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Genotyping harboring a second flagellin gene of *Salmonella enterica* Serovar Typhi in Indonesia endemic areas

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The genome of *S. Typhi* is highly conserved. However, *S. Typhi* strains from Indonesia were reported that harbored, instead of the *S. Typhi* specific Hd flagellin gene, a mutant flagellin gene (Hj) with a deletion in the conserved region or that carried, as a second flagellin gene, the z66 or Ind flagellin gene. Flagella may function in several properties include motility, cell entry, immune evasion and sensing of environmental conditions. The z66 and Ind flagellin genes were detected in, respectively, 23.1% and 26.5% of 363 *Salmonella enterica* serovar Typhi blood culture isolates from typhoid patients in east Indonesia and are associated with severe illness characterized by apathy and stupor (relative risk, 2.48; 95% confidence interval, 1.17-5.27). Multi-locus variable-number tandem repeat analysis identified 89 genotypes. The proximate location in papua of the homes of patients infected with almost identical genotypes containing the z66 gene is consistent with vertical transmission of the gene to their progeny. A spatial clustering of five divergent genotypes harboring the Ind gene revealed its horizontal transmission. Evidence to show capacity of *S. Typhi* to express different flagella increases the risk for severe disease characterized by apathy and stupor is presented. Spatial cluster analysis of the homes of typhoid patients provided supportive evidence for the vertical spread of the z66 flagellin gene to the progeny of two closely related genotypes and for the transfer of the Ind flagellin gene to several only distantly related genotypes revealing ongoing horizontal transmission. Cluster analysis of distinct genotypes may also be used to look for major sources of transmission and carriers. However, the large diversity in genotypes shows that the number of carriers can be large.

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