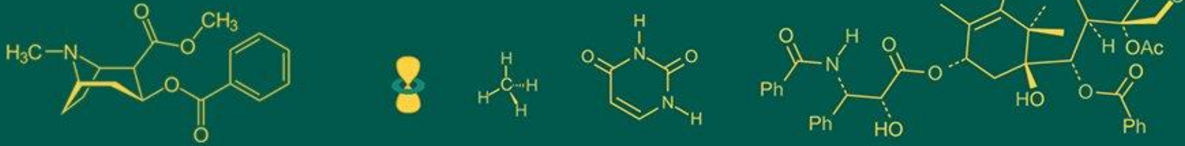

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A review on evaluating epidemiological parameters influencing the prevalence of Bovine Herpes Virus-1 (BoHV-I) infection in cattle

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Abstract
This review article provides an overview of Bovine Herpes Virus-1 (BoHV-1), including its characteristics, viral genome, proteins, and the latency of the virus. There are various serological surveys, as well as antigen and antibody detection methods, for assessing risk factors and sero-prevalence for BoHV-1 infection, although only a few are well established. The rate of Bovine Herpes Virus-1 infection is examined through molecular detection of antigens using Polymerase Chain Reaction and the detection of antibodies through Enzyme Linked Immuno Assay in infected cattle, which may be asymptomatic yet continue to transmit the virus within the environment and to other susceptible animals. The prevalence of BoHV-1 virus infection in cattle can be assessed based on age, species, and breed, which can significantly influence the progression of the disease.

Keywords: Bovine Herpes Virus-I (BoHV-I), Species, Age, breed, ELISA, PCR

Introduction
Bovine Herpes Virus-1 (BoHV-1) is responsible for causing a serious respiratory infection known as Infectious Bovine Rhinotracheitis (IBR) in high-producing cattle, as well as Infectious Pustular Vulvo-Vaginitis (IPV) in cows and Infectious Pustular Balanoposthitis (IPB) in bulls. BHV-1 has a global presence and shows significant variation in incidence and prevalence across different regions. The disease leads to a variety of clinical and pathological issues in affected cattle, resulting in substantial economic losses for the livestock industry due to decreased milk production, lower feed efficiency, and reproductive issues.

All age categories of cattle can contract the infection, but young calves after weaning are particularly vulnerable, likely due to a decline in colostral immunity. The first report of IBR in India was made by Mehrotra *et al.* (1976) [34]. Kiran *et al.* (2005) [24] identified this illness as one of the most widespread respiratory and reproductive viral diseases affecting cattle in India. Malmarugan *et al.* (2004) [29] noted the prevalence of IBR in buffaloes, recording rates of 2.75 percent and 81.0 percent, respectively, in India. Renukaradhya *et al.* (1996) [51] found sero-prevalence rates of 50.9 percent in cattle and 52.5 percent in buffaloes.

There are various sero-surveys and tests for antigen and antibody detection used to determine the risk factors and sero-positivity for BoHV-1 infection, although only some are clearly defined. Testing bulk milk with a gB specific ELISA provides insight into the previous spread of infection within the herd (Frankena *et al.*, 1997) [11]. The gE specific ELISA is appropriate only when over 10-15 percent of the herd is infected. Wellenberg *et al.* (1998) [73] found that bulk milk screenings may not adequately indicate freedom from BoHV-1 infection within the herd, and it is necessary to conduct tests on individual serum samples that were negative in the milk test.

At present, PCR is becoming an essential molecular technique for diagnosing various diseases due to its higher sensitivity and quicker results compared to virus isolation techniques (Moore *et al.* 2000) [40]. Even with colostral immunity in place, the virus remains dormant in the trigeminal ganglion of affected cattle.

Whenever these cattle experience stress for various reasons, they can shed the virus into the environment, potentially infecting other susceptible cattle. This may be attributed to immune evasion mechanisms and the reactivation of the virus following stress. Several intrinsic and extrinsic factors also affect the infection prevalence among the cattle population.

