

Campylobacter plasmids and their role in bacterial virulence

Lorna M. Friis

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Abstract

The increasing prevalence of diseases caused by *Campylobacter* has highlighted the need for more effective control and prevention of infections, and has boosted research into the biology of this organism. Plasmids in *Campylobacter* have previously been linked to the transfer of antibiotic resistance traits (Bradbury and Munroe, 1985). However, a recently sequenced Type IV Secretion System (TIVSS) on plasmid pVir of strain 81-176 has been proposed as the first potential plasmid-borne virulence determinant in *Campylobacter* (Bacon *et al.*, 2000, 2002).

This report discusses the genetic composition of an R plasmid from *Campylobacter coli* strain CC31, which exhibits a striking level of sequence similarity to the pTet plasmid of 81-176 despite their isolation almost twenty years apart on different continents (Batchelor *et al.*, 2004). A large TIVSS-encoding operon on plasmid pCC31 has been found to be essential for the conjugative transfer of pCC31. Also encoded on pCC31 are the *tet(O)* tetracycline resistance gene and a *Helicobacter pylori* restriction modification system homologue among genes of unknown function. In order to gain further insight into the function and conjugative properties of *Campylobacter* plasmids several pCC31 genes were investigated by mutational and phenotypic characterisation.

The Invasion Success Model was developed to evaluate *Campylobacter* invasion of epithelial cells and has enabled invasive properties to be statistically compared. This model highlights previously unknown parameters important for the assessment of invasion phenotypes. Strains NCTC 11168, CC31, 81-176 and genetic mutants thereof have been analysed by applying this model to data obtained using the gentamicin resistance assay.

The construction of a *Campylobacter* plasmid gene microarray specific for individual ORFs present in pVir and pCC31 has allowed a comparative plasmid analysis to be made. This has highlighted the extent of pCC31 conservation throughout *Campylobacter*. Although the precise host range of pCC31 is presently unknown, these findings indicate that plasmids play an important role in maintaining genome plasticity in *Campylobacter* species and may also mediate horizontal transfer of antibiotic resistance determinants and other virulence factors between *Campylobacter* and other pathogens.

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