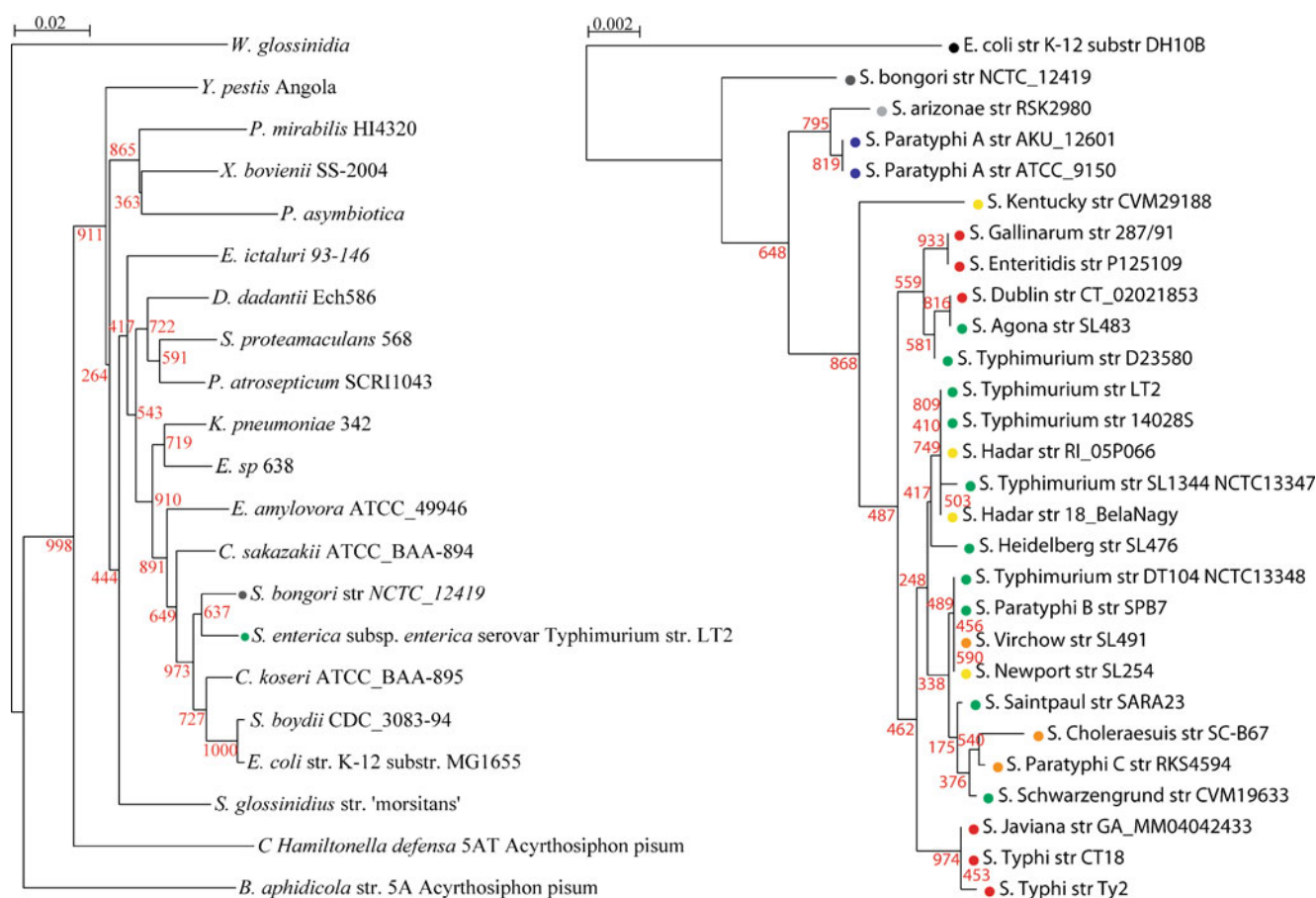


Figure 2 Phylogenetic analysis of 16S rRNA. (Left) 16S rRNA tree of different genus in the enterobacteria family, *Salmonella* is marked with color. (Right) 16S rRNA tree of 27 *Salmonella* genomes, colors indicate serogroups (see Table 1 for key). The *Salmonella* genomes of

Table 1 which are not presented here are absent because full length 16S rRNA could not be identified in most draft genomes (see “Materials and methods”). The bootstrap values, based on 1,000 iterations, are shown in red numbers, next to the branches

