

## **Virulotyping of *Salmonella enterica* subsp. *enterica* isolated from indigenous vegetables and poultry meat in Malaysia using multiplex-PCR.**

### **ABSTRACT**

The increased occurrence of *Salmonella* in local indigenous vegetables and poultry meat can be a potential health hazard. This study is aimed to detect the prevalence of twenty different virulence factors among *Salmonella enterica* strains isolated from poultry and local indigenous vegetables in Malaysia via an optimized, rapid and specific multiplex PCR assay. The assay encompasses a total of 19 *Salmonella* pathogenicity island genes and a quorum sensing gene (*sdiA*) in three multiplex reaction sets. A total of 114 *Salmonella enterica* isolates belonging to 38 different serovars were tested. Each isolate in under this study was found to possess up to 70% of the virulence genes tested and exhibited variable pathogenicity gene patterns. Reproducibility of the multiplex PCR assay was found to be 100% and the detection limit of the optimized multiplex PCR was tested with lowest detectable concentration of DNA 0.8 pg  $\mu$ l<sup>-1</sup>. This study demonstrated various *Salmonella* pathogenicity island virulence gene patterns even within the same serovar. This sets of multiplex PCR system provide a fast and reliable typing approach based on *Salmonella* pathogenicity islands, thus enabling an effective monitoring of emerging pathogenic *Salmonella* strains as an additional tool in *Salmonella* surveillance studies.

**Keyword:** Virulotyping; *Salmonella enterica*; *Salmonella* pathogenicity islands (SPIs); Multiplex PCR.