Cross Sectional Study of Enteric Pathogens in Wildlife and Cattle in Cheshire (UK)

Food-borne infection was estimated to be responsible for 1.4M human cases of enteric disease in England and Wales during 2000. The most frequent cause was Campylobacter, followed by Salmonella and verotoxigenic E. coli (VTEC). Domestic livestock are a known source of such pathogens, although their carriage in wildlife is less well understood.

The aims of the study were to determine the presence and distribution of these pathogenic organisms isolated from faeces of wild mammals, birds and cattle. A cross-sectional study was conducted on 6 farms (5 dairy and 1 beef) in Cheshire, NW England, between July 2004 and May 2005. Bacteria were isolated using standard microbiological techniques: Campylobacter species were determined by PCR; E. coli isolates were screened for virulence determinants and/or confirmed as 0157 by PCR; and Salmonella spp. were identified biochemically and serotyped.

Approximately 2600 samples were processed (40% rodents, 34% bird, 19% cattle and 7% other wildlife). Campylobacter spp were isolated from magpie (Pica pica), rabbit (Oryctolagus cuniculus), brown rat (Rattus norvegicus), bank voles (Clethrionomys glareolus), wood mouse (Apodemus sylvaticus) and cattle from six farms. There were marked differences in prevalence between species and farms. Only the beef farm was positive for E. coli 0157, however VTEC strains (eae, vt1 and vt2 genes) were isolated from all farms from cattle and wildlife. Salmonella spp., were rarely isolated except for a Salmonella Arizonae isolated from a wood mouse and Salmonella London from a badger on a farm which previously had an outbreak of this serotype.