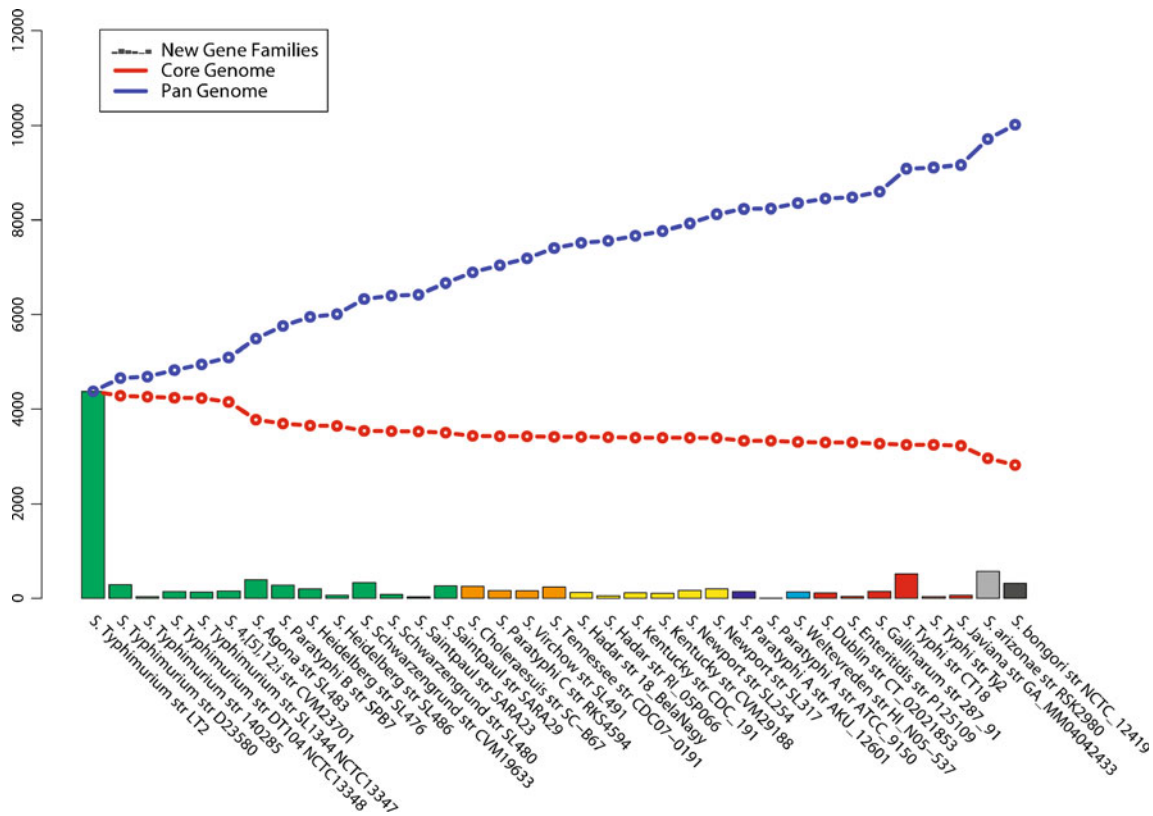
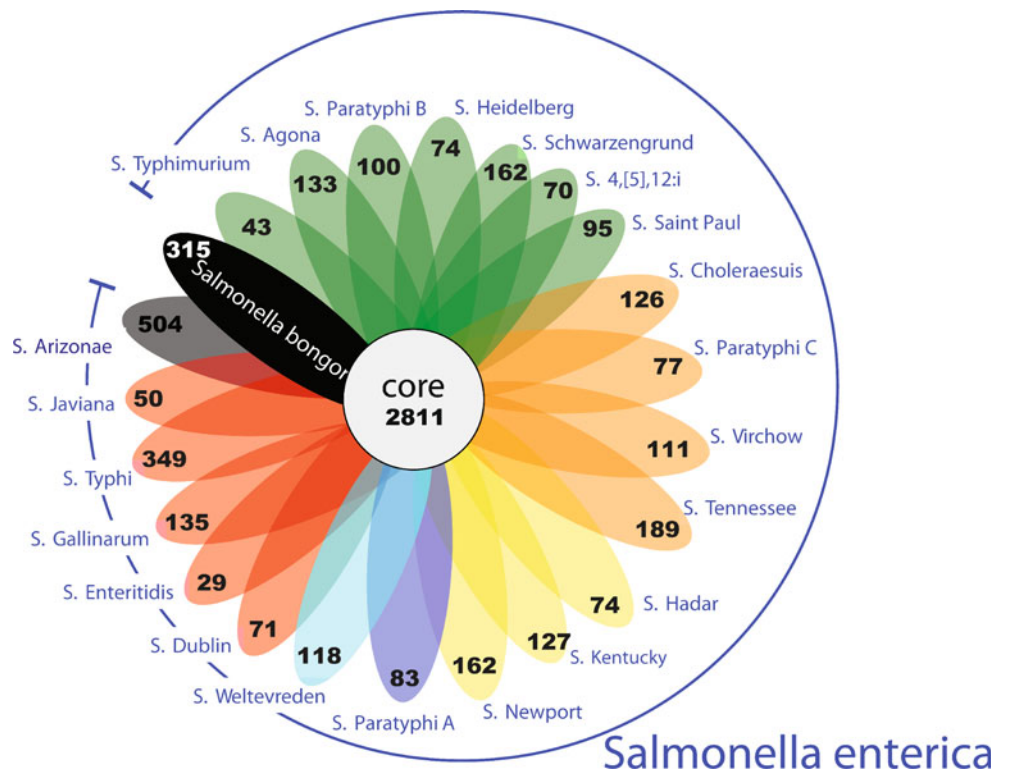


Figure 3 Pan- and core genome plot of 35 *Salmonella* strains. The red and blue lines show the progression in the core and pan genomes as more and more genomes are considered, while the columns indicate

the amount of novel gene families encountered. The color of the columns represents the serogroup as defined in Table 1 (see Table 1 for key)

Figure 4 Flowerplot of unique gene families in each *Salmonella* serovar. The figure presents the average number of gene families found in each genome as being unique to the serovar. Also given is the size of the core genome. The color of the petals represents the *S. enterica* serogroups (see Table 1 for key)