Retrospective view

In the United States during the 1950s, IBR was recognized as an emerging disease affecting feedlot and dairy cattle in Colorado and California. Based on the symptoms seen in infected cattle, various names were assigned to the disease, including red nose, dust pneumonia, necrotic rhinotracheitis, and necrotic rhinitis. In 1955, the US Sanitary Association confirmed the disease's name as infectious bovine rhinotracheitis. McKercher *et al.* (1955) [33] and Kendrick *et al.* (1958) [23] proposed the name infectious pustular vulvovaginitis. The close antigenic relationship between IBR and IPV was investigated by Gillespie *et al.* (1959) [16].
In Europe, BoHV-1 infection has been recognized for over a century. In the 1960s, only 10 percent of cattle in Great Britain were found to be serologically positive for IBR, but this figure increased significantly between the mid-1970s. By 1986, approximately 35 percent of cattle and 48 percent of herds in Europe demonstrated antibodies to IBR (cited by Ganguly *et al.*, 2008) [12]. Mehrotra *et al.* (1976) [34] first reported IBR in India from naturally infected crossbred calves in Uttar Pradesh. Numerous researchers (Sulochana *et al.*, 1982; Singh *et al.*, 1983; Manickam and Mohan, 1987; Satyanarayan and Babu, 1987; Mohan Kumar *et al.*, 1994; and Ganguly *et al.*, 2008) [62, 59, 32, 55, 37, 12] have documented the widespread occurrence of IBR in Kerala, Gujarat, Tamil Nadu, Andhra Pradesh, and Karnataka, respectively. During the 19th century, Buchner and Tommdorf identified BoHV-1 as a likely cause of the venereal form of infection observed in cattle in Germany (Muylkens *et al.*, 2007) [41].

Profile of BoHV-1

Bovine Herpes Virus-1 belongs to the Herpesviridae family, Alphaherpesvirinae subfamily, and Varicellovirus genus (Fenner *et al.*, 1987) [9]. Bovine Herpes Virus-1 is the only identified serotype, but it contains three subtypes: BoHV-1.1 (respiratory subtype), BoHV-1.2a (genital subtype), and BoHV-1.2b (encephalitic subtype), which are categorized based on endonuclease cleavage patterns and DNA technology. BoHV-1.1 causes severe respiratory disease and abortion, while BHV-1.2b strains tend to be less virulent. Subtypes 1.1 and 1.2a have been found in North America and parts of Europe. Meningo-encephalitis resulting from BoHV-1 in calves was previously classified as BoHV-1.3 but is now reclassified as BoHV-5 type (OIE, 2010) [46]. Goat herpes virus-6 (GHV-6) serotype shows a close antigenic relationship with BoHV-1 (Engels *et al.*, 1983) [8]. The phylogenetic analysis conducted in India has revealed that the predominant subtype studied so far is BHV-1.1 subtypes (Rahman *et al.*, 2011) [48].

The genome and proteins of BHV-1

The BoHV-1 genome is classified within group D and comprises a lengthy double-stranded DNA molecule, encoding a total of 70 proteins, among which 33 are structural and 15 are non-structural proteins (Ganguly *et al.*, 2011 and OIE, 2010) [13, 46]. The genome's overall molecular size ranges from 135 to 140 Kb. Proteins from the Alphaherpesvirinae subfamily are crucial for entry, pathogenicity, and the development of immunity in hosts. The viral genome features 12 enveloped glycoproteins, specifically gB, gC, gD, gE, gG, gH, gI, gL, gM, gK, gN, and Us9, of which ten are glycosylated and two are non-glycosylated. The gB, gC, and gD proteins are recognized as the primary proteins (Jones and Chowdhury, 2008) [22].

