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Campylobacter Typing Schemes and their use for Epidemiological Investigations

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Campylobacter is a common cause of bacterial gastroenteritis in Australia, however, the ability to identify causal factors has been hampered by the lack of a standard, useful and cost effective typing method. The aim of this study was to evaluate a number of Campylobacter subtyping methods for their suitability for use in epidemiological studies. Between January 1999 and August 2001, a case-control study of Campylobacter infection was conducted in the Hunter Valley, NSW, Australia. Risk factor information was obtained by conducting telephone interviews. One hundred and fifty three *C. jejuni* isolates from cases were tested using multiple (nine) typing methods; Lior biotyping, Serotyping, *fla A* typing (using 2 enzyme systems), PFGE, ribotyping, *fla A* short variable region gene sequencing, multi-locus sequence typing (MLST) and for antimicrobial sensitivity. The number of subtypes ranged from 4 (Lior Biotyping) to 63 (PFGE). The number of isolates in each subtype ranged from 1 (all methods except Lior biotyping) to 92 (Lior biotyping). Of the methods tested, 7 of 9 had subtypes with more than 20 isolates and all had subtypes with >5 isolates. The methods have been assessed for typeability, discriminatory power, ease of interpretation, speed, cost, and simplicity using an algorithm. To determine the public health usefulness of the methods, these assessments in conjunction with time-space clustering and association with risk factors have been undertaken. The findings from this study will be used to select the typing method(s) most appropriate for use in a national Campylobacter case-control study.