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SERO-PREVALENCE OF BLUE TONGUE VIRUS IN SMALL RUMINANTS OF THE STATE OF ASSAM

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Abstract–Bluetongue (BT) is an economically devastating viral disease transmitted to domestic and wild ruminants by certain species of Culicoides midges. In the recent years, BT has spread beyond the historically recognized geographical limits and there has been emergence of novel genotypes. Changes in the vector epidemiology and the potential for emergence of new vector species raises concerns of further spread. This study, therefore, was conducted to assess the seroprevalence of Bluetongue virus (BTV) in goats and sheep of Assam. A total of 671 sera samples were collected from goats and sheep belonging to different agro-climatic zones of Assam irrespective of age, sex and breed. The samples were screened for presence of BTV specific antibodies using indirect Enzyme Linked Immuno Sorbent Assay (iELISA). The locations of the study sites were marked using a GPS device and GIS facilities were used to correlate the disease prevalence with geo-climatic conditions. Out of 671 sera samples, 304 (45.31%) were found to be positive for the presence of BTV antibody out of which 295 (46.97%) samples were from goats and 9 (20.93%) from sheep. Among the six agro-climatic zones of Assam, the highest prevalence was detected in the Hills region (91.00%) and the lowest in the Central Brahmaputra Valley (25.00%). The seropositivity observed in this study herein calls for extensive surveillance for detecting the virus incursion in the entire susceptible host range and also for studying the vector population in order to implement comprehensive strategies to predict and control BTV occurrence.

INTRODUCTION

Bluetongue (BT) is an arthropod-borne viral disease of a wide range of wild and domestic ruminants. It can cause severe hemorrhagic disease with high morbidity and is therefore listed as a notifiable disease by Office International des Epizootics (OIE). It is caused by the Bluetongue virus which belongs to the genus *Orbivirus* of the family *Reoviridae* (Noaman *et al*., 2013). BT is mainly transmitted through the biting of insect vectors of the genus *Culicoides* (Diptera: Ceratopogonidae) and sheep are considered most susceptible while cattle, buffaloes and goats serve as reservoirs (Walton, 2004).

Worldwide at least 29 serotypes have been recognized but marked variation in the virulence has been observed even among the virus strains of the same serotype (Maclachlan, 2011). BTV has a double-stranded RNA genome which consist of 10 linear segments (Patel and Roy, 2014). It has the capacity to evolve rapidly with a marked mutation rate ranging from 0.52×10^{-4} to 6.94×10^{-4} substitution rate per site per year for segments 2, 3, 6, and 10 (Carpi *et al*., 2010). Both genome segment

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reassortment and mutation are known to generate genetic diversity among field strains of the virus (Mayo *et al*., 2020).

BTV infections have been reported from most of the tropical and subtropical regions of the world (Roy *et al*., 2011). For a long time, presence of BT was limited to a range between 40°N and 35°S but subsequently BTV strains began to spread worldwide (Samy and Peterson, 2016). From 1950 onwards, the disease has been recorded in Asia, Europe, Australia and North America and consequently has been recognized as an emerging transcontinental disease (Maclachlan, 2011). The transmission of BTV involves multiple factors *viz*. host–vector interactions, host–virus interactions, vector– virus interactions, and the effect of the environment (Moustaid *et al*., 2021). Climate change is believed to be a major driver of the recent appearance of BTV in some of the new regions (especially Northern Europe) especially since the increase in temperature of certain locations makes it suitable for the survivability of midges which can transmit diseases (USDA, 2016). In India, bluetongue was initially confined to exotic breeds of sheep but went on to become endemic in native breeds (Sreenivasulu *et al*., 2004). The first incidence of BT in India was reported in 1964 and since then various workers have documented the presence of most of the known serotypes of bluetongue virus (BTV) in the country either by virus isolation or by detection of serotype specific antibodies (Rao *et al*., 2016). Studies from different regions of India have shown variations in the BT seroprevalence which may be attributed to variations of breed and population density (Rao *et al*. 2016). However, similar studies on BTV in the northeastern states of India are sparse indicating towards the need to systematically analyse the disease and the potential risk factors in the region. The present study therefore, was designed to assess the prevalence of BTV antibodies in sheep and goats of Assam by including samples from the different agro-climatic zones of the state