Viral Latency

Cattle infected with BoHV-1 can shed the virus over an extended duration and may develop latency after recovering from the infection. Some cattle that experience bronchopneumonia during this time may become permanent carriers. Bovine Herpes Virus-1 persists in peripheral sensory ganglia such as the trigeminal, sacral, lumbar, or thoracic ganglia and can shed the virus in reaction to various stressors, which can lead to the spread of infection to immunocompromised cattle (OIE, 2004) [44]. During an acute phase, viral and sub-viral particles, along with cell-to-cell transmission (Winkler *et al.*, 1999) [74], can enter through the oral, nasal, or ocular routes, establishing infection in the sensory neurons of the trigeminal ganglion. According to Jones and Chowdhury (2008) [22], the abundant transcription of latency-related (LR) genes and the gE gene coding for glycoprotein E is linked to the latency of BoHV-1. Cattle that are latently infected remain lifelong carriers.

Disease occurrence

Globally, the genital form of BoHV-1 infection is more prevalent in Europe compared to the respiratory form, while digestive disorders are notably common in calves, especially in Belgium (Straub, 1991) [61]. In Sudan, Elhassan and colleagues (2006) [7] reported an impressive 73 percent sero-positivity based on the serum neutralization test (SNT), determining that SNT was the most effective and widely utilized technique among all tests in their study. In Australia, the first occurrence of infectious bovine rhinotracheitis (IBR) was noted in 1962 following an outbreak of vaginitis and rhinitis in cattle, based on virus isolation methods. The antibody prevalence in mature breeding cattle in Australia was found to be between 25 percent and 40 percent. Of the 80 percent of beef feedlot cattle that tested negative upon entering Australian farms, at least 60 percent were identified as sero-converters to BoHV-1 by the time of slaughter (Gu and Kirkland, 2008) [18]. The subtypes BoHV-1.1 and BoHV-1.2a have been reported in North America and various parts of Europe (OIE, 2010) [46]. In a study conducted in Egypt, Mahomoud *et al.* (2009) [31] observed a higher incidence (80 percent) of BoHV-1 in apparently healthy cattle raised on closed farms, compared to a lower incidence (62.5 percent) in cattle from open farms, with a significantly lower positivity rate in buffaloes. Although numerous countries worldwide have documented IBR, certain nations—specifically Austria, Denmark, Finland, Sweden, Italy, Switzerland, Norway, and parts of Germany—have achieved near-complete freedom from BoHV-1-IBR (OIE, 2010) [46]. Meanwhile, control measures for BoHV-1-IBR are ongoing in countries such as Australia, Belgium, Canada, India, Poland, Turkey, and the USA (Nandi *et al.*, 2009) [43].

Indian perspective

Mehrotra and his colleagues first identified Infectious Bovine Rhinotracheitis (IBR) in India in 1976. Since that time, it has been reported in every state across the country, establishing itself as an endemic disease. A cumulative sero-surveillance study conducted on 57, 009 serum samples between 1995 and 2010 revealed that 36 percent of these samples tested positive for IBR antibodies using the AB-ELISA method (Rahman, 2011) [48]. The indirect hemagglutination test was recognized as a highly sensitive and cost-effective method for assessing the prevalence of the economically significant BoHV-1-IBR (Kirby *et al.*, 1974) [25]. Additionally, Samal *et al.* (1981) [53] reported that 56.5 percent of cattle tested positive for IBR antibodies using the hemagglutination inhibition test. In efforts to identify antibodies against IBR in both vaccinated and experimentally infected animals, a study involving five different tests found a correlation in the results of three tests (PHA, VNT, and ELISA) (Edwards *et al.*, 1986) [6].

