論 文 要 旨

Diversification of *Escherichia albertii* H-Antigens and Development of H-Genotyping PCR

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Escherichia albertii is a recently recognized human enteropathogen that is closely related to *Escherichia coli*. As *E. albertii* sometimes causes outbreaks of gastroenteritis, rapid strain typing systems, such as the O- and H-serotyping systems widely used for *E. coli*, will be useful for outbreak investigation and surveillance. Although an O-genotyping system has recently been developed, the diversity of *E. albertii* H-antigens (flagellins) encoded by *fliC* genes remains to be systematically investigated, and no H-serotyping or genotyping system is currently available. Here, we analyzed the *fliC* genes of 243 genome-sequenced *E. albertii* strains and identified 73 sequence types, which were grouped into four clearly distinguishable types designated *E. albertii* H-genotypes 1-4 (EAHg1-EAHg4). Although there was a clear sign of intraspecies transfer of *fliC* genes in *E. albertii*, none of the four *E. albertii* H-genotypes (EAHgs) were closely related to any of the 53 known *E. coli* H-antigens, indicating the absence or rare occurrence of interspecies transfer of *fliC* genes between the two species. Although the analysis of more *E. albertii* strains will be required to confirm the low level of variation in their *fliC* genes, this finding suggests that *E. albertii* may exist in limited natural hosts or environments and/or that the flagella of *E. albertii* may function in a limited stage(s) in their life cycle. Based on the *fliC* sequences of the four EAHgs, we developed a multiplex PCR-based H-genotyping system for *E. albertii* (EAH-genotyping PCR), which will be useful for epidemiological studies of *E. albertii* infections.