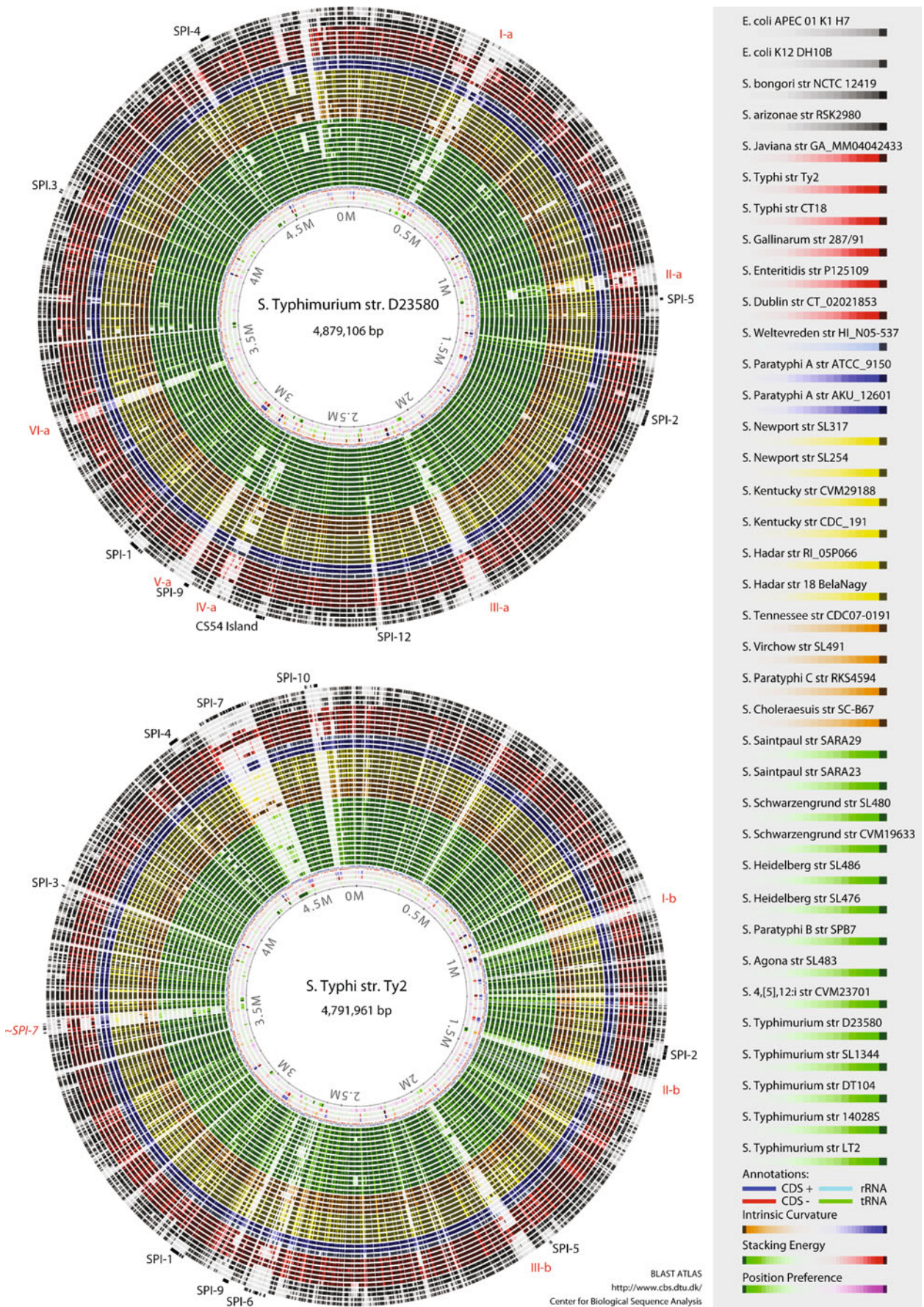


Figure 5 BLAST atlases of the 35 *S. enterica* and two *E. coli*. **a** BLAST atlas with *S. Typhimurium* str. D23580 as reference, representing the generalist strains. Six SPIs are marked on the atlas. **b** BLAST atlas with *S. Typhi* str. Ty2 as reference, representing a host-specific serovar. Four SPIs that were published along with the genome sequence are marked on the atlas. Generally, the *Salmonellas* show high homology with a few variable regions as SPIs. Also marked are several poorly characterized gene islands, I-a to VI-a and I-b to III-b (additional information in the [Supplementary Section](#))

total pan- and core genome, corresponding to the union and intersection of all genomes, respectively.

This approach differs from that of Tettelin et al. [30] in that we chose to rely on prodigal gene predictions as a method of coping with annotation biases. We also chose not to do permutations of the genomes as that would prevent us from visualizing the progression across serogroups. Even if the shape of the pan and core genome curves would be different for a different ordering of the genomes, the endpoints would remain the same, and thus the estimates of the size of the core and pan-genomes are unaffected by the order of the genomes.

Pan-genome Trees

The pan-genome tree is based on the absence or presence of each gene family in the serovars. The tree is constructed based on the Manhattan distance calculated from the BLAST matrix. Three different trees were constructed to show different groups of genes in the pan-genome. The “zero” tree counts all gene present only once as zero and the rest as one. The “shell” tree weighs genes that present in more number higher than genes in lower number. The “cloud” tree gives more weight to genes that present in lower number higher than genes in more number [35, 36].

BLAST Atlas

Comparisons from the BLAST were displayed using a reference genome in a BLAST atlas. All genes from the reference genome were aligned at the protein level by BLASTP with default settings against all other genomes. The presence and absence of genes are visualized in a circle, with increasing intensity of color representing greater similarity. The BLAST atlas also indicates properties of the DNA structure in the five innermost circles and the coding sequences (CDS), including rRNA and tRNA, in the following two circles [37].

The four innermost circles show structural parameters of the DNA. The position preference is used to measure the DNA flexibility, where dark purple means rigid DNA and dark green represents regions of anisotropic flexibility, that is, these regions with low-position preference (dark green on this scale) are likely not to be compacted by chromatin and could contain highly expressed genes [38, 39]. The

stacking energy is used to measure how readily the DNA will melt, where dark green means more stable and dark red that it will melt more easily. The intrinsic curvature describes how likely the DNA is to be curved. The dark orange indicates straight regions, whereas dark blue suggests strongly curved regions. Percent AT reveals regions having substantially different AT content compared to the rest of the genomes. Turquoise means low AT content and red means high AT content [40].

Identification of Gene Islands Across Genomes

GenBank entries for all SPIs listed for *S. enterica* in the Pathogenicity Island Database (PAI DB) were downloaded [41] and subjected to re-annotation using Prodigal with a training template constructed from the complete genomes [25]. The sequences of all proteins identified by Prodigal were subsequently aligned against all the Prodigal proteomes of all *Salmonella* in Table 1 to determine the absence or presence for each SPI in each genome. The identity score from the best match reported by BLASTP for each SPI protein was multiplied by the ratio of the alignment length to the total sequence length and averaged for all proteins in each SPI to arrive at an overall identity for each island. The island scores were clustered in both dimensions using the complete linkage method for hierarchical clustering available in the R software package [42].

Results and Discussion

The genomes of all fully sequenced *Salmonella* strains were compared and analyzed (Table 1). Observations on the amount of annotated genes in *Salmonella* revealed striking differences, particularly for *S. Typhi*, where the total number of reported genes for some genomes was as much as twice that of the average of all genomes with a corresponding decrease in the average gene length. Such biases, arising from differences in the methods by which the genomes were annotated and/or the data quality, lead to the accumulation of errors as more and more genomes are compared. To investigate this, all 45 initial genomes were subjected to de novo gene finding using two previously published gene finders: EasyGene [23, 24] and Prodigal [25]. The results were compared to the original annotations and while EasyGene generally displayed good performance, then for certain genomes the number of genes estimated was unrealistically low. A probable cause being that the pre-trained model upon which Easygene relies was insufficient to describe these. Prodigal has no such reliance and gave more consistent and believable genome sizes [data shown in [Suppl. Section](#)]. All genomes were then subjected to standardized gene finding using Prodigal.

Since more than half the genome sequences were not completely assembled, some of them being in thousands of contigs or more, a quality score described in Chain et al. 2009 [43] was calculated for all the genome sequences and is given in Table 1. The quality score ranges from 1 to 6, where 1 is described as finished and 6 as a standard draft. Based on this quality score and on the number of contigs, ten of the *S. Typhi* strains were excluded from most of this analysis (strains 404ty, AG3, E00-7866, E01-6750, E02-1180, E98-0664, E98-2068, E98-3139, J185, and M223). This left 35 genomes for the rest of the analysis

Pairwise Comparisons

The relation between the different genomes showed a conservation of the gene families between any two *Salmonella* isolates to be above 65% while the homology

of the gene families within each genome was generally less than 5% (Fig. 1). Similar comparisons within *E. coli* genomes show considerably more variation, with less than half the genes conserved between some *E. coli* strains [34]. We use the term “gene family” to describe a collection of copies of the same gene identified from different genomes or occasionally from duplication within the same genome. It is a process associated with a small, but unavoidable, degree of error. The construction of gene families is described in the “Materials and methods” section.