In Maharashtra, Chinchkar *et al.* (2002) [3] found that the prevalence of IBR in cattle was significantly higher at 33.91 percent compared to 31.0 percent in buffaloes. Sontakke *et al.* (2002) [60] reported that antibodies to IBR were present in 54.28 percent of cattle and 46.42 percent of buffaloes exhibiting clinical symptoms. They also noted that cattle and buffaloes suffering from conjunctivitis had a higher antibody prevalence of 62.5 percent, compared to 57.1 percent in those with rhinitis and other clinical signs. Ganguly *et al.* (2008) [12] identified a sero-positive rate of 85.29 percent in the cattle population of Nadia district in West Bengal, contrasting with a lower rate of 20.72 percent in Jalpaiguri district. Trangadia *et al.* (2010) [68] reported an overall sero-prevalence of 60.84 percent in organized cattle farms across India; however, they were unable to isolate the BoHV-1 virus from genital and nasal swabs using Madin-Darby Bovine Kidney (MDBK) cell lines. The prevalence of IBR antibodies in cattle and buffaloes in Gujarat and Andhra Pradesh was reported at 23.94 percent and 26.49 percent, respectively, according to Trangadia *et al.* (2012) [69]. The overall sero-positivity in India was highest in Tamil Nadu at 67 percent and lowest in Meghalaya at 34 percent. Regional prevalence rates were observed as 17 percent in Eastern India, 24 percent in Western India, 37 percent in Northern India, 39 percent in Northeastern India, and 25 percent in Central India, as reported by Rahman *et al.* (2011) [48].

Prevalence by species

BoHV-1 impacts a diverse array of animal species, including cattle, sheep, goats, water buffaloes, and various wild species such as antelope, wildebeest, hippopotamus, caribou, members of the Mustelidae family, and humans (Radostits *et al.*, 2007) [47]. The incidence of Infectious Bovine Rhinotracheitis (IBR) in buffaloes is lower than that observed in cattle (Suresh *et al.*, 1999; Sharma *et al.*, 2006) [63, 57]. In Tamil Nadu, the seroprevalence of IBR in buffaloes with reproductive disorders was found to be higher (40.30 percent) compared to those with respiratory infections (29.1 percent) (Suresh *et al.*, 1992) [64]. A study on antibody prevalence for IBR in Mithun cattle from Arunachal Pradesh, Mizoram, and Nagaland revealed positive rates of 38.46 percent, 18.8 percent, and 15.5 percent, respectively, with no positive cases in Mithun from Manipur (Rajkhowa *et al.*, 2004) [50]. Additionally, Bovine Herpes Virus-1 antibodies were detected in 60.1 percent of Yaks (*Peophagus grunniens*) at the National Research Centre for Yak in India (Nandi and Kumar, 2010) [42], with positivity rates of 67.7 percent in male Yaks, 62.6 percent in Yak cows, and 50.0 percent in Yak heifers.

Prevalence by age

All age groups of animals are susceptible to IBR; however, the disease is most prevalent in animals older than six months (Radostits *et al.*, 2007) [47]. Reports indicate that adult cattle are more susceptible than younger animals, likely due to increased exposure to BoHV-1 and the establishment of carrier status in older cattle (Dhand *et al.*, 2002) [5]. The lower prevalence in younger cattle may be attributed to maternal immunity (Fenner *et al.*, 1987) [9]. Unvaccinated herds of breeding or beef cattle are particularly vulnerable to outbreaks of the respiratory form of IBR and associated abortions. It has been noted that the prevalence in cattle aged nine years and older is higher compared to other age groups (Sharma *et al.*, 2006) [57].

Prevalence by Breed

The prevalence of infection is higher in crossbred cattle compared to non-descript cattle (Koppad *et al.*, 2007). No significant difference was observed in disease occurrence between crossbred and non-descript buffaloes (Suresh *et al.*, 1992) [64]. The incidence in female cattle may exceed that in males (Sharma *et al.*, 2006) [57]. A notably higher rate of sero-reactors has been identified in cattle from both organized and unorganized farms compared to buffaloes (Dhand *et al.*, 2002) [5], while cattle in closed farms exhibited a greater percentage of antibodies to IBR (Suresh *et al.*, 1999) [63]. Reports indicate that cattle in organized farms are more affected (Ganguly *et al.*, 2008) [12], similarly cattle and buffaloes in organized dairy farms were found to be equally susceptible (Trangadia *et al.*, 2010) [68].

