

**The academic year:** 2022-2023

**Author:** Ahmad Enferadi

**Title:** Molecular study of *Borrelia* species in the blood of sheep, goats and vector ticks in West Azarbaijan province

**Summary:**

Ticks are an important vector among arthropods and are associated with serious medical and veterinary problems. In this study, we studied on ticks that borne *Borrelia* spp from sheep, goats farms in different parts of west Azerbaijan province in Iran. Polymerase chain reaction (PCR) was performed using specific primers targeting *Borrelia* spp. genes. *Borrelia* spp. was identified through PCR. The positive PCR products were sending to Pishgam company for Sequencing. Sequenced data were analyzed and phylogenetic analysis was performed using maximum likelihood method in MEGA V.10. The detection rate of *Borrelia* spp. for *16SrRNA* gene 69 (n=542; 12.7%; 95%CI: 10.1%-15.8%) and 42 (n=542; 7.7%; 95%CI: 5.78%-10.1%) positive on *5S-23SrRNA* gene. These results are the first report in Iran to identifying *Borrelia* spp. these results showed that soft and hard ticks act as vectors of *Borrelia* spp. in Iran that can roll as important public health implications in their distribution areas. *Borrelia* species are spirochetes transmitted by ticks that are important in animals and humans. In most countries, there is still no molecular epidemiology of borreliosis in ruminants. Thus, this study aimed to assess the *Borrelia* spp. and the infection rate in ruminants in Iran. By detecting *Borrelia* spp., about 1,018 ruminants (456 goats and 562) were examined from different bioclimatic regions in West Azerbaijan Province by extracting DNA from their blood samples by polymerase chain reaction. The following prevalence rates were obtained: 3.55% (20/562), 2.13% (12/562), and 0.88% (5/562) in sheep, and gene *5s-23SrRNA* gene 0.87% (4/456), *16srRNA*, 1.75% (8/456), *ospA* gene 0.65% (3/456) in goats. The prevalence of *Borrelia* spp. was significantly different in small ruminants based on the farms and localities ( $P < 0.05$ ). The sheep and goats in humid areas (north of Iran) were more infected statistically than those in subhumid areas (south of Iran). In the present study, the main aim was to evaluate the existence of *Borrelia* spp. by extracting DNA from the blood samples via PCR in Iran. It is demonstrated that host species like sheep and goats may have a key role in natural Lyme disease cycles and other borreliosis diseases in Iran.

**Key words:** *Borrelia* spp., PCR, Blood, ticks, West Azerbaijan, Iran