For most strains, a greater degree of homology was observed within the serovars. This is particularly visible in the *S. Typhimurium* strains and the monophasic strain 4, [5],12:i- (darkly shaded region at the bottom of Fig. 1); the only documented difference between these strains is that the latter either lacks the entire phase 2 antigen gene *fljB* or contains partial deletions in *fljB* and an adjacent gene *hin*

Table 2 Salmonella pathogenicity islands used in this study, obtained from the pathogenicity island database

PAI ^a	Host strain	Insertion site	Accession	Size (kb)
SPI-1_CholeraesuisSC-B67	<i>S. Choleraesuis</i> SC-B67	<i>fhIA/mutS</i>	NC_006905_P5	43.5
SPI-1_TyphiCT18	<i>S. Typhi</i> CT18	<i>fhIA/mutS</i>	NC_003198_P5	41.9
SPI-1_TyphiTy2	<i>S. Typhi</i> Ty2	<i>fhIA/mutS</i>	NC_004631_P2	41.9
SPI-1_TyphimuriumLT2	<i>S. Typhimurium</i> LT2	<i>fhIA/mutS</i>	NC_003197_P3	44.3
SPI-2_CholeraesuisSC-B67	<i>S. Choleraesuis</i> SC-B67	<i>tRNA-val</i>	NC_006905_P3	41.8
SPI-2_TyphiCT18	<i>S. Typhi</i> CT18	<i>tRNA-val</i>	NC_003198_P3	41.6
SPI-2_TyphiTy2	<i>S. Typhi</i> Ty2	<i>tRNA-val</i>	NC_004631_P1	41.6
SPI-2_TyphimuriumLT2	<i>S. Typhimurium</i> LT2	<i>tRNA-valV</i>	NC_003197_P2	40.1
SPI-3_Dublin	<i>S. Dublin</i>	<i>tRNA-selC</i>	AY144490	10.1
SPI-3_CholeraesuisSC-B67	<i>S. Choleraesuis</i> SC-B67	<i>tRNA-selC</i>	NC_006905_P6	12.8
SPI-3_TyphiCT18	<i>S. Typhi</i> CT18	<i>tRNA-pro</i>	NC_003198_P7	16.9
SPI-3_TyphimuriumLT2	<i>S. Typhimurium</i> LT2	<i>tRNA-selC</i>	NC_003197_P4	16.6
SPI-4_CholeraesuisSC-B67	<i>S. Choleraesuis</i> str. SC-B67	<i>ssb/soxSR</i>	NC_006905_P7	26.7
SPI-4_TyphiCT18	<i>S. Typhi</i> CT18	<i>ssb</i>	NC_003198_P8	23.4
SPI-4_TyphimuriumLT2	<i>S. Typhimurium</i> LT2	<i>ssb/soxSR</i>	NC_003197_P5	23.4
SPI-4_TyphimuriumLT2_2	<i>S. Typhimurium</i> LT2	<i>ssb/soxSR</i>	AF060869	27.3
SPI-4_TyphimuriumST4-74	<i>S. Typhimurium</i> ST4/74	Not published	AJ576316	24.7
SPI-5_Dublin	<i>S. Dublin</i>	<i>tRNA-serT</i>	AF060858	9.7
SPI-5_TyphimuriumLT2	<i>S. Typhimurium</i> LT2	<i>tRNA-serT</i>	NC_003197_P1	9.1
SPI-6_TyphiCT18	<i>S. Typhi</i> CT18	<i>tRNA-asp</i>	NC_003198_P1	58.7
SPI-7_TyphiCT18	<i>S. Typhi</i> CT18	<i>tRNA-phe</i>	NC_003198_P9	133.6
SPI-7_TyphiTy2	<i>S. Typhi</i> Ty2	<i>tRNA-phe</i>	NC_004631_P3	131.7
SPI-8_TyphiCT18	<i>S. Typhi</i> CT18	<i>tRNA-phe</i>	NC_003198_P6	6.9
SPI-9_TyphiCT18	<i>S. Typhi</i> CT18	Not published	NC_003198_P4	15.7
SPI-10_TyphiCT18	<i>S. Typhi</i> CT18	<i>tRNA-leu</i>	NC_003198_P10	32.9
SPI-11_CholeraesuisSC-B67	<i>S. Choleraesuis</i> SC-B67	Gifsy-1 prophage	NC_006905_P2	15.7
SPI-12_CholeraesuisSC-B67	<i>S. Choleraesuis</i> SC-B67	<i>tRNA-pro</i>	NC_006905_P4	11.1
CS54island_TyphimuriumATCC14028	<i>S. Typhimurium</i> ATCC14028	<i>xseA/yfgK</i>	AF140550	25.3
SGI1_TyphimuriumDT104	<i>S. Typhimurium</i> DT104	<i>thdF</i>	AF261825	47.7

^a Downloaded from http://www.gem.re.kr/paidb/browse_pais.php?m=p#Salmonella%20enterica

