

INDIVIDUAL PREVALENCE ESTIMATES FROM FLOCK DATA WITH AND WITHOUT USING PRIOR INFORMATION AT FLOCK LEVEL

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Apparent prevalence data used in a survey study performed by Skjerve et al., (1996) were reanalysed and used in a simulation model to estimate true prevalence in mutton in Norway.

Authors sampled the prevalence data from the two largest slaughterhouses from each of the four most densely populated sheep districts in Norway. In the autumn slaughtering period (September to November 1993), 207 flocks were randomly selected. From each flock 10 animals were selected and blood samples were taken at bleeding. Sampling was performed twice at each slaughterhouse - at the beginning and at the end of the slaughtering period. The serum was collected and stored at -20 °C, until analysed by an ELISA technique mainly described by Ugglå et al. (1990) and Lunden et al. (1991).

The model consist of several parts: evaluation of true seroprevalence of *Toxoplasma gondii* in mutton in Norway and establishing an estimate of the volume of infected mutton distributed to the market; and estimate the probability for most important mutton products to be infected by *Toxoplasma gondii*.

The presentation will focus on the importance of using prior information for flocks when estimating individual prevalence within a stochastic risk model.