Title

Development of a Host Species-Specific Metabolic Fingerprint Database of Faecal Indicator Bacteria To Identify The Sources of Fecal Contamination in Surface Waters

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Abstract

A metabolic fingerprint database was used to trace the sources of faecal indicator bacteria in surface waters. The database comprising of enterococci and *Escherichia coli* from 9 animal species (i.e. cattle, horses, dogs, pigs, sheep, deer, kangaroos, ducks and chickens) and human (via septic tanks). In all, 526 enterococci biochemical phenotypes (BPTs) and 530 *E. coli* BPTs were obtained from 4057 enterococci and 3728 *E. coli* isolates tested. Of these 295 enterococci BPTs and 273 *E. coli* BPTs were unique to individual animal species. The remaining 231 enterococci BPTs and 257 *E. coli* BPTs were associated with multiple animal species. The database was used to trace the sources of faecal contamination in Eudlo Creek, Sunshine Coast region, Qld presumed to be contaminated by some of the above animal species. The mean diversity of enterococci (Di= 0.76 ± 0.05) and *E. coli* (Di= 0.88 ± 0.04) was high (maximum 1) in creek water samples indicating diffuse sources of faecal pollution. Altogether, 248 enterococci BPTs and 282 *E. coli* BPTs were found in water samples. In all, 71% of enterococci BPTs and 67% of *E. coli* BPTs from water samples were correctly classified as human and animals. Among enterococci, 26 (10%) BPTs were identical to humans and 152 BPTs (61%) were identical to animals referred to as animal-BPTs. Among *E. coli*, 36 (13%) BPTs were identical to humans and 151 (54%) BPTs were identical to animals. Of the animal-BPTs, 101 (66%) enterococci BPTs and 93 (62%) *E. coli* BPTs were also unique to individual animal groups. On the basis of these unique enterococci BPTs, chickens contributed 14% of contamination followed by humans (10%), dogs (7%) and horses (6%). For *E. coli*, humans contributed 13% of contamination followed by ducks (9%), cattle (7%) and chickens (6%). The developed metabolic fingerprint database was able to distinguish between human and animal sources as well as among animal species in the studied catchment. Both faecal indicator bacteria used in this study was in close agreement in terms of percentage contribution from individual animal species.