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Seroprevalence and host-related risk factors of infectious bovine rhinotracheitis in Indian bovines: a large-scale multi-state epidemiological study

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Abstract

Infectious bovine rhinotracheitis (IBR)/ infectious pustular vulvovaginitis (IPV), caused by *Varicellovirus bovinealpha1* (BoAHV-1), is a highly contagious disease of cattle and buffaloes, resulting in substantial economic loss to the global diary industry. The present study investigated the seroprevalence of IBR/IPV and associated host-related risk factors in Indian bovines using serum samples collected under breed improvement programmes between 2016 and 2024. Following data cleaning, 34,355 bovines from 213 districts across 13 states were included in the analysis. Antibodies against BoAHV-1 were detected using a commercial gB ELISA. The overall apparent and true seroprevalence of IBR were 31.95% (95% CI: 31.46–32.45%) and 31.13% (95% CI: 30.61–31.66%), respectively. Buffaloes exhibited significantly higher seroprevalence than cattle (37.69% *vs.* 26.10%) and remained at greater risk of seropositivity after adjustment for age, sex and geographical location (AOR = 1.57; 95% CI: 1.44–1.71; $p < 0.001$). Among cattle, indigenous breeds showed significantly higher seroprevalence than exotic and crossbred cattle, with indigenous cattle exhibiting 2.20-fold higher odds of seropositivity than exotic cattle ($p < 0.001$). Female animals and older age groups also showed significantly higher odds of seropositivity. In addition, IBR-seropositive animals were 2.42 times more likely to be seropositive for brucellosis ($p < 0.001$). The findings demonstrate widespread circulation of BoAHV-1 virus in Indian bovines and identify important host-related factors associated with seropositivity. The study provides valuable baseline epidemiological evidence to strengthen surveillance and develop effective IBR control strategies in India.

INTRODUCTION

Infectious bovine rhinotracheitis (IBR) is an economically important viral disease of cattle and buffaloes caused by *Varicellovirus bovinealpha1* (BoAHV-1; formerly bovine herpesvirus-1), a member of the genus *Varicellovirus*, subfamily *Alphaherpesvirinae*, and family *Herpesviridae* (Black et al. 2026; http://ictv.global/taxonomy). Depending on the route of infection and tissue tropism, BoAHV-1 may cause respiratory disease (infectious bovine rhinotracheitis), genital disease (infectious pustular vulvovaginitis and infectious balanoposthitis), conjunctivitis, abortion, neonatal disease and generalized infection in young calves. Acute infection is characterized by respiratory, ocular and reproductive manifestations, although subclinical infections are common (Muylkens et al. 2007; Biswas et al. 2013; Rimayanti et al. 2024; Sandhyarani et al. 2025). In addition to its direct clinical effects, BoAHV-1 is an important component of the bovine respiratory disease complex and can predispose animals to secondary bacterial and viral infections through its immunosuppressive properties (Biswas et al. 2013; Jones et al. 2019).

A characteristic feature of BoAHV-1 infection is the establishment of lifelong latency following primary infection. The virus persists in sensory ganglia and may reactivate periodically under conditions such as stress, transportation, parturition, corticosteroid administration or concurrent disease (Muylkens et al. 2007; Biswas et al. 2013; Chandrasekhar Reddy et al. 2020). Reactivated animals may shed virus without clinical signs, facilitating long-term persistence and transmission within susceptible populations and posing a major challenge to disease control programmes. Because infected animals generally remain

seropositive for prolonged periods, serological testing has become an important tool for epidemiological investigations, surveillance and disease control (Biswas et al. 2013; Sarangi et al. 2021b).

BoAHV-1 is distributed worldwide and remains endemic in many cattle-producing countries, although several European nations have successfully controlled or eradicated the disease through systematic surveillance, movement control, vaccination and test-and-slaughter programmes (Raaperi et al. 2014; Waldeck et al. 2021; Rimayanti et al. 2024). The infection is associated with substantial economic losses arising from reduced milk production, reproductive failure, neonatal calf mortality, impaired growth performance, trade restrictions and costs associated with disease prevention and control (Nandi et al. 2009; Biswas et al. 2013; Sibhat et al. 2018; Tejaswi et al. 2023; Kolech et al. 2025). Furthermore, increasing emphasis on the One Health approach and prudent antimicrobial use has highlighted the importance of controlling viral infections such as BoAHV-1 that can interact with other pathogens, exacerbate bovine respiratory disease and indirectly contribute to antimicrobial usage in livestock production systems (Nickell and White 2010; Ghoughal et al. 2026).

