Comparative Virulotyping of *Salmonella typhi* and *Salmonella enteritidis*

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**Abstract** Members of *Salmonella enterica* are important foodborne pathogens of significant public health concern worldwide. This study aimed to determine a range of virulence genes among typhoidal (*S. typhi*) and non-typhoidal (*S. enteritidis*) strains isolated from different geographical regions and different years. A total of 87 *S. typhi* and 94 *S. enteritidis* strains were tested for presence of 22 virulence genes by employing multiplex PCR and the genetic relatedness of these strains was further characterized by REP-PCR. In *S. typhi*, invA, prgH, sifA, spiC, sopB, iroN, sitC, misL, pipD, cdrB, and orfL were present in all the strains, while sopE, agfC, agfA, sefC, mgtC, and sefD were present in 98.8, 97.7, 90.8, 87.4, 87.4 and 17.2 %, of the strains, respectively. No *lpfA*, *lpfC*, *pefA*, *spvB*, or *spvC* was detected. Meanwhile, in *S. enteritidis*, 15 genes, *agfA*, *agfC*, *invA*, *lpfA*, *lpfC*, *sefD*, *prgH*, *spiC*, *sopB*, *sopE*, *iroN*, *sitC*, *misL*, *pipD*, and *orfL* were found in all *S. enteritidis* strains 100 %, followed by *sifA* and *spvC* 98.9 %, *pefA*, *spvB* and *mgtC* 97.8 %, and *sefD* 90.4 %. *cdrB* was absent from all *S. enteritidis* strains tested. REP-PCR subtyped *S. typhi* strains into 18 REP-types and concurred with the virulotyping results in grouping the strains, while in *S. enteritidis*, REP-PCR subtyped the strains into eight profiles and they were poorly distinguishable between human and animal origins. The study showed that *S. typhi* and *S. enteritidis* contain a range of virulence factors associated with pathogenesis. Virulotyping is a rapid screening method to identify and profile virulence genes in *Salmonella* strains, and improve an understanding of potential risk for human and animal infections.

**Keywords** REP-PCR · *Salmonella typhi* · *Salmonella enteritidis* · Virulotyping

**Introduction**

*Salmonella* spp. are important foodborne pathogens in humans and animals and pose significant public health concerns worldwide [1]. *Salmonella* establish an infection and cause illness through bacterially-expressed virulence factors interacting with host cells. *Salmonella* virulence factors play active roles in a broad range of pathogenic mechanisms, including adhesion, invasion, intracellular survival, systemic infection, fimbrial expression, antibiotic resistance, toxin production, and Mg$^{2+}$ and iron uptake [2, 3]. Many of these virulence factors are located in *Salmonella* pathogenicity islands (SPIs) and on plasmids [4–6]. At least 17 SPIs have been identified in different *Salmonella* serovars [7]. SPI-1 and SPI-2, which encode two separate type three secretion systems, TTSS-1 and TTSS-2, respectively, are the most prominent SPIs. SPI-1 encodes virulence genes responsible for invasion while SPI-2, which is absent in *Salmonella bongori*, encodes genes essential for systemic infection inside the host cells [2, 8]. Virulence plasmids encode genes for systemic disease in non-typhoid *Salmonella* serovars such as *Salmonella typhimurium*, *S. enteritidis*, *Salmonella dublin*, and *Salmonella choleraesuis*. On the other hand, *S. typhi* and