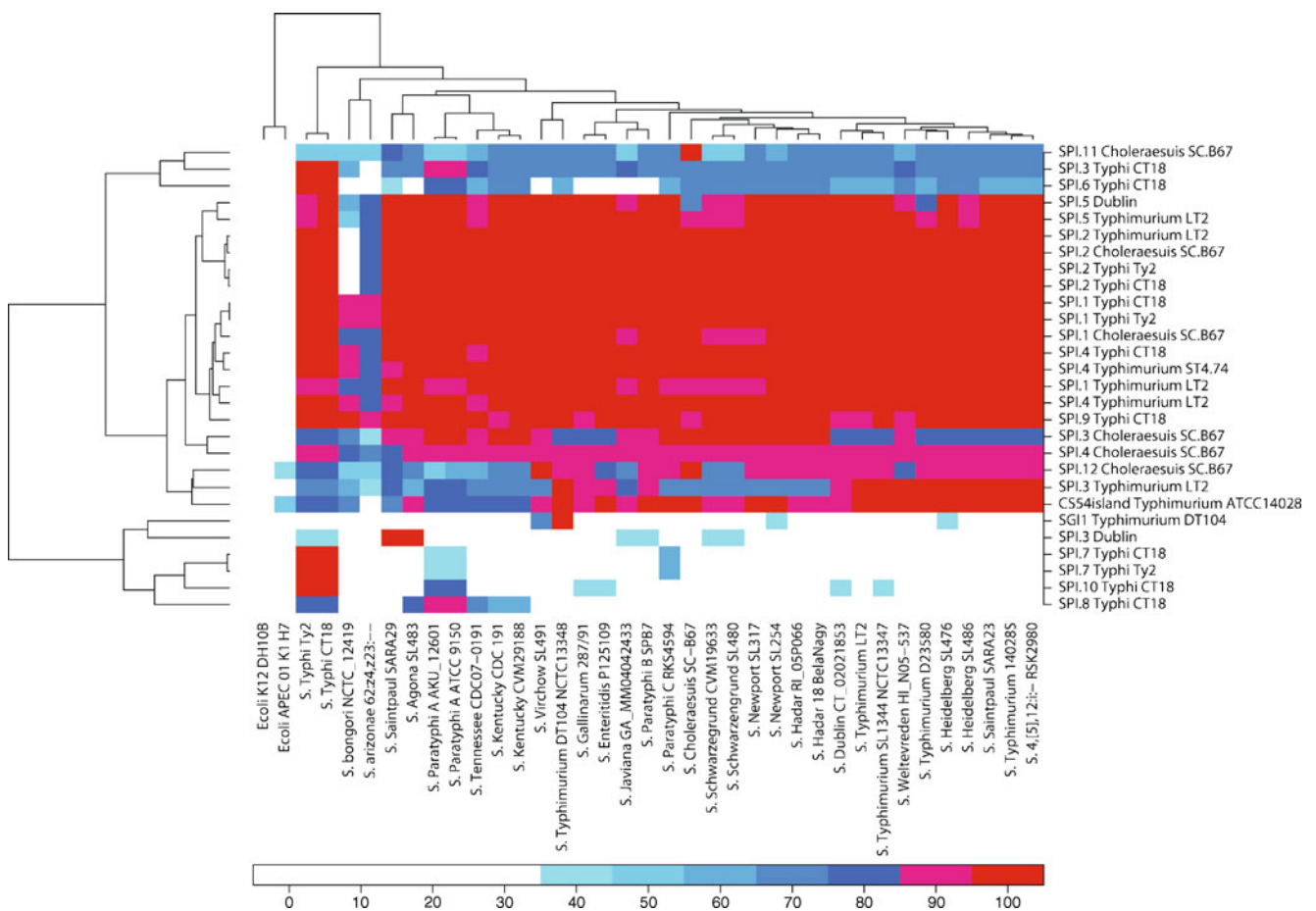


Figure 6 Heatmap of SPI conservation. SPIs from the Pathogenicity Island Database were aligned against genomes, and the average identity of all proteins in each SPI was hierarchically clustered in two dimensions. The vertical axis lists the SPIs while the genomes are located horizontally