MATERIALS AND METHODS

The study was conducted in the six agro-climatic zones of Assam consisting of the different districts. Goat and sheep population prevailing in different revenue villages were identified and accordingly blood samples without anti-coagulant were collected randomly. Sera were separated and stored for further analysis. A total of 671 serum samples were collected from goats (n=628) and sheep (n=43) irrespective of age, sex and breed during the period from January 2015 to December 2017. Antibodies against BTV were detected in the sera samples by using the indirect ELISA kit developed by ICAR-IVRI, Mukteswar.

The locations of the study sites were marked by their central coordinates of latitudes and longitudes using a GPS device and GIS facilities were used to correlate seroprevalence with agro-climatic conditions.

RESULTS AND DISCUSSION

Out of the 671 serum samples collected from six Agro-climatic zones of Assam, 304 (45.31%) were found to be positive for the presence of antibodies against BTV. The overall seroprevalence of 45.31% observed in this study is similar to the findings of Tigga *et al*. (2015) who reported 45.83% seroprevalence of BTV group specific antibodies in sheep, goat and cattle of Jharkhand state. In another study, comparable results were documented by Joardar *et al*. (2013) who observed 43.77% overall seroprevalence in cattle, sheep and goats from Assam. Among the six agro-climatic zones of Assam, the highest sero prevalence was detected in the sera samples collected from the Hills region (91.00%) followed by Barak Valley (46.15%), North Bank Plains (45.66%), Lower Brahmaputra Valley (32.76%), Upper Brahmaputra Valley (29.03%) and Central Brahmaputra Valley (25.00%). Antibodies against BTV were not detected in the sera samples collected from Goalpara, Darrang, Kokrajhar, Barpeta and Tinsukia District. Details of seroprevalence of BTV in goat and sheep in the six

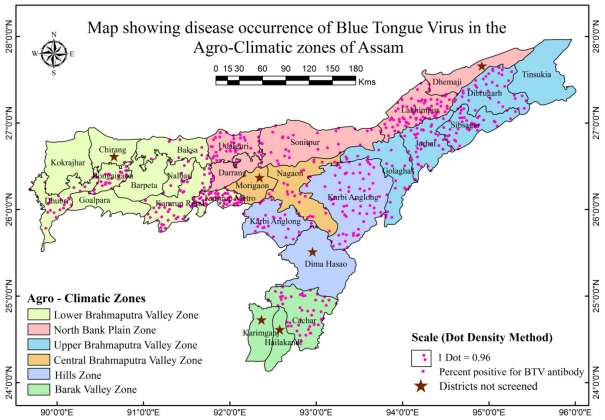

Fig. 1. Map showing Blue Tongue virus seroprevalence in the different Agro-Climatic zones of Assam

agro-climatic zones of Assam for the period of 2015-17 are depicted in Table 1 and Fig. 1. In a previous study, Joardar *et al*. (2013) reported that the prevalence of anti-BT antibodies in the different agro climatic zones of Assam ranged between 31-50%. They, however, had included only 4 agro climatic zones in their study.

Further our findings revealed higher seropositivity in goats i.e., 46.97% followed by 20.93% in sheep (Table 2). In other studies, involving goats, from Sunderbans area of West Bengal (De *et al*., 2008) and Udhampur district, Jammu province (Singh *et al*., 2009), 47% and 45.0% of the samples were found positive respectively. On similar lines, 43.33% of goat samples from Jharkhand were found positive by Tigga *et al*. (2015). However, a much lower seroprevalence of 31.79% was reported by Joardar *et al*. (2013) from goats of Assam, which may be attributed to the sample size variation with the present study. In our study, 628 samples were tested in comparison to the 195 included in the study conducted by Joardar *et al*. (2013).