India possesses the world's largest bovine population and the dairy sector plays a pivotal role in rural livelihoods, nutritional security and the national economy. IBR was first reported in India in 1976, and since then both the virus and serological evidence of infection have been documented from almost all regions of the country (Renukaradhya et al. 1996; Biswas et al. 2013; Das et al. 2014; Sarangi et al. 2021a; Naveena et al. 2022; Patil et al. 2022; Chandrasekhar Reddy et al. 2025). However, most investigations have been restricted to specific districts, states or production systems and were often based on relatively small sample sizes. Consequently, comprehensive epidemiological information on the distribution of IBR and the influence of major host-related risk factors at a broader geographical scale remains limited. Such information is essential for understanding disease dynamics and for designing effective surveillance and control programmes in the Indian dairy sector.

Therefore, the present study was undertaken to estimate the seroprevalence of IBR in Indian bovines using a large and geographically diverse sample population and to evaluate the association of seropositivity with species, cattle breed type, sex and age. In addition, the relationship between IBR and brucellosis seropositivity was investigated. The findings are expected to improve understanding of the epidemiology of IBR in India and provide evidence to support the development of effective surveillance, prevention and control strategies.

MATERIALS AND METHODS

Study design, source of samples and study population:

A retrospective cross-sectional study was conducted to estimate the seroprevalence of infectious bovine rhinotracheitis (IBR) in dairy bovines in India and to evaluate the influence of selected host-related factors on IBR seropositivity. Serum samples submitted to the National Dairy Development Board (NDDB) Research and Development Laboratory, Hyderabad, India, between January 2016 and December

2024 for IBR screening were included in the study. These samples originated from cattle and buffaloes enrolled in progeny testing and pedigree selection programmes implemented under the Rashtriya Gokul Mission across different states of India.

The initial dataset comprised 39,502 serum samples screened for antibodies against BoAHV-1. The dataset included duplicate records arising from repeated testing of the same animals, records lacking essential demographic information (species, breed, sex or location), and records for which animal traceability could not be established. In addition, samples collected from calves younger than nine months of age were excluded to minimize potential interference from maternally derived antibodies. For animals tested on multiple occasions, only the most recent test result was retained for analysis.

Following data cleaning and validation, a total of 34,355 individual animal records were included in the final analysis. The study population comprised cattle and buffaloes from 213 districts across 13 states of India, including 29 cattle breeds and 9 buffalo breeds. The dataset represented a broad spectrum of bovine genetic resources, agro-climatic zones and production systems within the Indian dairy sector.

Serological testing:

A commercially available ELISA kit (IDEXX IBR gB X3 Ab test, IDEXX Laboratories, USA) was used to detect antibodies directed against glycoprotein B of BoAHV-1. The test method has been found suitable for use in Indian cattle and buffalo populations (Sarangi et al. 2021b). The test was performed according to the manufacturer's instructions. Briefly, to the BoAHV-1 antigen-coated plates, 50 µL of wash solution (1X) was added to each well, followed by 50 µL of positive and negative control samples (supplied by the manufacturer with the kit), internal control samples (known positive and negative), and test samples. The plates were incubated for 2 hours ± 5 minutes at 37 ± 1°C. Following washing, 100 µL of ready-to-use conjugate was added to all wells, and the plate was incubated again for 60 ± 3 minutes at room temperature (18°C-26°C). Following washing, 100 µL of TMB –Substrate N.12 was added to all wells and the plate was incubated for 10 ± 1 minutes at 18–26ºC in a dark place for enzymatic reaction. Finally, 100 µL of stop solution N.3 was added to each well to stop the reaction and the optical density (OD) values were read with an ELISA reader (Synergy HT, BioTek) at 450nm. The blocking percentage was calculated as per the formula suggested by the manufacturer: $100 \times [NCx_{(A450)} - Sample_{(A450)}]/[NCx_{(A450)}]$. The samples were considered positive when the blocking percentage was ≥ 55%; suspect when the blocking % was ≤ 45 to < 55%; and negative when the blocking % was < 45.

Quality control:

All testing was performed in an ISO/IEC 17025:2017-accredited laboratory in accordance with established quality management procedures. The test method was included within the laboratory's accredited scope of testing. Quality assurance measures included the use of trained and competency-assessed personnel, calibrated equipment, verification of new ELISA kit lots prior to routine use, and

testing of internal positive and negative control sera in duplicate on every ELISA plate, in addition to the manufacturer-supplied controls. Test results were accepted only when both kit controls and internal quality control samples met predefined acceptance criteria. Internal quality assurance was further supported through blind sample testing, duplicate testing and retesting of previously analysed samples. Suspect samples were routinely verified using alternative ELISA platforms and serum neutralisation tests. External quality assurance was ensured through regular participation in proficiency testing programmes conducted by the Veterinary Laboratories Agency Quality Assurance Scheme (VETQAS), Animal and Plant Health Agency (APHA), United Kingdom, with 100% concordance achieved in all proficiency testing rounds. In addition, as part of a WOAH laboratory twinning project, 60 serum samples were independently tested by the World Reference Laboratory for IBR (APHA, United Kingdom) in 2023, and complete agreement was observed between the results of the two laboratories.

