Makale Adı: First molecular detection of Anaplasma species in cattle from Kyrgyzstan; molecular identification of human pathogenic novel genotype Anaplasma capra and Anaplasma phagocytophilum related strain

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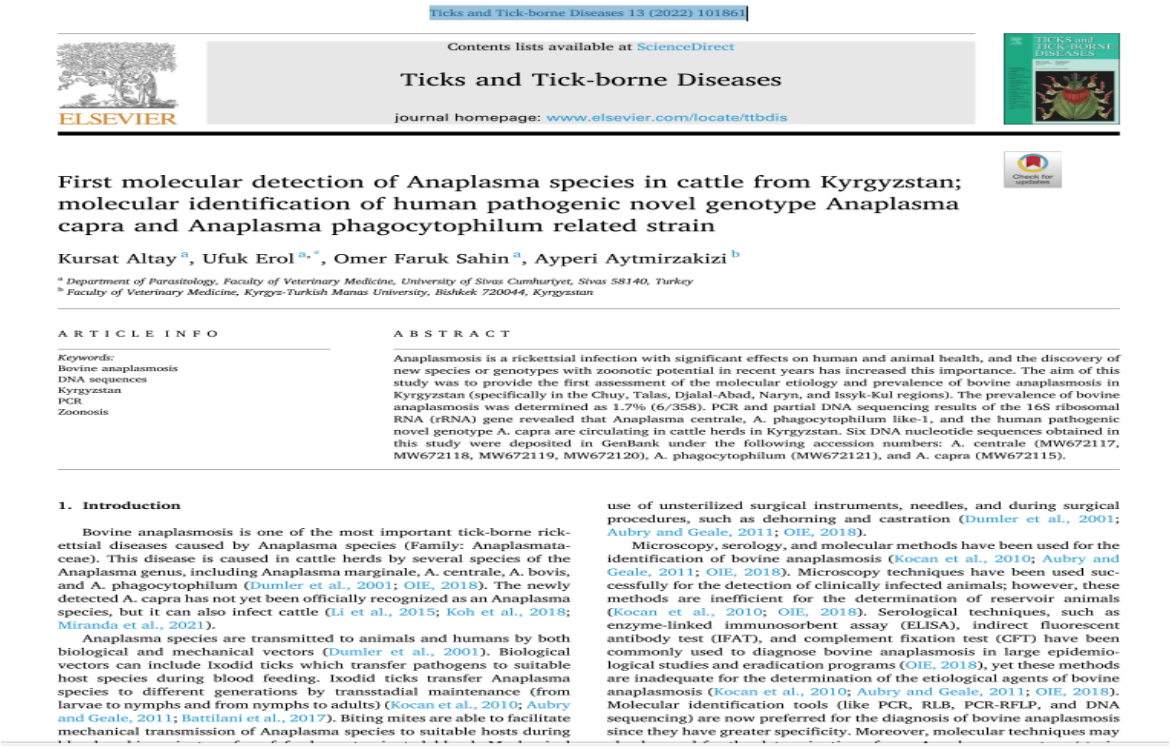

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First molecular detection of Anaplasma species in cattle from Kyrgyzstan; molecular identification of human pathogenic novel genotype Anaplasma capra and Anaplasma phagocytophilum related strain

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ABSTRACT

Anaplasmosis is a rickettsial infection with significant effects on human and animal health, and the discovery of new species or genotypes with zoonotic potential in recent years has increased this importance. The aim of this study was to provide the first assessment of the molecular etiology and prevalence of bovine anaplasmosis in Kyrgyzstan (specifically in the Chuy, Talas, Djalal-Abad, Naryn, and Issyk-Kul regions). The prevalence of bovine anaplasmosis was determined as 1.7% (6/358). PCR and partial DNA sequencing results of the 16S ribosomal RNA (rRNA) gene revealed that Anaplasma centrale, A. phagocytophilum like-1, and the human pathogenic novel genotype A. capra are circulating in cattle herds in Kyrgyzstan. Six DNA nucleotide sequences obtained in this study were deposited in GenBank under the following accession numbers: A. centrale (MW672117, MW672118, MW672119, MW672120), A. phagocytophilum (MW672121), and A. capra (MW672115).

1. Introduction

Bovine anaplasmosis is one of the most important tick-borne rickettsial diseases caused by Anaplasma species (Family: Anaplasmataceae). This disease is caused in cattle herds by several species of the Anaplasma genus, including Anaplasma marginale, A. centrale, A. bovis, and A. phagocytophilum (Dumler et al., 2001; OIE, 2018). The newly detected A. capra has not yet been officially recognized as an Anaplasma species, but it can also infect cattle (Li et al., 2015; Koh et al., 2018; Miranda et al., 2021).