As far as sheep are concerned, a seroprevalence of 20.93% was observed in the present study. In contrast, a higher seroprevalence of 58.82%, 57.66% and 43.68 % were reported by Joardar *et al*. (2013) from Assam, Panda *et al*. (2011) from West Bengal and Tigga *et al*. (2015) from Jharkhand respectively. In a much earlier study, Naresh and Prasad (1995) had reported a seroprevalence of 23.5% in goats from the states of Haryana, Himachal Pradesh and Punjab. In a metanalytic study performed by Rupner *et al*. (2020), the region wise sub-group analysis revealed the highest BT seroprevalence in sheep from the central zone (53%), goats from the East zone (48%), cattle from the East zone (52%), and

Table 1. Sero-Prevalence of Blue Tongue in goat and sheep from different Agro-climatic zones of Assam

Agro-climatic zones	Districts	Total number of samples assessed	No. positive (%)	Total number of samples assessed According to Agro-climatic zone wise	No. positive (%)
Upper Brahmaputra Valley	Golaghat	28	6 (21.43)	62	18 (29.03)
	Jorhat	14	6 (42.86)		
	Sivsagar	7	3 (42.86)		
	Dibrugarh	8	3 (37.50)		
	Tinsukia	5	0 (00.00)		
Central Brahmaputra Valley	Morigaon	0	0 (00.00)	16	4 (25.00)
	Nagoan	16	4 (25.00)		
Lower Brahmaputra Valley	Nalbari	47	4 (8.51)	293	96 (32.76)
	Bongaigaon	11	3 (27.27)		
	Goalpara,	1	0 (00.00)		
	Baksa	30	3 (10.00)		
	Kamrup Metro	27	18 (66.67)		
	Kamrup Rural	130	63 (48.46)		
	Dhubri	21	5 (23.81)		
	Barpeta	17	0 (00.00)		
	Kokrajhar	9	0 (00.00)		
	Chirang	0	0 (00.00)		
Hills	KarbiAnglong	114	104 (91.00)	114	104 (91.00)
	DimaHasao	0	0 (00.00)		
Barak Valley Zone	Cachar	13	6 (46.15)	13	6 (46.15)
	Karimganj	0	0 (00.00)		
	Hailakandi	0	0 (00.00)		
North Bank Plain Zone	Darrang	40	0 (00.00)	173	79 (45.66)
	Sonitpur	41	11 (26.83)		
	Udalguri	5	2 (40.00)		
	Dhemaji	0	0 (00.00)		
	Lakhimpur	87	66 (75.86)		
Grand Total		671	304 (45.31)		

Table 2. Sero-prevalence of Blue Tongue in different species in Assam

Sl. No.	Species	No. of samples screened	No. of samples positive (%)
1	Goat	628	295 (46.97)
2	Sheep	43	9 (20.93)
	Total	671	304 (45.31)

buffalo from North zone (93%). This highlights the variability in the results observed in the seroprevalence studies conducted in the different states of the country involving different species of animals. Studies on BTV seroprevalence in the neighbouring countries also reported species specific variation. In a metalysis including data from 1988 to 2019 collected from different parts of China, the seroprevalence of bluetongue in different species showed significant variation and the highest seroprevalence of 39.8% was recorded in buffalo while the lowest (4.3%) was found in yak. They also observed a positive correlation within a certain range between the seroprevalence of bluetongue and the species distribution of Culicoides (Gong *et al*., 2021). In another study carried out in Punjab Province of Pakistan (Sohail *et al*., 2019), the seroprevalence was found to be higher in goats (40.75%) followed by buffalo (29.34%), sheep (18.40%) and cattle (17.94%).

CONCLUSION

This study confirms BTV sero prevalence in the small ruminant population of Assam indicating towards the high probability of occurrence of clinical disease in future. Therefore, there is a need to emphasize on the risk factors for preventing potential outbreaks and also design comprehensive surveillance programmes to include all susceptible domestic and wild animals. Further, identifying the vectors and establishing their distribution pattern would provide invaluable insights towards predicting the course of the disease in this part of the world.

Conflict of Interests

The authors declare that no conflict of interests exist.

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