

**Modeling of *Mycobacterium avium* subsp. *paratuberculosis* in farm bulk tank milk**

Okura, H., Nielsen, S.S. and Toft, N., University of Copenhagen, Department of Large Animal Sciences, Denmark; [ssn@life.ku.dk](mailto:ssn@life.ku.dk)

*Mycobacterium avium* subsp. *paratuberculosis* (MAP) in milk of bovine origin is suspected of being implicated Crohn's disease in humans. Pasteurization is considered to reduce the concentration of MAP by at least 4 to 5  $\log_{10}$ . This study aimed at estimating the level of MAP in milk at farm level and simulating the effect of different control options at different infection prevalences. The concentration of MAP in milk was estimated using a hierarchical simulation model representing individual cows in a herd while taking both direct and indirect contamination with MAP into account. Parameters included true within-herd infection prevalences with cows in different infection stages, which were used to estimate prevalences of milk and fecal shedders, and subsequently MAP concentrations in milk and feces. Cows in different infection stages were considered with different risks of excreting MAP testing positive. Furthermore, direct MAP contamination of milk was related to infection stages while indirect contamination was associated to within-herd prevalence and distribution of infection stages. Control options implemented included discarding of milk based on diagnostic test results. Median MAP load in farm bulk tank milk at within-herd infection prevalences from 7.5 to 60% were estimated to 0.74-6.81 cfu/ml, of which the contribution of direct contamination was less than 1%. Maximum concentration at the prevalence of 60% could be 1186 cfu/ml caused by shedding of high amounts of MAP in feces from super-shedders. At the prevalence of 15%, discarding milk from test positive cows would result in discarding 11% of milk and reduce the MAP level by 80%. The model was relatively simple yet capable of capturing true infection status and associated contributions from milk and feces. Further knowledge on distribution of fecal excretion from infected cows is required because very few 'super-shedders' might play a major role. The results can be used for a formal risk assessment including effects such as pasteurization.