

Source attribution of *Campylobacter* infection by exposure modelling

Knowledge on the relative importance of the different sources of human campylobacteriosis is important in order to implement effective disease prevention and control measures. It is well known that the incidence of campylobacteriosis differs among age groups. The objective of this study was to assess the relative importance of three key exposure pathways (traveling abroad, poultry meat, pet contact) for different age groups in Switzerland. Using a stochastic exposure model we linked data on *Campylobacter* incidence for the years 2002 – 2007 with data on the three exposure pathways, the results of a case-control study and other studies describing risk factors for campylobacteriosis.

Mean values for the population attributable fractions (AFp) over all age groups and years were 27% (95%CI 17-39) for poultry consumption, 27% (95%CI 22-32%) for traveling abroad, 8% (95%CI 6-9%) for pet contact and 39% (95%CI 25-50%) for other risk factors. In children and elderly people, the exposure through poultry consumption was more important than traveling abroad, whereas in adult age groups, this was reversed. Daily pet contact had a certain importance as a risk factor in children and elderly persons but was relatively less important for young and middle aged adults. In young children, >50% of *Campylobacter* cases were attributed to risk factors not considered in the model, whereas in elderly people this percentage was significantly lower with a mean value over the years of 25%. Other factors may include direct contact to farm of animals like cattle or poultry, drinking raw milk or untreated water and recreational activities like swimming in open water.

Our model provides reasonable results when using data available for Switzerland, but the uncertainty remains high. The output of the model could be improved with the integration of more accurate input data to estimate the infection rate per exposure, which could be obtained by new case-control studies or genotyping studies.