Short chain fatty acids (SCFA) are end-products of intestinal bacterial fermentation. The concentrations of fermentation metabolites are closely related to the microbial activity that occurs in various digestive compartments. The fermentation products may vary qualitatively and quantitatively, especially within the colon. The Simulator of the Human Intestinal Microbial Ecosystem (SHIME), an *in vitro* dynamic and multicompartment model of the human intestinal tract, can be adapted to mimic the piglet gastrointestinal tract. In this context, a quantitative method, based on solid phase microextraction gas chromatography coupled to mass spectrometry (SPME–GC–MS), was developed for the determination of seven short chain fatty acids, *i.e.* acetic, propionic, butyric, isobutyric, valeric, isovaleric and hexanoic acids, in samples coming from this experimental *in vitro* gastrointestinal model. The advantage of the SPME-GC–MS technique is that the seven compounds could be determined in a single run, after a simple and rapid sample treatment, without any other extraction than the automatic SPME. The developed method was validated in accordance to the European and US FDA guidelines and showed good specificity/selectivity. In addition, limits of detection and quantification ranged from 8 to 72 mg L^{-1} and from 16 to 144 mg L^{-1}, respectively. Two internal quality control samples spiked at different concentrations were analyzed to assess the trueness of the developed method, which ranged between 97.7 and 122.4% of the expected value, for the seven compounds analyzed. The method was successfully applied to twenty samples coming from a gastrointestinal model, with different inocula. The developed method might be used as a general method for measuring SCFA in biological samples.

Development of an analytical method to detect short-chain fatty acids by SPME-GC–MS in samples coming from an *in vitro* gastrointestinal model

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