Comparison of the efficacy of an existing versus a locally developed metabolic fingerprint database to identify non-point sources of faecal contamination

Warish Ahmed, Jack Tucker, James Harper, Ron Neller and Mohammad Katouli Faculty of Science, Health and Education, University of the Sunshine Coast, Maroochydore DC, Qld

Summary

We developed a large metabolic fingerprint database from enterococci and *Escherichia coli* by carefully testing 4057 enterococci and 3728 *E. coli* isolates from 10 host groups. This database proved to be highly representative and identified the sources of faecal contamination when applied locally. In order to identify whether this database can be used in other catchments, we initially assessed the representativeness and the stability of the database by comparing it to isolates that were external to the database. We then compared the efficacy of our large database with a locally developed one to identify sources of faecal contamination in a costal lake.

Methodology

1 A biochemical fingerprinting method was used to develop both the existing database (from Eudlo Catchment) and the local database (from Currimundi Catchment).



3 The host groups included humans, cattle, horses, pigs, sheep, chickens, ducks, deer, kangaroos and dogs.

4 BPTs of host groups from both the existing database and the local database were compared to create a merged database. The efficacy of all the databases were separately evaluated in ecological study.



6 Representativeness and stability of the existing database were assessed by comparing with isolates that were external to the database.

Aim

To assess the representativeness and stability of a large existing database of enterococci and Escherichia coli and to evaluate its efficacy to identify the sources of faecal contamination in a cross-catchment study within the same geographical area.

Results

1 In all, 649 enterococci and 505 *E. coli* isolates were typed with the biochemical fingerprinting method from 7 sites. A total of 197 enterococci BPTs and 179 *E. coli* BPTS were obtained. These BPTs were compared to the databases to predict their likely sources.

Databases	Human Specific (%)		Animal non-specific (%)	
	Enterococci	E.coli	Enterococci	E. coli
Local Existing Merged	6% 7% 9%	7% 8% 10%	44% 55% 66%	46% 57% 63%

2 Certain BPTs from water samples were also specific to animals species. The percentage contribution from animal species has been shown below.



Conclusions

1 The existing large database is representative enough to identify faecal indicator bacterial contamination in other catchments within the same geographical area.

2 This existing database will eliminate the need for developing specific database for each catchment.

3 The degree of reliability of any such a database relies on the stability of the fingerprints of faecal indicators, which should be assessed before its application in cross-catchment studies.