

## Current Epizootic Situation of Q Fever in Polish Cattle

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**Abstract :** Q fever (coxiellosis) is an infectious disease of animals and humans caused by *C. burnetii* and widely distributed throughout the world. Cattle and small ruminants are commonly known as shedders of *C. burnetii*. The aims of this study were the evaluation of seroprevalence and shedding of *C. burnetii* in cattle. Genotypes of the pathogen present in the tested specimens were also identified using MLVA (Multiple Locus Variable-Number Tandem Repeat Analysis) and MST (multispacer sequence typing) methods. Sampling was conducted in different regions of Poland in 2018-2021. In total, 2180 bovine serum samples from 801 cattle herds were tested by ELISA (enzyme-linked immunosorbent assay). 489 specimens from 157 cattle herds such as: individual milk samples (n=407), bulk tank milk (n=58), vaginal swabs (n=20), placenta (n=3) and feces (n=1) were subjected to *C. burnetii* specific qPCR. The qPCR (IS1111 transposon-like repetitive region) was performed using Adiavet COX RealTime PCR kit. Genotypic characterization of the strains was conducted utilizing MLVA and MST methods. MLVA was performed using 6 variable loci. The overall herd-level seroprevalence of *C. burnetii* infection was 36.74% (801/2180). Shedders were detected in 29.3% (46/157) cattle herds in all tested regions. ST 61 sequence type was identified in 10 out of 18 genotyped strains. Interestingly one strain represents sequence type which has never been recorded previously. MLVA method identified three previously known genotypes: most common was J but also I and BE were recognized. Moreover, a one genotype has never been described previously. Seroprevalence and shedding of *C. burnetii* in cattle is common and strains are genetically diverse.

**Keywords :** *Coxiella burnetii*, cattle, MST, MLVA, Q fever

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