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Molecular characterisation of Australian *Campylobacter jejuni* isolates with antibiotic resistance

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Campylobacter is a common cause of bacterial gastroenteritis in Australia. Between January 1999 and August 2001 Campylobacter isolates were collected as part of a case-control study conducted in the Hunter Valley, New South Wales, Australia. The study evaluated a number of subtyping methods for their suitability for use in epidemiological studies. One hundred and fifty three *C. jejuni* isolates from human stools were submitted for antibiotic susceptibility testing, to 10 antimicrobial agents, and PCR-RFLP of the *flaA* gene, using *Ddel* digestion. The results were analysed to determine the correlation, if any, between antibiotic resistance profiles and molecular types. Resistance was observed in 120 (78%) isolates with 13 resistotypes represented. The most common resistotypes were ampicillin (A; 32%), ampicillin-roxithromycin (AR; 24%), no resistance (NIL; 22%) and roxithromycin (R; 11%). Levels of erythromycin and quinolone resistance were low. Twenty five *flaA* types were represented. There were 15 *flaA* types among isolates from resistotype A, 13 among A-R isolates, 10 among R isolates, and 12 among sensitive isolates. *FlaA* types 2, 4, 6 and 10 were found among the 4 major resistotypes and *flaA* type 16 was only found among A isolates. *FlaA* types 1, 8, 11, and 15 were: acquired overseas with expressed quinolone resistance; and acquired locally with or without resistance. The antimicrobial profile may not be dependant on the molecular type but rather the result of exposure to antimicrobial use. Although no particular correlation was observed among the isolates analysed, *flaA* typing demonstrated isolate diversity and resistotyping provided a useful epidemiological marker.