Statistical analysis:

For analysis, the dataset containing individual animal information, sample sources, and other relevant information, including test results, was maintained in a Microsoft Excel® spreadsheet. For further analysis, all suspect samples were treated as negative to obtain a dichotomous outcome. Under this classification, the diagnostic sensitivity and specificity of the IDEXX IBR gB ELISA were previously determined to be 96.47% and 97.21%, respectively (Sarangi et al. 2021b).

Apparent prevalence was calculated as the proportion of ELISA-positive animals among the total animals tested. True prevalence and corresponding 95% confidence intervals (CI) were estimated by adjusting for the diagnostic sensitivity and specificity of the assay using Epitools (Sergeant et al. 2018).

Differences in seroprevalence among species, cattle breed types, sex categories and age groups were assessed using the chi-square test. Univariable associations between IBR seropositivity and explanatory variables were evaluated by calculating odds ratios (OR) and 95% confidence intervals from contingency tables. The association between IBR seropositivity and *Brucella* seropositivity was also assessed using odds ratio analysis.

To identify factors independently associated with IBR seropositivity, multivariable logistic regression analysis was performed in Jamovi version 2.7 (The jamovi project 2025), with IBR serostatus as the binary outcome variable. Variables with biological relevance and/or significant associations in univariable analyses were included in the multivariable models. Adjusted odds ratios (AOR) and 95% confidence intervals were estimated after controlling for potential confounding effects. Statistical significance was considered at $p < 0.05$. Three multivariable logistic regression models were constructed. The primary model included species and sex as explanatory variables and utilized the complete dataset (n = 34,355) while adjusting for state-level variation. Since age information was available for a subset of animals, a secondary model was developed using records with complete age information (n = 18,426) to evaluate the independent effect of age on IBR seropositivity. This model included species, sex and age group as explanatory variables while adjusting for state. A third model

was restricted to cattle and was used to assess the association between breed type and IBR seropositivity after adjustment for sex, age group and state (n = 8,896). Adjusted odds ratios (AOR), 95% confidence intervals were calculated for all multivariable models. Model significance was assessed using likelihood-ratio chi-square tests.

RESULTS

Seroprevalence of IBR:

Screening of 34,355 bovines by gB ELISA test revealed an overall apparent seroprevalence of 31.95% (95% CI: 31.46–32.45%), while the estimated true prevalence after adjustment for test sensitivity and specificity was 31.13% (95% CI: 30.61–31.66%). Considerable variation in seropositivity was observed across Indian states (Fig. 1). Seropositive animals were detected in all surveyed states, indicating widespread circulation of the pathogen across diverse agro-climatic regions of the country. Species-wise analysis revealed a significantly higher true seroprevalence in buffaloes [37.69% (95% CI: 36.86–38.52%)] than in cattle [26.10% (95% CI: 25.43–26.77%)] ($p < 0.001$) (Table 1). Among cattle, indigenous breeds exhibited the highest seroprevalence [36.16% (95% CI: 35.09–37.24%)], followed by exotic [18.41% (95% CI: 16.86–20.05%)] and crossbred cattle [17.45% (95% CI: 16.54–18.40%)], with significant differences observed among breed categories ($p < 0.001$) (Table 1). Breed-level analysis demonstrated substantial variation in seropositivity among individual breeds. Among breeds represented by more than 400 animals, the highest seroprevalence was recorded in Banni buffaloes (78.1%), followed by Pandharpuri (57.9%) and Mehsana buffaloes (45.9%). Murrah buffaloes constituted the largest breed group included in the study (n = 11,534) and showed a seroprevalence of 34.0%. Among cattle breeds, Tharparkar (41.4%), Kankrej (40.3%) and Sahiwal (36.4%) exhibited comparatively high seropositivity.

Table 1
Apparent and true seroprevalence of infectious bovine rhinotracheitis (IBR) in bovines according to species, breed type, sex, age group and state

