Title

Population Similarity Analysis of Faecal Indicator Bacteria: A Predictive Tool to Trace the Sources of Faecal Contamination in Surface waters

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Abstract

A biochemical fingerprint method (the PhPlate system) was used to type and compare faecal indicator (i.e. enterococci and *Escherichia coli*) bacterial populations from 9 animal species human (via septic tanks) and compared with the same indicator bacterial populations from surface water samples during the wet and dry season in order to rapidly predict the dominant sources(s) of faecal contamination in surface waters. Eudlo Creek, Sunshine Coast, Qld was chosen as the site of investigation. The number and diversity (di) of enterococci and *E. coli* in the creek significantly increased during the wet season with regards to dry season. In general, enterococci populations from water samples showed higher population similarity with those found in animals. A higher population similarity for both faecal indicator bacteria was observed in wet season with regards to dry season. For both indicators, highest population similarities were observed in dogs followed by horses, cattle and kangaroos. In contrast, a low population similarity was observed for both faecal indicator bacteria from humans with water samples during the wt and dry season. The results indicated that analysis of enterococci populations has advantages over *E. coli* with regards to predict the dominant sources(s) of faecal contamination in the studies creek. We conclude that population similarity analysis as used in this study can be used to predict the sources of faecal contamination in surface waters.