Mode of Transmission

Direct contact between infected and susceptible cattle is the primary method of transmission (Muylkens *et al.*, 2007) [41]. Contaminated aerosols arise from materials expelled through exhalation, sneezing, and coughing by infected animals (Mars *et al.*, 1999) [30]. The transmission of Infectious Bovine Rhinotracheitis (IBR) is largely dependent on the abundance of viral sources present in the infected materials. Potential viral carriers include nasal secretions, droplets from coughing, genital fluids, semen, as well as fetal fluids and tissues. Bovine Herpes Virus-1 can persist for up to one year in semen preserved in liquid nitrogen (Nandi *et al.*, 2009) [43]. This virus can be transmitted through both natural mating and artificial insemination, with venereal transmission being a significant route for genital diseases. Additionally, Bovine Herpes Virus-1 can be transmitted via inanimate objects. Mechanical transmission of BoHV-1 in cattle can also occur through ticks (*Ornithodorus coriaceous*) (Straub, 1991) [61]. The risk of BoHV-1 infection increases with direct contact and high-density cattle populations (Van Schaik *et al.*, 2002; Vonk Noordegraaf, 2004) [70, 72]. The virus found in vaginal and preputial secretions is less likely to result in IBR transmission to other animals. Cattle that are latently infected act as carriers for susceptible cattle (Thiry *et al.*, 1987) [66], complicating control measures. It has been noted that sheep are unlikely to transmit BHV-1 to cattle (Hage,

1997) [19]. Experimental infection in rabbits via intra-conjunctival or intranasal routes may also be feasible (Meyer *et al.*, 1996) [35].

Disease development

The virus enters the mucous membrane of the upper respiratory tract and tonsils through nasal inhalation, where it replicates in high quantities. Subsequently, the virus spreads to the conjunctivae and ultimately reaches the trigeminal ganglion via neuro-axonal transport. Infected cattle exhibit significant clinical signs such as serous nasal discharge, mucopurulent discharge, salivation, fever, loss of appetite, and depression within 2 to 4 days post-incubation (OIE, 2008) [45]. Following a respiratory infection, viral shedding occurs for 10 to 14 days, with titers ranging from 10^8 to 10^10 TCID50. Samples for diagnosing BoHV-1 infection can be obtained from nasal, ocular, and genital swabs. Clinically affected animals may display ocular, respiratory, reproductive, alimentary, and central nervous system issues, and young calves may experience a generalized neonatal infection (Gibbs and Rweyemam, 1977) [15]. The introduction of new animals to a farm frequently triggers an outbreak of Infectious Bovine Rhinotracheitis (IBR). In cases of reproductive tract infection, the virus proliferates in the mucous membranes of the vagina and prepuce, becoming latent in the sacral ganglia, where it may persist in the neurons for the animal's lifetime (OIE, 2008) [45].

Diagnostic tools

Enzyme linked sorbent assay (ELISA)