Variable	Description	Total	Apparent prevalence		True prevalence	
			% positivity	95% CI	% positivity	95% CI
Species	Buffalo	14929	38.09	37.32–38.88	37.69	36.86–38.52
	Cattle	19426	27.24	26.62–27.87	26.10	25.43–26.77
Cattle Breed type	Crossbred	7852	19.14	18.29–20.03	17.45	16.54–18.40
	Exotics	2740	20.04	18.58–21.58	18.41	16.86–20.05
	Indigenous	8834	36.67	35.67–37.68	36.16	35.09–37.24
Sex	Male	15710	25.07	24.40-25.76	23.79	23.07–24.52
	Female	18645	37.75	37.06–38.45	37.32	36.58–38.07
Age	< 2 years	10990	21.87	21.10-22.65	20.36	19.55–21.20
	2–5 years	2887	30.45	28.80–32.15	29.52	27.76–31.34
	> 5 years	4549	45.68	44.24–47.13	45.78	44.24–47.33
State	Andhra Pradesh	1095	13.42	11.53–15.57	11.35	09.33–13.64
	Chhattisgarh	203	91.13	86.42–74.32	94.30	89.27–97.70
	Gujarat	9127	32.75	31.79–33.72	31.98	30.96–33.02
	Haryana	7553	38.85	37.75–39.95	38.49	37.32–39.67
	Karnataka	33	39.39	24.68–56.32	39.07	23.37–57.14
	Kerala	295	6.44	4.16–9.84	3.90	1.46–7.53
	Madhya Pradesh	192	29.17	23.20-35.95	28.16	21.78–35.40

Variable	Description	Total	Apparent prevalence		True prevalence	
			% positivity	95% CI	% positivity	95% CI
	Maharashtra	3313	30.00	28.47–31.59	29.05	27.41–30.74
	Punjab	5487	27.08	25.92–28.27	25.93	24.69–27.20
	Rajasthan	2315	38.23	36.27–40.23	37.83	35.74–39.96
	Tamil Nadu	1407	24.73	22.55–27.05	23.42	21.09–25.90
	Uttar Pradesh	2935	28.45	26.85–30.11	27.39	25.68–29.16
	Uttarakhand	400	21.75	17.99–26.05	20.24	16.22–24.83
Total		**34355**	**31.95**	**31.46–32.45**	**31.13**	**30.61–31.66**

Female animals exhibited a higher seroprevalence [37.32% (95% CI: 36.58–38.07%)] than males [23.79% (95% CI: 23.07–24.52%)] ($p < 0.001$). An age-related increase in seropositivity was also observed. Animals younger than two years exhibited a prevalence of 20.36% (95% CI: 19.55–21.20%), whereas animals aged 2–5 years and > 5 years had prevalences of 29.52% (95% CI: 27.76–31.34%) and 45.78% (95% CI: 44.24–47.33%), respectively.

Univariable analysis of risk factors:

Univariable analysis identified significant associations between IBR seropositivity and species, breed type, sex and age (Table 2). Buffaloes were 1.64 times more likely to be seropositive than cattle (OR = 1.64; 95% CI: 1.57–1.72; $p < 0.001$). Female animals exhibited significantly higher odds of seropositivity than males (OR = 1.81; 95% CI: 1.73–1.90; $p < 0.001$). Compared with animals younger than 2 years, bovines aged 2–5 years and > 5 years had 1.59-fold (95% CI: 1.45–1.77) and 3.01-fold (95% CI: 2.79–3.24) higher odds of seropositivity, respectively ($p < 0.001$). Among cattle breeds, crossbred cattle had significantly lower odds of seropositivity than indigenous cattle (OR = 0.41; 95% CI: 0.38–0.44; $p < 0.001$), whereas no significant difference was observed between exotic and indigenous cattle (OR = 0.94; 95% CI: 0.85–1.05; $p = 0.3075$).

Table 2
Univariable logistic regression analysis of factors associated with infectious bovine rhinotracheitis (IBR) seropositivity in bovines

Variable	Description	% positivity	Odds Ratio	95% CI	*p* value
Species	Buffalo	37.69	**1.64**	**1.57–1.72**	< 0.001
	Cattle	26.1	1.00		
Cattle Breed type	Exotics	18.41	1.00	0.85 to 1.05	0.3075
	Crossbred	17.45	0.94	0.83–1.06	0.31
	Indigenous	36.16	2.53	2.28–2.81	< 0.001
Sex	Female	37.32	**1.81**	**1.73 to 1.90**	< 0.001
	Male	23.79	1.00		
Age	< 2 years	20.36	1.00		
	2–5 years	29.52	**1.59**	**1.45 to 1.77**	< 0.001
	> 5 years	45.78	**3.01**	**2.79 to 3.24**	< 0.001

Multivariable analysis of risk factors:

Multivariable logistic regression analysis was performed to identify factors independently associated with IBR seropositivity while controlling for geographical variation among states (Table 3). In the primary model utilizing the complete dataset (n = 34,355), both species and sex were significantly associated with IBR seropositivity. Buffaloes had significantly higher odds of seropositivity than cattle (AOR = 2.20; 95% CI: 2.07–2.34; $p < 0.001$), while female animals had 2.13-fold higher odds of seropositivity than males (AOR = 2.13; 95% CI: 2.03–2.24; $p < 0.001$).

