PARASITOLOGICAL AND MOLECULAR INCIDENCE OF *Trypanosoma evansi* IN DROMEDARY CAMELS OF GUJARAT, INDIA

Bhupendrakumar J. Thakre¹, Binod Kumar¹, Nilima N. Brahmbhatt² and Krishna Gamit³

¹Department of Veterinary Parasitology, ²Animal Diseases Diagnosis Laboratory, Veterinary Clinical Complex; ³Department of Livestock Production Management, College of Veterinary Science and Animal Husbandry, Junagadh Agricultural University, Junagadh-362001, Gujarat, India

**ABSTRACT**

The present study was aimed to assess the incidence of *T. evansi* infections in camel in Saurashtra region of Gujarat, India, through microscopy and polymerase chain reaction (PCR) methods. Blood samples were collected from 192 camels, randomly. The diagnostic sensitivity and specificity of Field’s stain, Giemsa stain and RoTat1.2 polymerase chain reaction (PCR) assays for detection of *T. evansi* in blood samples was evaluated. *T. evansi* infection recorded in camels based on Field’s stain, Giemsa stain and RoTat1.2 PCR assays was 3.23%, 8.85% and 22.39%, respectively. Sensitivity of Field’s stain was 35.29% while PCR test had 100% sensitivity in comparison to Giemsa stain for the detection of *T. evansi* in blood samples. The analytical sensitivity of newly developed RoTat1.2 PCR assay was determined as 1.07 pg of purified whole blood genomic DNA. Epidemiologically, *T. evansi* was an important pathogen in camels of all age groups but more prevalent in adult animals and in monsoon season.

**Key words:** Camels, Field’s Stain, Giemsa stain, Polymerase chain reaction (PCR), RoTat1.2 VSG gene, Trypanosomosis

*T. evansi* infection is widely prevalent in different parts of India and is of significant economic importance in livestock production (Mahran, 2004; Juyal *et al*, 2007). The disease has been reported from almost all states of India viz., Haryana, Punjab, Uttar Pradesh and Jammu and Kashmir in northern India; Rajasthan, Gujarat and Maharashtra towards west andhra Pradesh, Karnataka, Tamil Nadu towards south and Bihar and West Bengal in eastern India (Juyal *et al*, 2007; Ravindran *et al*, 2008; Kumar *et al*, 2015; Maharana *et al*, 2016). Though, the disease has been studied for the past many decades, the definite diagnosis still suffers from low sensitivity and specificity and as a result, the epidemiology of the disease is far from completely understood. The parasitological examinations frequently fail to detect patent infections because parasitemia is scanty in peripheral blood in chronic forms (Killick-Kendrick, 1968; Abdel-Rady, 2008). Antibody detection based serological diagnosis has limitations of differentiation between current and past infections, persistent titres and the occurrence of false-positive results (Bhutto *et al*, 2010). Accordingly, very high rate of prevalence of *T. evansi* in camels was recorded through various serological tests such as CATT/*T. evansi*, formol gel test, ELISA/VSG RoTat1.2, immune trypanolysis compared to PCR and standard trypanosome detection methods (STDM) (Tehseen *et al*, 2015; Hassan-Kadle *et al*, 2019).

Alternatively, polymerase chain reaction (PCR) has been developed for detection of trypanosomes (Masiga *et al*, 1992; Claes *et al*, 2004; Aradaib and Magid, 2006; Konnai *et al*, 2009; Ghorui *et al*, 2012; Elhaig *et al*, 2013). PCR assays have been designed to target different genome sequences and there exists a consensus regarding the difference of sensitivity and specificity between the different PCR methods (Taylor *et al*, 2008; Pruvot *et al*, 2010; Sengupta *et al*, 2010; Tehseen *et al*, 2015). However, the sensitivity of the specificity of different available primers is varying (Pruvot *et al*, 2010; Padmaja, 2012). Based upon Rode Trypanozoon antigen type (RoTat) 1.2., a variable surface glycoprotein (VSG) gene, the *T. evansi* is classified as Type A (presence of RoTat1.2 gene) and Type B (absence of RoTat1.2 gene). *T. evansi* Type A is commonly found while Type B is rare and only reported from some part of Africa (Li *et al*, 2020). Based on the specificity of the targeted gene (Urakawa *et al*, 2001) and wide spread nature of *T. evansi* type A, the present study was aimed to identify *T. evansi*