LC–QTOF-MS identification of porcine-specific peptide in heat treated pork identifies candidate markers for meat species determination

ABSTRACT

The purpose of this study was to identify porcine-specific peptide markers from thermally processed meat that could differentiate pork from beef, chevon and chicken meat. In the initial stage, markers from tryptic digested protein of chilled, boiled and autoclaved pork were identified using LCóQTOF-MS. An MRM method was then established for verification. A thorough investigation of LCóQTOF-MS data showed that only seven porcine-specific peptides were consistently detected. Among these peptides, two were derived from lactate dehydrogenase, one from creatine kinase, and four from serum albumin protein. However, MRM could only detect four peptides (EVTEFAK, LVVITAGAR, FVIER and TVLGNFAAFVQK) that were consistently present in pork samples. In conclusion, meat species determination through a tandem mass spectrometry platform shows high potential in providing scientifically valid and reliable results even at peptide level. Besides, the specificity and selectivity offered by the proteomics approach also provide a robust platform for Halal authentication.