Table 3
Multivariable logistic regression analysis of factors associated with infectious bovine rhinotracheitis (IBR) seropositivity in bovines

Variable	Description	Adjusted Odds Ratio (AOR)	95% CI	*p* value
Model I (Primary model; All animal; n = 34,355)*				
Species	Buffalo	**2.20**	**2.07–2.34**	< 0.001
	Cattle (Ref.)	1.00	-	-
Sex	Female	**2.13**	**2.02–2.24**	< 0.001
	Male (Ref.)	1.00		
Model II (Age-adjusted model; All bovines with age data; n = 18,426)**				
Species	Buffalo	**1.57**	**1.44–1.71**	< 0.001
	Cattle (Ref.)	1.00	-	-
Sex	Female	**1.32**	**1.17–1.49**	< 0.001
	Male (Ref.)	1.00		
Age	2–5 years	**1.45**	**1.29–1.64**	< 0.001
	> 5 years	**2.18**	**1.91–2.49**	< 0.001
	< 2 years (Ref.)	1.00	-	-
Model III (Cattle only model; n = 8,698)***				
Breed type	Indigenous	2.20	1.81–2.67	< 0.001
	Crossbred	0.81	0.63–1.04	0.096
	Exotic (Ref.)	1.00	-	-
Sex	Female	1.72	1.44–2.05	< 0.001
	Male (Ref.)	1.00		
Age	2–5 years	**2.11**	**1.78–2.50**	< 0.001
	> 5 years	**2.07**	**1.71–2.52**	< 0.001
Ref. = Reference category				
* Model I adjusted for state.				
** Model II adjusted for state and included only animals with available age data.				
*** Model III adjusted for state and included only cattle with co				
mplete breed, age and sex information.				

Variable	Description	Adjusted Odds Ratio (AOR)	95% CI	*p* value
Model I (Primary model; All animal; n = 34,355)*				
	< 2 years (Ref.)	1.00	-	-
Ref. = Reference category				
* Model I adjusted for state.				
** Model II adjusted for state and included only animals with available age data.				
*** Model III adjusted for state and included only cattle with co				
mplete breed, age and sex information.				

To evaluate the effect of age, a secondary multivariable model was constructed using animals for which age information was available (n = 18,426). Inclusion of age in the model reduced the magnitude of the species and sex associations observed in the primary model, indicating that age acted as a confounding factor. Nevertheless, both variables remained significantly associated with IBR seropositivity after adjustment. Buffaloes exhibited 1.57-fold higher odds of seropositivity than cattle (AOR = 1.57; 95% CI: 1.44–1.71; $p < 0.001$), while females had 1.32-fold higher odds of seropositivity than males (AOR = 1.32; 95% CI: 1.17–1.49; $p < 0.001$). A significant age-dependent increase in IBR seropositivity was observed, with animals aged 2–5 years and > 5 years exhibiting 1.45-fold (95% CI: 1.29–1.64; $p < 0.001$) and 2.18-fold (95% CI: 1.91–2.49; $p < 0.001$) higher odds of seropositivity, respectively, compared with animals younger than 2 years (Table 3).

A separate multivariable logistic regression model was developed for cattle to assess the effect of breed type while adjusting for sex, age and state (n = 8,896). Indigenous cattle had significantly higher odds of IBR seropositivity than exotic cattle (AOR = 2.20; 95% CI: 1.81–2.67; $p < 0.001$), whereas no significant difference was observed between crossbred and exotic cattle (AOR = 0.81; 95% CI: 0.63–1.04; $p = 0.096$). Female cattle had significantly higher odds of seropositivity than male cattle (AOR = 1.72; 95% CI: 1.44–2.05; $p < 0.001$). Age was also independently associated with IBR seropositivity within cattle populations, with animals aged 2–5 years and > 5 years exhibiting 2.11-fold (95% CI: 1.78–2.49; $p < 0.001$) and 2.07-fold (95% CI: 1.71–2.52; $p < 0.001$) higher odds of seropositivity, respectively, compared with cattle younger than 2 years (Table 3).

Association between IBR and brucellosis seropositivity

The association between IBR and brucellosis serostatus was evaluated in animals, with results available for both diseases (Table 4). Brucella seropositivity was detected in 659 IBR-positive animals and 595 IBR-negative animals. Bovines seropositive for IBR were significantly more likely to be seropositive for brucellosis than IBR-negative animals (OR = 2.42; 95% CI: 2.16–2.71; $p < 0.001$), indicating a strong positive association between the two infections.

