Identification of livestock faecal contamination in surface waters using chemical and microbiological tools

Cattle and pig manure may contain pathogenic micro-organisms that can be transferred to soil through spreading on fields and thence to surface water. Such faecal pollution may pose risks to human health, especially in sensitive areas which support recreational shellfish harvesting, swimming and other uses where the public may come into direct contact with the water. Furthermore, the new European Directive on bathing waters (2006/7 /CE) requires the establishment of bathing water profiles, which require identification of sources of pollution. As the bacteria currently monitored to assess faecal pollution (E. coli, faecal coliforms and enterococci) do not distinguish between faecal pollution of water from animal and human sources, host-specific markers would be useful for the identification of faecal pollution. Recently, the concept of "Microbial source tracking" has been proposed (Scott et al., 2002). It includes biological and chemical methodologies that could be used to identify the dominant sources of faecal contamination in surface waters. Among specific markers, steroids, intensity peaks and their ratios of three-dimensional fluorescence excitationâ'emission matrix (3D-EEM) spectroscopy, F+ RNA bacteriophages (FRNAPH) genotypes, host specific Bacteroidales and Lactobacillus appear to be interesting tools to distinguish human from animal faecal pollution (Leeming et al., 1996, Seurinck et al., 2005, Blanch et al., 2006; Mieszkin et al., 2009, Naden et al., 2009, Marti et al., 2010). The aim of this study was to compare the suitability of chemical and microbiological markers to identify farm livestock sources of faecal contamination found in the environment. Four types of markers were tested: (i) the ratio of coprostanol/coprostanol+24-ethylcoprostanol (R1, expressed in percentage) and sitostanol/coprostanol (R2), (ii) tryptophan and fulvic-like fluorescence ratios (Bio/Geo and (V+VI/III)), (iii) genotypes of F-specific RNA bacteriophages (animal genotypes I and IV and human genotypes II and III) and (iv) bacterial markers belonging to Bacteroidales (human-specific HF183, ruminant-specific Rum-2-Bac and pig-specific Pig-2-Bac markers) and to the pig-specific Lactobacillus amylovorus.

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