USE OF PULSED-FIELD GEL ELECTROPHORESIS IN SUBTYPING OF OVINE CAMPYLOBACTER FETUS ISOLATES FROM NETHERLANDS

RUWANI KALUPAHANA[1], LINDA VAN DER GRAAF[2] , JAAP WAGENAAR [2,3] AND MARCEL A.P. VAN BERGEN[2]

1. Faculty of Veterinary Medicine and Animal science, University of Peradeniya
2. Animal Sciences Group, Division of Infectious diseases, P.O.Box 65, 8200AB, Lelystad, The Netherlands
3. Faculty of Veterinary Medicine, Department of Infectious Diseases and Immunology, Utrecht University, P.O.Box 80165, Utrecht, The Netherlands

For some epidemiological purposes such as outbreak investigation, tracing of source of infection or contamination, it is important to identify the relatedness of a group of bacterial isolates. Among several other techniques pulsed field gel electrophoresis (PFGE) is one of the genetic fingerprinting methods that can be used in molecular epidemiology. The value of PFGE in outbreak investigation in animals as well as human disease outbreaks has been shown.

In PFGE the genomic DNA of each bacterial isolate is digested with restriction enzymes which reveal large DNA fragments. These fragments are subsequently separated by PFGE to create a genetic "fingerprint" which is specific for that isolate. To identify the relationship between isolates, the obtained restriction profiles are compared.

In the present study, PFGE was used to determine the relatedness of a group of 31 *C.fetus* bacterial isolates recovered from mainly Dutch ovine abortion cases.

The species *C. fetus* is divided in to two subspecies: *C.fetus* subsp.*venerealis*, the causative agent of bovine genital campylobacteriosis and *C. fetus* subsp. *fetus* with a broader host range and associated with abortions in cattle and sheep. A polymerase chain reaction (PCR) was employed to confirm the species and to differentiate *C.fetus* subsp. *fetus* from *C.fetus* subsp. *venerealis*. Out of 58 bacterial isolates 31 were identified as *C.fetus* subsp. *fetus* while one sample was positive for *C.fetus* subsp. *venerealis*. The 31 isolates of *C.fetus* subsp. *fetus* were further studied by PFGE using the restriction enzyme *Sma*I. PFGE patterns were normalized and analysed using Bionumerics version 3.5 soft ware. According to the resulting dendogram it seems that there are two main clusters, which indicates a limited variation in the (Dutch) ovine *C.fetus* population. As expected *C.fetus* subsp. *venerealis* clustered at a greater distance. However, coming to a definite conclusion requires the comparison of a number of dendograms obtained with the use of different restriction enzymes on the same group of isolates.