

Innovative semi-quantitative multiplex single primer pair PCR method for simultaneous detecting some obligate intracellular piroplasms

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Received: 15.12.2025

Accepted: 20.05.2026

Abstract

The causative agents of piroplasmosis, *Babesia* spp. and *Theileria* spp. infect ruminants in the livestock industry with high economical losses worldwide. The early diagnosis of the disease can help manage the successful treatment. Giemsa staining is a common method used worldwide for diagnosis of piroplasmosis which unfortunately can be accompanied with some serious problems like suitable blood smears and quality of staining and needs high experience. Serological methods like ELISA or IFAT was also used in some laboratories. The molecular methods based on DNA analysis preferably used in many laboratories are accurate and reliable. The aim of the present study was to introduce a simple and innovative semi-quantitative multiplex PCR method which can be helpful for simultaneously detection of *Babesia* spp. and *Theileria* spp. For this aim, we used primers derived from 18S rRNA genes which can amplify simultaneously the DNA from hosts (ruminants and ticks) and also from *Babesia* spp., and *Theileria* spp with different easily distinguishable PCR products. Our results showed that, as was expected, the different length of amplicons generated from *Theileria* spp. and *Babesia* spp. make it possible to differentiate these parasites from each other on the same agarose gel. Interestingly, since the same primer pair can also amplify the 18S rRNA from host cells with larger amplicon compared to the parasites, this property can be used for semi-quantitative analysis of the parasite burden in the samples. It is necessary to mention that the introduced primer pair (VetUTPiro) can be used for differential diagnosis of babesiosis and theileriosis as well as for semi-quantitative multiplex PCR analysis of the parasite burden consequently for controlled therapy management.

Key words: *Theileria* spp., *Babesia* spp., Semi-quantitative multiplex PCR, Therapy management, Sheep

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