SHEDDING OF *COXIELLA BURNETII* IN DAIRY CATTLE AND POSSIBILITY OF TRANSMISSION VIA ALIMENTARY ROUTE

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Estimation of herd-level prevalence of *C. burnetii* shedding in the Polish dairy cattle and identification of the pathogen's genotypes and STs using multiple-locus variable number tandem repeat analysis (MLVA) and multispacer sequence typing (MST) methods. Moreover, the possibility of transmission of the pathogen via alimentary route was evaluated.

In total 2635 bovine serum samples from 969 cattle herds were tested by ELISA/CFT test. Moreover 1439 specimens such as: individual milk samples (n=897), bulk tank milk (n=101), vaginal swabs (n=409), placenta (n=32); were subjected to *C. burnetii* specific qPCR. The qualitative real-time PCR, detecting IS1111 element was performed. The 49 samples with the lowest Ct values were selected for genotyping by MLVA-6 and MST methods. MLVA was performed using 6 variable loci. Amplification products were run on *ABI 3500 Genetic Analyser* and electropherograms were evaluated with *GeneMapper* software. MST was performed as previously described by Glazunova et al. (2005). Ten different intergenic spacers: Cox 2, 5, 18, 20, 22, 37, 51, 56, 57 and 61 were amplified and after purification products were subjected to sequencing. Moreover, to assess the possibility of transmission of the pathogen via alimentary route, an experiment on guinea pigs was conducted.

Average seroprevalence for bovine herds was 24.46 % (969/237). Molecular analysis by real-time PCR revealed the presence of *C. burnetii* DNA in 88 (31.54 %) of tested cattle herds. Positive results were obtained for placenta specimens as well as for swabs from reproductive tract, however the most common was shedding in milk. Five previously described MLVA genotypes: I, J, BG, BE, NM and two novel PL1 and PL2 were identified in 31 out of 49 samples. Two sequence types: ST16 and one newly discovered, named ST61, were identified in field samples using MST technique. After *per os* administration of the pathogen, one guinea pig developed seroconversion and the presence of *C. burnetii* DNA was detected using real-time PCR in testicles and intestine of some animals.

The research confirmed that level of prevalence of *C. burnetii* in dairy cattle herds in Poland is significant and similar to other European countries. It should be highlighted that MLVA and MST profiles identified in this research were different from profiles of the strain involved in the Q fever outbreak in The Netherlands as well as from genotypes of the outbreak strains isolated in Poland the 20th century. However, some of them as genotype I, J, NM and ST16 have been previously recorded in humans, therefore zoonotic threat cannot be ruled out. The results of conducted experiment did not exclude the possibility of infection by alimentary route.

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