

Dietary Effects on *Escherichia coli* O157 and Serotype Diversity of Shiga Toxin-Producing *Escherichia coli* in Feedlot Cattle Faeces

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Ruminants have been considered as a principle reservoir for the *E. coli* O157, a shiga toxin-producing *E. coli* (STEC) responsible for severe abdominal illness in humans. The shedding of *E. coli* O157 and other STEC serotypes in ruminants has been suggested to be influenced by the diet components. This study was designed to evaluate the impact of dietary manipulation on i) the shedding of *E. coli* O157:H7 and ii) the diversity of STEC in feedlot cattle faeces. Thirty steers were initially adapted to high grain diet (G). Then, they were allocated into 3 groups which assigned one of the 3 diets containing (1) molasses, Rhodes grass hay (RM); (2) high grain diet (G); and (3) Rhodes grass hay (R) fed continuously for 14 days before the animals were sent to slaughter as described elsewhere (Gilbert et al 2008). Faecal samples were collected on 2 days during the final week of the adaptation period and at days 6, 8 and 14 after the new diet were introduced. Samples were also taken from the faeces, hide and carcass at lairage.

Escherichia coli O157 was intermittently isolated throughout the trial. Although *E. coli* O157 was initially isolated from 3 animals during the adaptation period, no animals were identified as positive for *E. coli* O157 by immunomagnetic separation method (IMS) 5 days later. Interestingly, *E. coli* O157 was never repeatedly isolated from any of these animals at any other time during the trial. Following the segregation of animals into dietary groups, *E. coli* O157 was only isolated on one occasion during the 14 day period, from one animal fed the R diet. A single hide sample from an animal fed the RM diet was found to be positive for *E. coli* O157, but the corresponding faecal and carcass samples from this animal were not positive for *E. coli* O157 by IMS. No diet-induced effects on *E. coli* O157 prevalence or concentration could be determined.

To further investigate the diversity of the faecal non-O157 STEC, approximately 2000 individual colonies from hydrophobic grid membrane filters (HGMF) processed from the same trial from faecal samples at day 13 and lairage collections (Gilbert et al 2005) were picked and screened for the virulence genes (*eaeA*, *hlyA*, *stx1* and *stx2*). The HGMF coupled with colony hybridization with probes for the virulence genes were specifically used for the detection of complex shiga toxin-producing *E. coli* (cSTEC; Gilbert et al 2008) and thus all the isolates were assumed to be cSTEC. Therefore, based on the result of the virulence genes profile tested above, a total of 84 isolates (R, 13; G, 14 and RM, 57) were selected for serotyping and phenotypic characterization.

The 84 isolates belonged to 36 different serotypes. All the serotypes were reported as STEC elsewhere with the exception of O10:HR and O37:H4 serotypes which were reported in our study for first time. However, only 5 serotypes (14%) were found to produce toxin in our investigation. Cattle fed RM diet had more diversity of serotypes (28 serotypes) than cattle fed G or R diet (8 and 11 serotypes respectively) (Figure 1). Isolates more frequently isolated included Ont:H14, Ont:H8 and O103:H7. None of the serotyped *E. coli* was O157 or contained specific O157 genes. Three isolates (8%) were found to produce enterohaemolysin and 11% produce α -hemolysin. These results are consistent with previous studies showing a low prevalence rate for *E. coli* O157 and indications that diet may be a contributing factor of determining the diversity of faecal STEC.

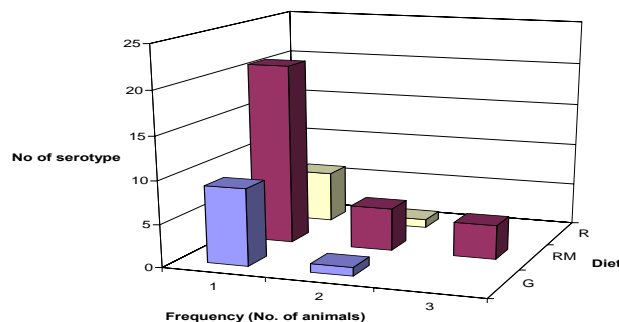


Figure 1. Effect of diet type on the serotype diversity of Shiga Toxin-Producing *Escherichia coli* in feedlot cattle faeces (R= Rhodes grass; RM= Rhodes grass and molasses; G= high grain diet)

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