

Makale Adı: Buffaloes as new hosts for Anaplasma capra: Molecular prevalence and phylogeny based on *gltA*, *groEL*, and 16S rRNA genes

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Buffaloes as new hosts for *Anaplasma capra*: Molecular prevalence and phylogeny based on *gltA*, *groEL*, and 16S rRNA genes

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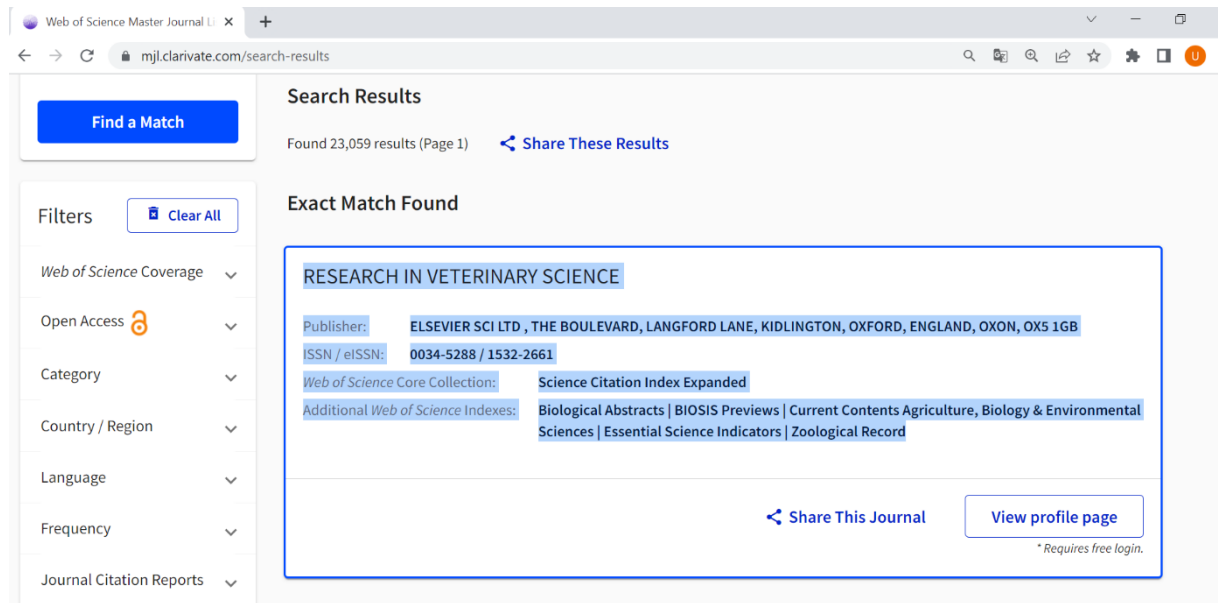
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ABSTRACT

Anaplasma capra is a tick-borne pathogen that was discovered for the first time in goats in China in 2012. The studies carried out from the first detection in China to the present have revealed the presence of this species in eight countries including Angola, France, Iranian, South Korea, Kyrgyzstan, Malaysia, Spain, and Türkiye in three continents (Africa, Asia, and Europe). It has also been determined that humans, sheep, cattle, dog, and wild animals are the hosts of *A. capra*. It was investigated whether water buffaloes were the host of *A. capra* using nested-PCR and DNA sequencing in this study. The prevalence of *A. capra* in Turkish water buffalo herds was investigated and phylogenetic analyzes were performed on the basis of *gltA*, *groEL*, and 16S rRNA genes. A total of 364 water buffalo blood samples were examined in terms of *A. capra* using *gltA* gene species-specific nested-PCR. *A. capra* were detected in 52 of 364 (14.28%) blood samples. There was no statistically significant difference between the prevalence, gender, and age parameters. The *gltA*, *groEL*, and 16S rRNA genes in randomly selected three positive samples were sequenced. *A. capra* isolates obtained from water buffaloes in this study shared 85.20–100%(*gltA*), 89.84–100%(*groEL*), and 99.82–100%(16S rRNA) nucleotide similarity with *A. capra* isolates present in GeneBank. Phylogenetic analyses of *gltA* and *groEL* genes revealed that *A. capra* divided in two

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