Anaplasma species are transmitted to animals and humans by both biological and mechanical vectors (Dumler et al., 2001). Biological vectors can include Ixodid ticks which transfer pathogens to suitable host species during blood feeding. Ixodid ticks transfer Anaplasma species to different generations by transstadial maintenance (from larvae to nymphs and from nymphs to adults) (Kocan et al., 2010; Aubry and Geale, 2011; Battilani et al., 2017). Biting mites are able to facilitate mechanical transmission of Anaplasma species to suitable hosts during use of unsterilized surgical instruments, needles, and during surgical procedures, such as dehorning and castration (Dumler et al., 2001; Aubry and Geale, 2011; OIE, 2018).

Microscopy, serology, and molecular methods have been used for the identification of bovine anaplasmosis (Kocan et al., 2010; Aubry and Geale, 2011; OIE, 2018). Microscopy techniques have been used successfully for the detection of clinically infected animals; however, these methods are inefficient for the determination of reservoir animals (Kocan et al., 2010; OIE, 2018). Serological techniques, such as enzyme-linked immunosorbent assay (ELISA), indirect fluorescent antibody test (IFAT), and complement fixation test (CFT) have been commonly used to diagnose bovine anaplasmosis in large epidemiological studies and eradication programs (OIE, 2018), yet these methods are inadequate for the determination of the etiological agents of bovine anaplasmosis (Kocan et al., 2010; Aubry and Geale, 2011; OIE, 2018). Molecular identification tools (like PCR, RLB, PCR-RFLP, and DNA sequencing) are now preferred for the diagnosis of bovine anaplasmosis since they have greater specificity. Moreover, molecular techniques may

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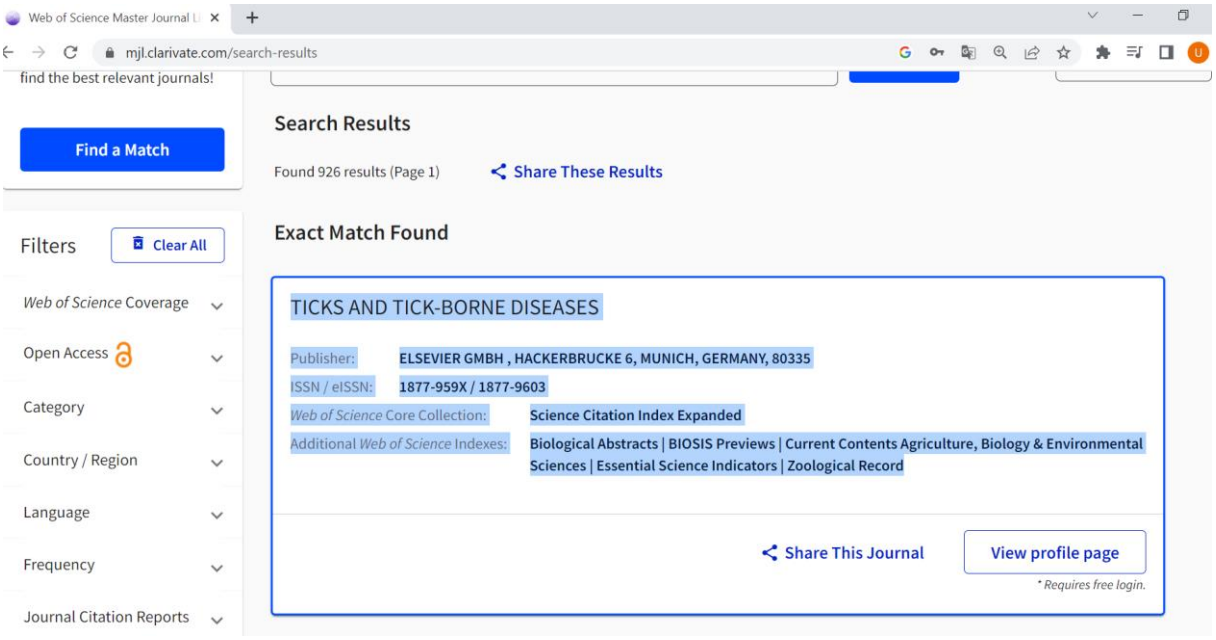

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