Table 4
Association between infectious bovine rhinotracheitis (IBR) and brucellosis seropositivity in bovines

		IBR		Odds Ratio	95% CI	*p* value
		Positive	Negative			
Brucellosis	**Positive**	659	595	2.42	2.16–2.71	< 0.001
	Negative	10031	21940			

DISCUSSION

The present investigation revealed a high burden of IBR-associated seropositivity in Indian dairy bovines, with an overall true seroprevalence of 31.13% (95% CI: 30.61–31.66%). Since vaccination against IBR is not routinely practised in India, the detected antibodies are likely to reflect natural exposure to the virus. The widespread occurrence of seropositive animals across all surveyed states further supports the endemic status of the infection in the country. The prevalence observed in the present study was remarkably similar to that reported in a recent nationwide survey by Patil et al. (2022) and to estimates from Ethiopia, Belgium and Ireland (Sibhat et al. 2018; Barrett et al. 2018; Boelaert et al. 2000; Asmare et al. 2023). In contrast, substantially higher seroprevalence has been reported from Pakistan, Brazil, Kazakhstan and certain regions of Egypt, whereas lower estimates have been documented from Kenya, Egypt and Nepal (Fernandes et al. 2019; Rehman et al. 2020; Kipyego et al. 2020; Mahmoud and Ali 2022; Paudel et al. 2022; Karabassova et al. 2026). Collectively, these findings indicate that IBR remains widely distributed globally, although its prevalence varies considerably between regions and production systems.

Variation in seroprevalence across countries and regions is likely influenced by differences in herd density, production systems, management practices, breeding methods, biosecurity measures, sampling strategies and diagnostic tests employed (Segura-Correa et al. 2016; Kipyego et al. 2020; El-Sheikh et al. 2024; Karabassova et al. 2026). Notably, the prevalence observed in the present study was substantially lower than the 51.6% reported by Renukaradhya et al. (1996), one of the earliest multi-state investigations of IBR seroprevalence in India. Although direct comparisons between studies should be interpreted cautiously because of differences in study design, geographical coverage and sampled populations, the relatively lower prevalence reported in recent nationwide investigations may reflect improvements in breeding practices and disease control measures implemented in the Indian dairy sector over the past three decades. In particular, the widespread adoption of artificial insemination and implementation of the Minimum Standard Protocol for Production of Bovine Frozen Semen issued by the Department of Animal Husbandry and Dairying (DAHD), Government of India, may have contributed to reducing dependence on natural service and limiting the dissemination of infection through contaminated semen. While the impact of these interventions cannot be quantified from the present study, they may have played an important role in reducing venereal transmission and restricting the spread of infection within Indian dairy populations.

A major finding of the present study was the significantly higher seroprevalence in buffaloes (38.1%) than in cattle (27.2%). This association remained significant after adjustment for age, sex and geographical location, with buffaloes showing 1.57-fold higher odds of seropositivity. Similar observations have been reported from India and other endemic regions (Renukaradhya et al. 1996; Trangadia et al. 2010; El-Sheikh et al. 2024), although some studies have reported either higher prevalence in cattle or no significant species-wise differences (Verma et al. 2014; Patil et al. 2022). The higher seropositivity in buffaloes may partly be attributable to exposure to antigenically related alphaherpesviruses, particularly *Varicellovirus bubalinealpha1* (formerly called bubaline alphaherpesvirus-1, BuAHV-1), which shares substantial antigenic similarity with BoAHV-1 and may induce antibodies detectable by gB-based ELISA assays. Recent evidence from India has demonstrated a high seroprevalence of BuAHV-1 in buffalo populations (Chandrasekhar Reddy et al. 2025), suggesting that a proportion of ELISA-positive buffaloes may have been exposed to BuAHV-1 rather than BoAHV-1 alone. Differences in management practices may also contribute to the higher seropositivity recorded in buffaloes. Supporting this hypothesis, exceptionally high seroprevalence was observed among buffaloes in Banni (78.1%), Pandharpuri (57.9%), and Mehsana (45.9%). Banni buffaloes are traditionally reared by Maldhari pastoral communities under extensive grazing systems in Kutch, Gujarat, while Pandharpuri buffaloes are largely restricted to their native breeding tract in southern Maharashtra. The high seroprevalence observed in these geographically localized breeds suggests long-term endemic circulation of alphaherpesviruses within their native populations.