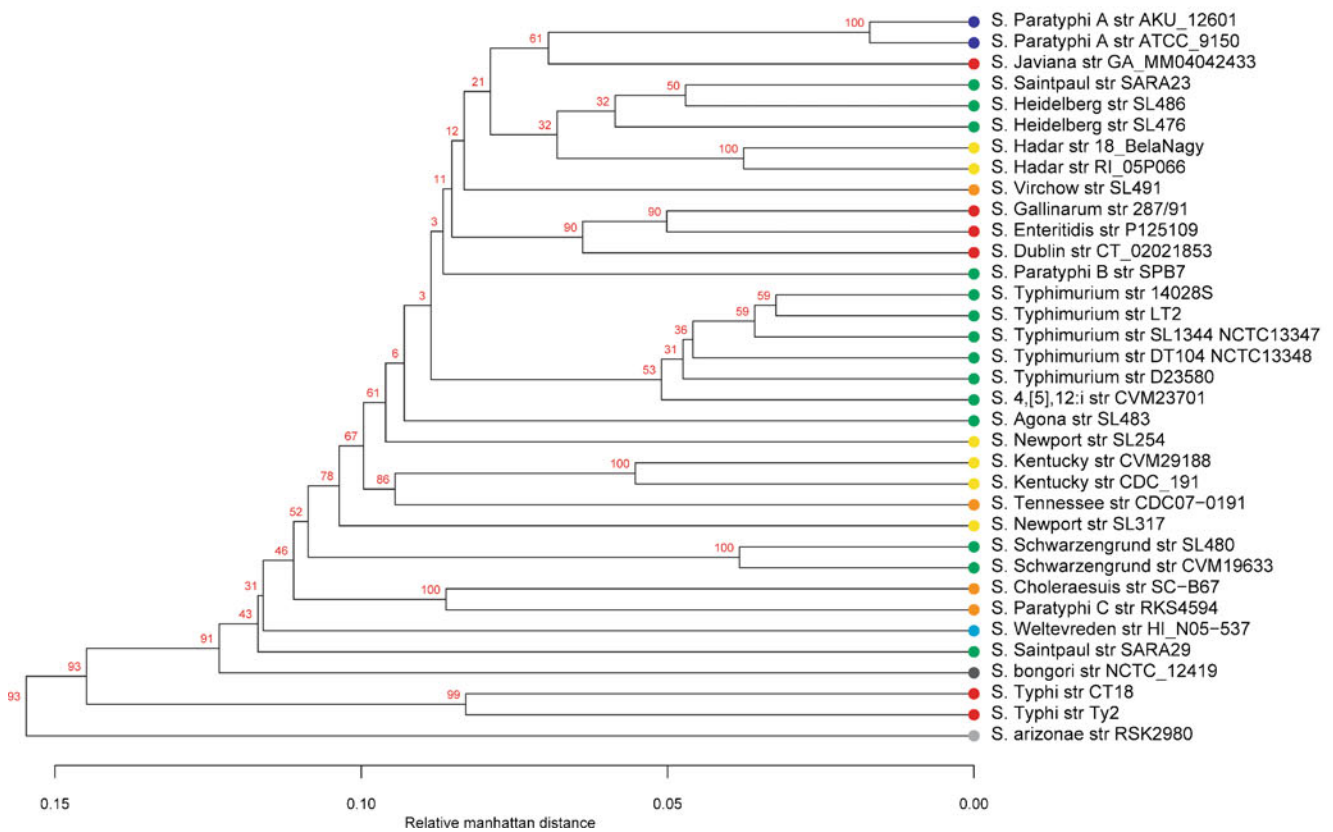
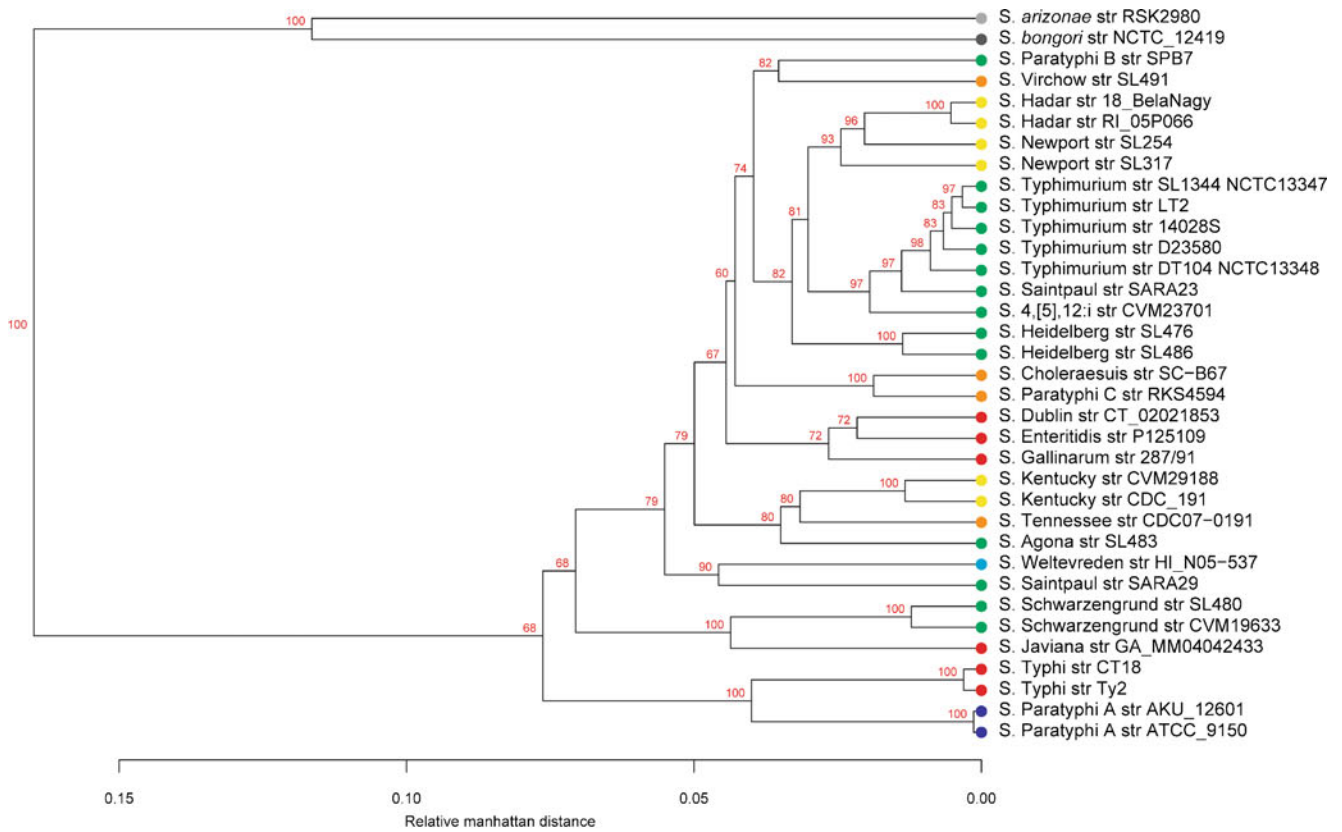
[44–46]. It is noteworthy that *S. Dublin* str. CT_02021853, *Salmonella* Enteritidis str. P125109, and *Salmonella* Gallinarum str. 287/91 (upper right in Fig. 1) display a higher degree of gene family homology than the norm for cross-serovar comparisons. Furthermore, *Salmonella* Saintpaul str. SARA23 stands out by displaying a relatively high degree of similarity to most other strains in cross-serovar comparisons. A similar behavior was not observed for *S. Saintpaul* str. SARA 29; however, results observed for that genome are marred and brought into doubt by a poor quality score of 5 for the sequence.

Evolutionary Relationships

16S rRNAs are functionally conserved and relatively long, making them ideal for phylogenetic studies. Two phylogenetic trees were constructed based on 16S rRNA and are shown in Fig. 2. The sequences were identified using RNAmmer [26] which was not able to find sufficiently high-quality sequences for all draft sequences (due to the difficulty in assembling large repeated regions like the

rRNA operons from short read lengths). This makes the 16S rRNA comparison between all the strains in this study impossible, but it was possible to find reliable, full-length 16S rRNA genes in 27 of the *Salmonella* strains.

Studies of the evolutionary relationship of *Salmonellae* within *Enterobacteriaceae* have defined the *Salmonella* genus and the division into the two species [47, 48]. The relationship between the *Salmonellae*, on subspecies and species level, has been extensively studied based on MLEE [49], microarray [50], and four housekeeping genes [51]. Figure 2 shows a 16S rRNA phylogenetic tree of 20 enterobacteria giving a good description of the relationship of the different genera, as well as a tree based on the 16S rRNA of the sequenced genomes within the *Salmonella* genus. Although there is some overlap between the 16S rRNA similarity and serotype within the genus, the correlation is far from complete. Another interesting observation is that strains known for being host specific—*S. Dublin*, *S. Gallinarum*, and *S. Choleraesuis*—are grouped together with strains known for having a broader range of hosts, e.g., *S. Typhimurium* and *S. Enteritidis*, again



◀ **Figure 7** Pan genome family trees based on the absence and presence of gene families. In the *upper panel*, the tree is constructed by weighting gene families higher the more genomes they are present in. The *lower panel* shows the opposite scheme where genes present in smaller numbers are weighted higher. The serogroup colors are defined in Table 1

showing that host specificity and the degree of invasiveness is not necessarily linked to evolutionary relationship.

The human-restricted serovars *S. Typhi* and *S. Paratyphi A* show high proteome similarity in Fig. 1, but in the 16S rRNA relationship, the *S. Paratyphi A* are grouped distant from the rest of the *Salmonella* subsp. *enterica* including the *S. Typhi* genomes, which are found with the generalist pathovar *Salmonella* Javiana. The two non-specific paratyphoid pathovars *S. Paratyphi B* and *S. Paratyphi C* neither show gene homology nor much evolutionary relatedness in 16S similarity to the *S. Paratyphi A*. Interestingly, *S. Paratyphi C* consistently cluster with *S. Choleraesuis*, both in protein similarity and 16S rRNA similarity. Indeed, a recent study has shown that *S. Paratyphi C* is likely to have diverged from *S. Choleraesuis* even though the serovars differ in the host they infect [52].

