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Parasitology

Parasitological and molecular investigation of *Trypanosoma evansi* in dromedaries from Greater Cairo, Egypt

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ABSTRACT. In Egypt, camel trypanosomiasis is widespread. From October 2021 to March 2022, we collected 181 blood samples from apparently healthy one-humped camels (*Camelus dromedarius*) in Cairo and Giza Governates. The objective of this study was to assess infection rates of trypanosomes using blood smear examination and PCR-sequencing assays. Trypanosomes were detected in 8.3% (15/181) of camels by blood smear and in 23.8% (43/181) by PCR targeting the internal transcribed spacer (ITS). Based on blood smear and ITS-PCR results, and the absence of tsetse flies in the study area, we hypothesized that the *Trypanosoma* species was likely *T. evansi*. Validation using PCR based on the variant surface glycoprotein (VSG) of T. evansi Rode *Trypanozoon* antigen type (RoTat) 1.2 (RoTat 1.2 VSG gene) on ITS-PCR-positive samples (n=43) confirmed that 88.4% (38/43) were RoTat 1.2 *T. evansi*, while 11.6% (5/43) were non-RoTat 1.2 *T. evansi*. This marks the second report of non-RoTat 1.2 *T. evansi* in dromedary camels in Egypt. Considering the underestimated zoonotic risk of *T. evansi* in Egypt, there is a potential threat to humans, underscoring the need for a "One Health" approach to safeguard animal and human health.

KEYWORDS: *Camelus dromedarius*, Egypt, ITS-PCR, RoTat 1.2 VSG PCR, *Trypanosoma evansi*

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Trypanosoma evansi, a member of the *Trypanozoon* subgenus, causes "surra," a life-threatening disease in camels transmitted mechanically by biting insects. Surra manifests acute symptoms like fever, anaemia, and weakness, or chronic illness [16]. The disease is widespread from North Africa to Southeast Asia and is enzootic in Egypt [3, 5, 7, 17, 18, 40, 43, 46]. While *T. evansi* is the main pathogen causing camel trypanosomiasis, studies in Sudan [31] and Iran [6] also identified *T. vivax* as a second cause of camel trypanosomiasis. In Kenya, *T. vivax*, *T. brucei*, and *T. congolense* were found in camel blood [19]. Mixed infections with *T. evansi*, *T. vivax*, and *T. congolense* were reported in Saudi Arabia [2] and *T. simiae* in camels from Somalia [22].

Egypt's escalating demand for affordable, high-quality protein has driven the large-scale import of camels from neighboring countries such as Sudan and Ethiopia. Upon arrival, these camels undergo quarantine at border facilities like Abu Simbel and Shalateen before being transported to slaughterhouses or dispersed across key animal markets such as Berkash near Cairo and Daraw near Aswan. These markets are crucial hubs in Egypt's domestic animal trade, facilitating the movement of livestock across regions. However, the extensive cross-border trade of animals poses a significant risk for the spread of infectious diseases, including trypanosomiasis, potentially transforming localized outbreaks into global health threats.

Members of the *Trypanozoon* subgenus (*T. evansi*, *T. brucei*, and *T. equiperdum*) were considered distinct species, but phylogenetic studies suggest *T. evansi* and *T. equiperdum* should be subspecies of *T. brucei* [28, 54]. Trypanosomes are known for their kinetoplast DNA (kDNA). *Trypanosoma brucei* kDNA comprises 20–50 maxicircles (about 23 kb) and thousands of minicircles (about 1 kb), while

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