Another notable findings of the present study was the significantly higher seroprevalence in indigenous cattle compared with exotic and crossbred cattle. After adjustment for potential confounders, indigenous cattle had 2.20-fold higher odds of seropositivity than exotic cattle. Similar findings have been reported earlier (Danu et al. 2024; El-Sheikh et al. 2024), although several earlier studies suggested greater susceptibility of exotic and crossbred cattle to infection (Saravanajayam et al. 2015; Sibhat et al. 2018; Ortiz-Gonzalez et al. 2022; Ghougal et al. 2026). However, seropositivity is influenced not only by host susceptibility but also by the intensity and duration of exposure to infection. Therefore, the higher seroprevalence observed in indigenous cattle in the present study should not necessarily be interpreted as evidence of greater biological susceptibility. Rather, it may reflect differences in management practices, production systems and exposure opportunities. Indigenous cattle are commonly maintained under extensive or semi-intensive systems involving communal grazing, natural breeding and frequent contact with neighbouring herds, whereas exotic and crossbred cattle are often managed under more intensive systems with better reproductive management and biosecurity. The relatively high seroprevalence observed in indigenous breeds such as Tharparkar (41.4%), Kankrej (40.3%) and Sahiwal (36.4%) supports the hypothesis that differences in exposure opportunities and management practices may be more important than genetic susceptibility in explaining the observed breed-wise variation.

Female animals showed significantly higher seropositivity than males in both univariable and multivariable analyses. Although females remained at higher risk after adjusting for age and geographical location, the association became weaker after adjustment, indicating that part of the observed sex difference was influenced by the greater proportion of older animals among females

retained for breeding and milk production. Similar observations have been reported previously (Kaddour et al. 2019; Ortiz-Gonzalez et al. 2022; Danu et al. 2024). However, contradictory findings have also been reported, suggesting that sex is likely a secondary risk factor influenced by management practices and herd structure rather than an inherent biological predisposition (Raaperi et al. 2014; Waldeck et al. 2021; El-Sheikh et al. 2024; Ghougal et al. 2026).

Age was identified as an important risk factor for IBR seropositivity, with animals aged 2–5 years and > 5 years exhibiting 1.45-fold and 2.18-fold higher odds of seropositivity, respectively, compared with animals younger than two years. This finding is consistent with numerous previous studies that have identified age as one of the most important and consistent risk factors associated with BoAHV-1 infection (Raaperi et al. 2014; Saravanajayam et al. 2015; Segura-Correa et al. 2016; Sibhat et al. 2018). The higher seroprevalence observed in older animals is most likely attributable to cumulative exposure over time and the lifelong latent nature of BoAHV-1 infection. Periodic reactivation of the virus helps maintain detectable antibody levels for extended periods, allowing infected animals to remain seropositive and act as a source of infection for susceptible animals.

An additional finding of the present study was the significant association between IBR and brucellosis seropositivity, with IBR-positive animals being 2.42 times more likely to be seropositive for brucellosis. Similar associations between IBR seropositivity and other infectious diseases, including brucellosis, bovine viral diarrhoea, Q fever, neosporosis and leptospirosis, have been reported previously (Waldeck et al. 2021; Sarangi et al. 2021a; Naveena et al. 2022). A plausible explanation for this association is the immunosuppressive nature of BoAHV-1 infection increasing susceptibility to secondary infections (Biswas et al. 2013; Jones 2019). Nevertheless, the observed association may also be influenced by shared epidemiological risk factors, including management practices, breeding systems and biosecurity measures that facilitate exposure to multiple pathogens within the same production system.

The high seroprevalence of IBR observed in the present study highlights the need for implementation of comprehensive control measures. Although artificial insemination and semen screening programmes have likely reduced venereal transmission, these measures alone are insufficient to control a disease characterized by lifelong latency and periodic viral reactivation. Several countries have successfully controlled or eradicated IBR through integrated programmes combining glycoprotein E (gE)-deleted marker vaccines with surveillance and movement control. Previous studies have demonstrated that vaccination can substantially reduce BoAHV-1 transmission within herds, with the basic reproduction number (R_0) declining from approximately 2.8–7.0 in unvaccinated populations to levels approaching or below the threshold required for sustained transmission (reviewed in Raaperi et al., 2014; Brock et al., 2020). In India, field evaluation of a commercially available inactivated gE-deleted marker vaccine demonstrated significant reductions in disease occurrence and abortion rates in endemic dairy herds (Sarangi et al. 2020). Furthermore, gE-deleted marker vaccines have been shown to confer protection against BuAHV-1 infection in buffaloes (Montagnaro et al. 2015; Martucciello et al. 2023). Considering the endemic nature of IBR in India, preventive vaccination using marker vaccines may be particularly beneficial in organized dairy herds, milk-shed areas and regions implementing breed improvement

programmes such as progeny testing and pedigree selection. Such interventions would help reduce virus circulation, improve reproductive performance and increase the availability of IBR-free breeding stock. However, vaccination should form part of a broader control strategy that includes enhanced surveillance, routine testing of breeding animals and semen, strengthened farm biosecurity, regulation of animal movement and farmer awareness programmes. Adoption of such an integrated approach would reduce the burden of IBR while improving herd productivity and sustainability of dairy production systems.

