

Comparison of Genome Sequence of *Salmonella enterica* serovar Typhimurium LT2 with *Salmonella* Genome Sequences, and Genotyping of Salmonellae Using PCR

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The minimal number of genes of *Salmonella enterica* serovar Typhimurium LT2, which expected specific to *Salmonella*, was selected using the BLAST program. These selected 152 genes were compared with 11 genome sequences of *Salmonella* serovars including *Salmonella* subspecies I, IIIb and *S. bongori* (V), and clustered 17 groups based on comparison patterns. Representing each 17 group, total 38 primer sets were constructed and PCR was performed with various *Salmonella* strains to establish a comprehensive DNA-based scheme for identification of *Salmonella* subspecies and the major *Salmonella* serovars, which cause disease in human and domestic animals. Analysis of PCR patterns showed that *Salmonella enterica* subspecies I were critically divided from other subspecies and *Salmonella* strains belongs to subspecies I were clustered based on their serovars. In addition, the signature genes of *Salmonella*, *S. enterica* serovar Typhimurium and *Salmonella* subspecies I were suggested and evaluated using PCR. These results would apply to rapid and convenient method for identification of the *Salmonella* serovars attainable by non-specialized laboratories, and showed that the comparison of genome sequence has a potential application in epidemiologic and taxonomic study and characterization of *Salmonella*.