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Prevalence and Genetic Diversity of Human Diarrhoeagenic *Escherichia coli* Isolates by Multilocus Sequence Typing

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Highlights:

- The study facilitated an overall understanding of human DEC from worldwide.
- CC10 was the most widely distributed CC, comprising 276 isolates with 85 STs.
- *fumC* and *gyrB* sequence variation observed were more abundant than the other genes.
- The population structure of five common DEC pathotypes was highly diversified.
- Isolates with the same ST or CC were heterogeneous for different pathotypes.

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