During adaptation to a new niche, changes in the *Salmonella* genome can occur, for example by horizontal gene transfer, rearrangement, and duplication, but also by gene excision and pseudogene formation [53]. Due to this, an analysis of their gene similarity at different levels which includes differences and similarities in the SPIs, is better at describing the relationship between the strains with different host specificities.

The *Salmonella* core genome

The core genome consists of all the gene families present in all the *Salmonella* strains, whereas the pan-genome consists of all gene families found in any of the *Salmonella* strains. A plot of the evolution of the pan- and core genome as more and more genomes are considered is seen in Fig. 3. The core genome of 35 sequenced *Salmonella* is 2,811 gene families, and the pan-genome is 10,015; the corresponding numbers within the *Salmonella* subsp. *enterica* are 3,224 and 9,161. The first genome under consideration was *S. Typhimurium* str. LT2, and when the second genome, *S. Typhimurium* str. D23580 is added, the size of the pan-genome grows slightly while the core genome decreases. This trend continues as more and more strains are added reaching a milestone first with the addition of a second serovar and again when *Salmonella* subsp. *arizonae* is added.

While the exact size of the pan- and core genome is dependent on the amount of genomes under analysis as well as the chosen methodology, it is clear that *Salmonella* exhibits what has tentatively been called a “closed” pan-

genome structure [54]. This is in contrast to the close relative *E. coli* which clearly displays an open pan-genome structure [55], but congruent with other pathogens such as *Yersinia pestis*, *Listeria*, or *Campylobacter jejuni* [35, 56, 57]

In most cases, the addition of a second or third isolate of a given serotype has much less impact than the addition of the first, although exceptions exist. Most notably, the addition of a genome which is fragmented and incomplete affects the size of the core and pan-genome proportionally more than the addition of a completed genome. For example, consider the fragmented *S. Saintpaul* str. SARA29 and the proportional increase in novel gene families observed for it relative to *S. Saintpaul* str. SARA23. This can be accurate—while the sharing of serotype suggests a similarity for the entire proteome, it need not be the case—two strains of the same serotype can, potentially, be very different. Another explanation exists, however, since incomplete genomes may not always contain the full sequence for genes otherwise present, and such truncated genes might erroneously be identified as novel gene families.

We identified the average number of gene families unique to each serotype, encountered in each genome and visualized the result in Fig. 4. The analysis shows that the average number of distinct gene families varies considerably from serotype to serotype, but is at least weakly correlated to genome size (Table 1). Amongst the *S. enterica*, serovar *S. Typhi* clearly stands out having the highest number of unique gene families; this is likely due to the presence of several large pathogenicity islands characteristic to the serovar [19, 58]. The smallest number of unique gene families was found in serovar *S. Enteritidis* which is among the smaller *Salmonella* genomes, although *S. Javiana* is the smallest. Interestingly, the *Salmonella* subsp. *arizonae* genome has almost twice the number of unique genes compared to *S. bongori*, although it remains a subspecies of *S. enterica* while the latter is recognized as a separate species.

BLAST Atlas of *S. Typhimurium* D23580 and *S. Typhi* Ty2

The BLAST atlas is a visualization of gene conservation in a number of species against a single reference genome (Fig. 5). The BLAST atlas thus shows which genes from the reference genome are present in the other genomes. As references, we selected the genome of the pathogens *S. Typhimurium* str. D23580 and *S. Typhi* str. Ty2 because they are human-adapted and human specific, respectively. Also, a recent study did a thorough analysis of SPIs in *S. Typhi* CT18 with the generalist *S. Typhimurium* LT2 [14]. The proteomes of the *Salmonella* and *E. coli* strains were aligned against the reference genomes illustrating similarity

by color intensity. The general picture is that the *Salmonella* strains are highly conserved, with most genetic variation being concentrated in specific variable regions, as can be seen in Fig. 5.

The *E. coli* genomes show the lowest number of BLAST hits to the reference *Salmonellas*, in particular little homology exists in the regions containing the different SPIs which are important for virulence in *Salmonella*. Between the *Salmonella* genomes, the conservation of the SPIs was generally high but with notable differences, particularly for *S. Typhi* str. Ty2 where SPI-7, the characteristic *S. Typhi* pathogenicity island, is clearly unique to that serovar. SPI-7 has previously been reported in both serovars *S. Paratyphi C* and *S. Dublin* [59–61], but our analysis finds only fragments of SPI-7 in these serovars, not the complete island. In the *S. Typhi* str. Ty2 genome, a part of SPI-7 was found duplicated, marked in Fig. 5 by the red SPI-7 label. This duplicated part is the principle fragment of SPI-7 conserved in *S. Dublin* but not in *S. Paratyphi C* suggesting that the island may consist of several independently mobile parts.

Most of the SPIs have been under intense study. SPI-1 and SPI-2 encode type III secretion systems [17]. T3SS of SPI-1 is important for the penetration of intestinal epithelium, whereas the T3SS of SPI-2 is also considered important after access to macrophages [62, 63], although not all studies on its role in macrophage survival are congruent [64]. SPI-3 contains ten ORFs in six transcriptional units and encodes proteins with little known functional relation to each other. The most important is the Mg²⁺ transporter, a putative ToxR regulatory protein and a putative AIDA-I adhesion [65]. The function of SPI-4 is mostly unknown, but has been shown in a mouse model to contribute to intestinal inflammation [66]. The SPI-4 encodes a type I secretion system, T1SS, and a substrate protein of the T1SS, SiiE [67]. SPI-5 was first located in *S. Dublin* and is mainly composed of effector proteins [68].

In addition to the established SPIs that are present in most members of the *Salmonella* subsp. *enterica*, the atlases also reveal several genomic regions which are absent from most or all *Salmonella* genomes. These regions are gene islands likely of viral origin. For example, the region marked “I-a” is flanked by several genes encoding integrase/recombinase-like proteins and contains several phage-related proteins. Similar images can be seen for the regions marked II-a to VI-a. In all cases, though, the majority of the proteins in the inserts are without any well-described functions, which makes the impact on the host difficult to gauge. This may be “junk DNA,” and their conservation in certain isolates of *Salmonella* can be attributed to the proliferation of the responsible phages. Alternatively, some of these proteins may confer selective

advantages for the host, thus providing an evolutionary incitement for their retention.

