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A Longitudinal Study of *Campylobacter* Spp. on a New Zealand Dairy Farm

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ABSTRACT

Although *Campylobacter* is a common cause of gastroenteritis in humans in New Zealand, the source of infection usually remains unknown. However, the high frequency of human infection may be due to the relatively low infectious dose. *Campylobacter jejuni* and some other *Campylobacter* species are commonly found as commensals in livestock including cattle which may be reservoirs for a number of *Campylobacter* species.

The objective of this study was to estimate the prevalence of *Campylobacter* carriage in healthy dairy cows at the study farm. The combined epidemiological and microbiological investigation was useful in conducting a longitudinal study of Massey University No. 4 Dairy Farm in this project. The project surveyed cows of different ages in the herd at different times over the study period. In order to determine whether strains of *C. jejuni* isolated from the cows were identical, Pulse-Field Gel Electrophoresis was applied to examine the similarities among *C. jejuni* isolates.

Based on the results of an initial pilot study, selecting a suitable sample size of dairy cows for planned sampling events saved time and cost in estimating the *Campylobacter* prevalence. In this study, on a basis of the results of pilot study, a sample size of about 60 animals was selected in order to estimate 90 % confidence level within 10% accuracy. Finally, the results of prevalences of *Campylobacter* at different samplings were applied to calculate 95% confidence intervals for prevalences in different populations.

The survey of different age groups of the same herd at different times within the period 8/6/00 to 5/10/00, found significant differences in isolation rates. For example, the prevalences of both *C. jejuni* and other *Campylobacter* species during dry off period were higher than before calving and after calving. The prevalence of *Campylobacter* carriage by heifers had the highest ranges between 72.1% and 91.0% compared with other populations. Yearling group had relatively prevalence of *C. jejuni* infection but the

prevalence of other *Campylobacter* species was 35%, but the reason is unclear. Moreover, *C. jejuni* strains 74 and 75 was isolated from the pond of this study farm display distinct restriction patterns and are different from the 15 strains from cattle. Although some identical strains occurred across the 1st and 2nd samplings, variation within and between sampling events was evident. In addition, wild birds may be important reservoirs of *C. jejuni* infection of cows. Thus, in this study *Campylobacter jejuni* has a very complex ecologic cycle involving water and animals. Another significant explanation is that some animals may be recovering or recovered carriers or *Campylobacter* may be present in only localized areas or shed intermittently in faeces. Table 10 shows the changes in *Campylobacter* status within different stages of sampling. However, from the present study, there is insufficient evidence to indicate which is a major contributory factor in the causation of infection with *Campylobacter*.

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