Clinical investigations and molecular analyses of re-emerging Mycoplasma bovis outbreaks in Switzerland

Paola Pilo[1], Michèle Bodmer[2*], Joachim Frey[1], and Adrian Steiner[2]*

[1]Institute for Veterinary Bacteriology, [2]Clinics of Ruminants, Vetsuisse, University of Bern, CH-3012 Bern
[*] Both applicants contributed equally to this study

Key words
Mycoplasma bovis, bovine mycoplasmosis, pneumonia, mastitis, arthritis, Switzerland

Aim of the study
The aim of this study was the collection of clinical, epidemiological and bacteriological data about the "new" Mycoplasma bovis outbreaks.

Material and methods
Case and control herds were visited twice and samples collected during one year. All samples were first tested for M. bovis by real-time PCR. All isolates were compared genetically by IS element typing. Moreover, several factors were analyzed in the analysis for risk factors.

Results and significance
In total, 2577 samples from 38 herds were analyzed for the presence of *M. bovis* using real-time PCR. Thereof 114 samples tested positive for *M. bovis*. Forty-five *M. bovis* isolates could be cultured from these samples. In general, the IS element profiles of *M. bovis* isolated in this study from different herds showed considerable variations. They also strongly differed from *M. bovis* that were isolated occasionally in previous years and from the type strain. The IS element profiling showed that *M. bovis* strains are herd specific and transmitted within one herd suggesting that animal traffic in the sense of spreading the disease is probably not as important as believed for a long time. The results suggest that strains were present in carrier animals beforehand and that secondary events must be at the bases of the outbreaks observed. Since descriptive statistics are not completed yet we cannot make out any patterns in the occurrence of the disease. However, preliminary results of the logistic regression analysis show some interesting points: The factor “brand of milking parlour” has to be seen as a classical confounder and may be linked to many breeding farms milking with the same brand of system. Therefore we can conclude that in the population of our case herds the breeding farms were probably over-represented. Linked with cattle breeders in comparison to ordinary farmers is the factor “high milk production” which was also a significant risk factor. The “presence of immunosuppressant factors” was significantly associated with being case herds. In contrast intensive animal traffic can also be seen as a stress factor may impairing the immune system giving rise to mycoplasmosis. An interesting factor is also the “resting area with straw bedding” which was significant in both logistic regression procedures.

Publications, posters and presentations
Marlis Aebi, Michèle Bodmer, Joachim Frey, Paola Pilo. Genetic profiles of Swiss *Mycoplasma bovis* isolates are herd-specific. *Submitted to Veterinary Microbiology*.

Bigna Rossetti, Marlis Aebi, Joachim Frey, Paola Pilo. Realtime PCR for direct detection of *Mycoplasma bovis* from clinical samples. In Proceedings of the European *Mycoplasma* Meeting: What’s New in Mycoplasmology?. 48. 22-24 June 2011. Weybridge, United Kingdom.

Bigna Rossetti, Joachim Frey, Paola Pilo. 2010. Direct detection of *Mycoplasma bovis* in milk and tissue samples by realtime PCR. Mol. Cell. Probes. 24(5): 321-323.

***Project** 1.10.17*

***Project duration** September 2010-October 2011*