Objectives: Shigella species and E. coli are very closely related and their differentiation is needed from a clinical and veterinary perspective. Shigella species are always considered pathogenic whereas E. coli can be either pathogenic or part of the commensal flora. Shigella spp and E. coli are to date difficult to distinguish using MALDI-TOF MS. Tedious and time-consuming biochemical and serological methods are conventionally used and their differentiation remains a diagnostic challenge. The objective of this study was to set up a simple MALDI TOF MS method that could be implemented routinely in the laboratory allowing to distinguish these closely related species.

Methods: In this study, 106 well characterized strains of Shigella and E. coli including the pathogenic serovar 0157 were used to acquire 400 MALDI TOF MS spectra using a simple extraction procedure. After processing of the spectra, a predictive identification model was built and discriminative peaks were identified. Data exploration was also performed using multi-dimensional scaling (MDS).

Results: An estimation of performance by cross-validation and data exploration via MDS showed that 100% of E. coli 0157 strains were well identified at the serogroup level. Non-0157 E. coli and the four Shigella species (S. boydi, S. dysenteriae, S. flexneri and S. sonnei) were identified to the species level in 82%, 89%, 90%, 100% and 95% of the cases, respectively. Several discriminative peaks allowing the differentiation of the species were also highlighted. The validation of the prediction model on an external dataset of 62 Shiga-toxin producing E. coli (STEC) strains from different serogroups (excluding 0157) showed that 100% of the strains could be identified to the species level. However, identification at the serogroup level was not possible.

Conclusions: This study showed that the closely related Shigella spp and E. coli can be distinguish at the species level using MALDI TOF MS. In this study, it was not possible to distinguish serogroups, with 0157 being the single positive exception. This finding could be of great importance in the management of outbreaks and in epidemiological and surveillance studies.