Although the concentration of immunoglobulin in milk is lower than that found in serum, the gE ELISA demonstrates a high sensitivity for detecting antibodies against BHV-1 in milk (Mach and Pahud, 1971). Likewise, the gE Milk ELISA has been recognized as a more sensitive and specific test compared to the serum gE ELISA (Wellenberg, 1998) [73]. Shome *et al.* (1997) [58] reported that the AB-ELISA identified 89 percent of 203 samples as positive for antibodies to IBR in cattle. Additionally, Suresh *et al.* (1999) [63] found that 38.01 percent of 3, 428 cattle screened for IBR antibodies tested positive, declaring AB-ELISA as the most effective technique among five methods evaluated. In Maharashtra, Chinchkar *et al.* (2002) [3] utilized Dot ELISA and found that 58.13 percent of crossbred cattle had IBR antibodies, suggesting exposure to the virus. Regardless of breed, age, parity, health status, and management practices, Rajesh *et al.* (2003) [49] reported sero-prevalence in 28 to 110 cattle in Kerala. The gB specific ELISAs exhibit greater sensitivity for detecting antibodies in serum samples. Indirect ELISAs and gB blocking ELISAs showed highly comparable sensitivity and specificity (Beer *et al.*, 2003). The Enzyme Linked Immunosorbent Assay technique has gradually supplanted the Viral Neutralization test. Various ELISAs are employed for antibody detection in serum samples; however, Kramps *et al.* (2004) [27] identified antibodies to BoHV1-IBR in milk, while the AB-antibody ELISA indicated a 45.01 percent serum antibody prevalence for BoHV-1 infection in bulls in Punjab State. In comparison with the results from three other techniques, PCR was deemed a more sensitive method than virus isolation in bulls (Deka *et al.*, 2005) [4].

A monoclonal antibody-based blocking ELISA for Infectious Bovine Rhinotracheitis indicated that 30 percent of bulls tested positive for BoHV-1 infection, whereas PCR targeting the gB gene revealed a positivity rate of 42 percent (Jain *et al.*, 2009) [20]. Given that some samples were positive by ELISA but negative by PCR, and vice versa, Jain *et al.* (2009) [20] recommended employing both serological and PCR diagnostic methods. They also found that 15 out of 50 breeding bulls tested positive using the antibody-based blocking ELISA. In a separate study, Mahmoud *et al.* (2009) [31] concluded that ELISA was the quickest, most reliable, cost-effective, and straightforward test available, making it an ideal choice for screening large animal populations within herds. Indirect ELISAs are recognized as the most sensitive tests for detecting BHV-1 antibodies in milk (OIE, 2010) [46]. In another investigation involving 595 cattle and buffalo, 362 were identified as positive via ELISA, with the highest prevalence noted in the central region of India, followed by the southern, western, and northern regions (Trangadia *et al.*, 2010) [68]. This study reported an overall prevalence rate of 60.84 percent but was unable to isolate BoHV-1 from nasal or genital samples, even after multiple passages in Madin Darby Kidney (MDBK) cell lines.

Polymerase Chain Reaction (PCR)

Vilcek *et al.* (1994) [71] successfully detected herpes virus DNA in samples from reindeer, red deer, and goats using PCR assays, and they also identified BoHV-1 in semen and serum samples. When comparing PCR with virus isolation tests conducted on experimentally inoculated bulls with BoHV-1 at various post-inoculation days, the analysis revealed that 24 positive results were obtained from virus isolation in egg yolk extended semen samples, 51 from fresh semen, and 118 from PCR assays out of 162 semen samples tested. Frank *et al.* (1995) [10] concluded that bulls infected intra-preputially could excrete the BoHV-1 virus for a longer duration than through other infection routes. In countries where BoHV-1 is endemic, PCR screening could prove to be a cost-effective method to mitigate the spread of the BHV-1 virus through semen by enabling early and rapid diagnosis (Gee *et al.*, 1996) [14]. A molecular differential diagnosis between the wild type Bovine Herpesvirus-1 and the gE negative strain was conducted using PCR assays, with specificity confirmed through restriction enzyme analysis and DNA sequencing of the amplicons (Schynts *et al.*, 1999) [56]. The findings indicated that PCR could serve as a valuable tool for monitoring the dissemination of live marker vaccines and the gE genotype of viral field isolates. Tiwari *et al.* (2000) [67] discovered that the simple boiling water method was adequate for PCR amplification, suggesting that simultaneous extraction of purified DNA was not necessary for comparing PCR products. Moakhar *et al.* (2003) [36] indicated that PCR is highly applicable for screening BoHV-1 infected aborted fetuses in cattle and for the early detection of BHV-1 in tissue culture viral isolates, noting that PCR is a more time-efficient assay compared to virus isolation and the Neutralization test.