Distribution of SPIs across genomes

We extracted all *S. enterica* genomic islands from the Pathogenicity Island Database (PAI DB) (Table 2) [41]. The proteomes of each island were aligned against the proteomes of the species in Table 1, and the average identity for each island was clustered in a heat map (Fig. 6).

Since many SPIs were historically first identified as being present in *Salmonella* but absent in *E. coli* (strain K-12) [17], it is not surprising that no SPI proteins were found in *E. coli* K-12. Because of the diversity within the *E. coli* species, other non-K12 strains might potentially contain SPI proteins, but for the APEC strain at least, no significant similarity was found. Even within *Salmonella* many SPI proteins are found exclusively within *Salmonella* subsp. *enterica* and not in *S. bongori* or *Salmonella* subsp. *arizonae* which supports the hypothesis that these islands are an integral part of what gives *Salmonella* subsp. *enterica* its genetic identity. The same can be said for serovar *S. Typhi* where the exclusivity of the characteristic typhoid SPIs is clearly seen.

The SPIs appear very well conserved despite being isolated from different serovars. The different versions of SPI-1 in particular, cluster perfectly together, but also SPI-2 and SPI-4 follow identical distributions. Only SPI-3 is in discord; the four different versions of SPI-3 are clearly not identical copies of the same island, as illustrated by the leftmost dendrogram which divides the islands into at least three distinct versions. Most apparent is the SPI-3 isolated from *S. Dublin*, which clusters together with otherwise Typhi-specific islands. It is clearly separate from the other versions of SPI-3 and shares no homology with them. The island is also present in only very few genomes. The *S. Typhi* CT18 SPI-3 is also a distinct version of SPI-3 found within the two genomes of the serovar, with partial alignments to non-Typhi genomes only. Unlike the *S. Dublin* SPI-3 which is an almost unique SPI-3; it consists of a core shared with the remaining two copies of SPI-3 and a part which is unique. It is the shared core which aligns with the non-Typhi genomes, while the unique part is found in *S. Typhi* alone. The remaining two copies of SPI-3 are much closer to each other. The SPI-3 *S. Typhimurium* str. LT2 is found with a perfect alignment in the other *S. Typhimurium*s and in *S. Heidelberg*, but only to a lesser degree in most other genomes, many of which instead show perfect conservation to the SPI-3 from *S. Choleraesuis*.

In all cases, the variance between the islands arises from certain specific proteins being either present or absent and not from general mutational drift. It is, however, unclear what the consequences for a given cell of having one version of SPI-3

as opposed to another, but could potentially impact the organism's pathogenicity quite profoundly.

There is a good correlation between the clustering of the topmost dendrogram and the serotype, but it is not perfect. For example, the antibiotic resistance island SG11 from *S. Typhimurium* str. DT104 appears to be more or less unique to that particular strain and causes it to cluster away from the other *S. Typhimurium*s. Another example is the SPI-3 *S. Dublin* originally identified in serotype *S. Dublin*, but here it was found only in *S. Agona* and *S. Saintpaul* str. SARA29 and appears completely absent in the sequenced *S. Dublin* str. CT_02021853. This is not an error; the SPI was identified from a different isolate of *S. Dublin* than the one which lies sequenced in GenBank. Rather, this emphasizes that the distribution of SPIs is not always linked to serotype.

Pan-genome Tree

Two dendrograms constructed from the overall genomic content in *Salmonella* are illustrated in Fig. 7 by weighing the presence of non-core gene families according to two different schemes. The upper panel in Fig. 7 shows a dendrogram where gene families are weighted higher the more strains they are present in, while the lower panel displays a tree made from weighing gene families higher the fewer genomes they are present in [36]. In general, the two representations illustrate the impact of the choice of method on what relations are observed.

The human-restricted serovars, *S. Paratyphi* A and *S. Typhi*, show close relation in the first dendrogram emphasizing genes present in most serovars, but when we give more weight to genes present in few strains, this image reverses and the two organisms become far apart. This is likely the result of SPI-7 being present only in *S. Typhi* which will be much more significant when rare genes are weighted the highest. In the two representations, the *S. Typhi* genomes have also changed orientation in relation to *S. bongori* and *Salmonella* subsp. *arizonae*, being more distantly related to the rest of *Salmonella* subsp. *enterica* than *S. bongori* when rare gene families are weighted the highest. The two different *S. Newport* serovars show more or less the same relative distance in both dendrograms, but cluster with *S. Kentucky* instead of *S. Hadar* when gene families present in few strains are weighed higher. The *S. Typhimurium* strains cluster together in both plots. The same can be seen for *S. Paratyphi* C and *S. Choleraesuis*, and for *S. Gallinarum*, *S. Enteritidis*, and *S. Dublin*.

Conclusion

A comparative genomic analysis of 35 *Salmonella* genomes with standardized gene findings provides insight into the

relationship between the different serovars as well as offering a glimpse into the relationship of *Salmonella* subsp. *enterica* to subsp. *arizonae* and *S. bongori*. Generally, the *Salmonellas* show fairly high similarity in protein sequences when visualized by the BLAST atlas or BLAST Matrix, where the identity between the genomes within *Salmonella* subsp. *enterica* ranges from 65% to 99%. Although exceptions exist, the pan-genome study shows that the addition of each new isolate of *S. enterica* reveals relatively few novel genes, and even fewer genes if an isolate of the same serotype has already been considered.

In general, the number of *Salmonella* “core genes” (2,800) seems relatively large, compared to other bacterial genera. For example, there are roughly a thousand core genes found in *E. coli*, in *Bacteroides*, and also in *Vibrio* genomes [31–33]. Similarly, the pan-genome size of *Salmonella* is smaller than that found for other genera, reflecting a less open pan-genome for *Salmonella*.

Many of the previously characterized pathogenicity islands in *Salmonella* were found throughout all genomes within *Salmonella* subsp. *enterica*, with notable exceptions such as SPI-6 and SPI-7 found only in serovar *S. Typhi*; SPI-3 seems to exist in several similar but distinct versions. The presence of these rare SPIs undoubtedly plays a substantial role in giving the host genomes their characteristic phenotypes. Further studies into the importance of these SPIs for host-specificity/preference of different serovars are needed.

In addition to the *Salmonella*-specific genomic islands (SPIs), there are other genome islands in *Salmonella* genomes, which are also found in other organisms. Many of these appear to be of viral origin, and are strain specific. Compared to *E. coli*, the pan-genome of *Salmonella* genome seems fairly static, and genomic islands, in particular SPIs could represent an important avenue for the evolution of the *Salmonella* genus.

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