



Development of microbial and chemical MST tools to identify the origin of the faecal pollution in bathing and shellfish harvesting waters in France

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Résumé en anglais	<p>The microbiological quality of coastal or river waters can be affected by faecal pollution from human or animal sources. An efficient MST (Microbial Source Tracking) toolbox consisting of several host-specific markers would therefore be valuable for identifying the origin of the faecal pollution in the environment and thus for effective resource management and remediation. In this multidisciplinary study, after having tested some MST markers on faecal samples, we compared a selection of 17 parameters corresponding to chemical (steroid ratios, caffeine, and synthetic compounds), bacterial (host-specific Bacteroidales, Lactobacillus amylovorus and Bifidobacterium adolescentis) and viral (genotypes I-IV of F-specific bacteriophages, FRNAPH) markers on environmental water samples (n = 33; wastewater, runoff and river waters) with variable Escherichia coli concentrations. Eleven microbial and chemical parameters were finally chosen for our MST toolbox, based on their specificity for particular pollution sources represented by our samples and their detection in river waters impacted by human or animal pollution; these were: the human-specific chemical compounds caffeine, TCEP (tri(2-chloroethyl)phosphate) and benzophenone; the ratios of sitostanol/coprostanol and coprostanol/(coprostanol+24-ethylcopstanol); real-time PCR (Polymerase Chain Reaction) human-specific (HF183 and B. adolescentis), pig-specific (Pig-2-Bac and L. amylovorus) and ruminant-specific (Rum-2-Bac) markers; and human FRNAPH genogroup II.</p>

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