Deka *et al.* (2005) [4] reported that 14 out of 24 bull semen samples tested positive for the 468bp gI gene fragment using PCR, while 11 samples were confirmed positive through virus isolation techniques. The presence of Bovine Herpes Virus-1, specifically the gB and gE genes, was detected in semen samples from naturally infected bulls via PCR assay, which demonstrated sensitivity comparable to that of the virus isolation test (Grom *et al.*, 2006) [17]. Jhala

et al. (2007) [21] indicated that PCR-based assays are a rapid and sensitive method for screening bulls at semen collection centers. Jain *et al.* (2009) [20] found that 46.53% and 42.57% of semen samples from bulls in Gujarat tested positive for BoHV-1 infection using gB and gC gene-based PCR, respectively. The open reading frame of the gB gene from BoHV-1 genomic DNA was amplified and utilized in PCR cloning by Momtaz and Abbasian (2009) [39]. The Polymerase Chain Reaction amplification of the gB gene from semen samples indicated a 42% incidence rate of BHV-1 infection among bulls in Gujarat, with a higher incidence observed in cattle (50%) compared to buffaloes (34.61%) (Jain *et al.*, 2009) [20]. Rodriguez Medina *et al.* (2009) [52] noted that even under optimal thermal cycling conditions, a thymidine kinase (tk) based PCR method developed for detecting Bovine Herpesvirus-1 was unsuccessful in identifying the gene from either heterologous or other bovine viruses; however, it successfully amplified a BoHV-1 fragment of 202bp, leading researchers to regard this PCR method as specific. Real-Time PCR was effective in detecting buffaloes experimentally inoculated with a field strain of BoHV-1 from cattle (Teresa Scicluna *et al.*, 2010) [65]. Chandranaik *et al.* (2010) [2] conducted extensive screening of semen samples from four southern Indian states, identifying four samples with cytopathic changes in cell lines, which were confirmed using real-time PCR techniques. The percentage of IBR positivity in cattle bulls (40.81%) was notably higher compared to buffalo bulls (38.46%). The semen from breeding bulls tested positive for the gC gene PCR at a rate of 39.60%, surpassing that of buffalo bulls.

Conclusions

The incidence of BoHV-1 infection appears to rise with age, being more prevalent in older animals than in younger ones. A higher occurrence is likely in older female cattle and pluriparous animals due to the stress associated with high milk production. Additionally, intensive farming practices, which involve close contact among animals during parturition and milk production, may contribute to increased prevalence of BoHV-1 infection. In contrast, younger animals exhibit a lower prevalence of BoHV-1, potentially due to the presence of maternal antibodies or immunity. While there is no significant difference in the prevalence of BoHV-1 infection across breeds, it has been documented among Mithun and Yak species in India. Most infected cattle remain asymptomatic, allowing the virus to circulate between the environment and susceptible animals. The virus can maintain latency in the trigeminal ganglion of affected cattle, and stress from various factors can trigger its shedding into the environment, posing a risk of infection to other susceptible cattle. This phenomenon can be attributed to immune evasion mechanisms and the reactivation of the virus under stress. Furthermore, the prevalence of BoHV-1 infection is influenced by a variety of intrinsic and extrinsic factors.

No single diagnostic method can simultaneously identify both antigens and antibodies, and it is possible for a sample to yield a positive result with one test while appearing negative with another. ELISA is a quick, cost-effective, and highly specific assay for measuring antibody levels in the serum and milk of animals, making it crucial for identifying latent virus carriers in control programs, international trade regulations, sero-epidemiological research, sero-surveillance during eradication efforts, and assessing antibody responses in vaccination studies. PCR has emerged as a vital molecular technique for diagnosing various diseases due to its rapidity and sensitivity. This molecular tool is instrumental in detecting, genetically characterizing, and identifying genetic variations that may exist among circulating field strains of BoHV-1.

Competing Interests

The author declare that they have no competing Interests

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