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Original Article

Molecular Identification of *Neospora caninum* Infection in Aborted Fetuses of Sheep, Cattle, and Goats in Mazandaran Province, Northern Iran

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Abstract

Background: We aimed to identify *Neospora caninum* DNA in the brain samples of aborted fetuses of cattle, goats, and sheep in Mazandaran, northern Iran, using PCR.

Methods: In total, 133 aborted fetuses (51 sheep, 78 cattle, and 4 goats) were randomly collected from different stages of gestation in various regions of Mazandaran, Iran, from Mar 2016 to May 2017. The DNA was extracted from all the brain samples using phenol chloroform isoamyl alcohol instructions. The *Nc-5* gene was used for the detection of *N. caninum* DNA by nested-PCR assay.

Results: The detection of *N. caninum* DNA was confirmed by the observation of a 227 bp band in 24 samples of 133 aborted fetuses (18.1%). The highest prevalence rate of *N. caninum* was detected in the cattle (20.5%) followed by the sheep (15.6%); however, no positive cases were reported in the goats. The highest and lowest prevalence rates of the infection were reported as 23.8% and 8.6% in Qaemshahr, and Behshahr, respectively. The prevalence rate of infection (32%) in the early gestational period was higher than those in the middle (15%) and late (3.8%) gestational periods.

Conclusion: The obtained data of the present study indicated that *N. caninum* infection may partly be responsible for abortion and economic loss in livestock farming in Mazandaran Province.



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