The present study has several important strengths. It represents the largest study conducted on IBR seroprevalence in India in terms of the number of animals analysed and includes a diverse population of cattle and buffaloes representing 29 cattle breeds and 9 buffalo breeds. Serological testing was performed using a validated commercial ELISA, and prevalence estimates were adjusted using experimentally determined diagnostic sensitivity and specificity values. The study however, has certain limitations that should be considered while interpreting the findings. The study was retrospective and observational in nature, and therefore the identified associations should not be interpreted as causal relationships. In addition, the gB ELISA used in the study could not differentiate antibodies induced by BoAHV-1 from those induced by related alphaherpesviruses such as BuAHV-1, BoAHV-5 and CpAHV-1. Furthermore, the samples were originally collected for breed improvement programmes and not specifically for epidemiological investigation of IBR; consequently, complete randomization was not possible and the study population may not be fully representative of the national bovine population. Nevertheless, the large sample size, extensive geographical coverage, broad breed representation and inclusion of samples collected over a nine-year period (2016–2024) provide robust baseline information on the epidemiology of IBR in Indian bovines. These findings can guide surveillance activities, inform disease control policies and support the development of a national IBR control programme in India.

CONCLUSION

The present study provides a comprehensive assessment of IBR seroprevalence in Indian bovines based on the largest animal-level dataset analysed to date in the country. The estimated true seroprevalence of 31.13% confirms that IBR and related alphaherpesvirus infections remain widely distributed and endemic in Indian dairy populations. Buffaloes, indigenous cattle, female animals and older bovines exhibited significantly higher odds of seropositivity, highlighting the influence of host and management-related factors on disease occurrence. The significantly higher seropositivity observed in buffaloes and indigenous cattle suggests that exposure patterns, husbandry practices and the possible contribution of antigenically related alphaherpesviruses such as BuAHV-1 may play an important role in shaping the epidemiology of the disease in India.

The findings emphasize the need for strengthening surveillance and implementing integrated control strategies, including enhanced biosecurity, continued monitoring of breeding animals and semen, and strategic use of marker vaccines, particularly in organized dairy herds and breed improvement programmes. The study provides valuable baseline information for future epidemiological investigations and offers a scientific foundation for the development of a national IBR control programme in India.

Declarations

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Author Contribution:

LNS and PNM conceived and designed the study. AP and SS performed laboratory testing and contributed to data compilation. AP and KSNL were involved in data validation, curation and resource management. LNS conducted the statistical analyses. LNS, AP and KSNL were responsible for quality assurance and quality control of laboratory testing. LNS prepared the initial draft of the manuscript, and PNM critically reviewed and edited the manuscript. All authors contributed to interpretation of the results, reviewed the manuscript and approved the final version for publication.

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Competing Interests: The authors declare competing interest related to this article.

Data availability: All the data related to the study are given in the manuscript. The raw datasets of the current study are available from the corresponding author on reasonable request.

Ethical approval: The present study was based on retrospective analysis of laboratory data generated from routine infectious bovine rhinotracheitis (IBR) and brucellosis screening activities conducted under progeny testing and pedigree selection programmes. No animals were sampled or subjected to additional procedures specifically for this investigation. Consequently, approval from an Institutional Animal Ethics Committee was not required. All samples had been collected as part of routine disease surveillance and breed improvement activities, and all data were analysed in anonymized form.

References

1. Asmare K, Aragaw K, Sibhat B, Abayneh T, Gelaye E, Getachew B, Egan S (2023) Seroprevalence and risk factors associated with bovine herpesvirus 1 (BHV-1) infection in dairy cattle in southern and central Ethiopia. Prev Vet Med. 217:105959. https://doi.org/10.1016/j.prevetmed.2023.105959;
2. Barrett D, Lane E, Lozano JM, O'Keeffe K, Byrne AW (2024) Bovine Herpes Virus Type 1 (BoHV-1) seroprevalence, risk factor and Bovine Viral Diarrhoea (BVD) co-infection analysis from Ireland. Sci Rep 14(1):867. https://doi.org/10.1038/s41598-023-50433-5
3. Barrett D, Parr M, Fagan J, Johnson A, Tratalos J, Lively F, Diskin M, Kenny D (2018) Prevalence of Bovine Viral Diarrhoea Virus (BVDV), Bovine Herpes Virus 1 (BHV 1), Leptospirosis and Neosporosis, and associated risk factors in 161 Irish beef herds. BMC Vet Res 14(1):8. https://doi.org/10.1186/s12917-017-1324-9.)

4. Biswas S, Bandyopadhyay S, Dimri U, Patra PH (2013) Bovine herpesvirus-1 (BHV-1) - a re-emerging concern in livestock: a revisit to its biology, epidemiology, diagnosis, and prophylaxis. Vet Q 33(2):68–81. https://doi.org/10.1080/01652176.2013.799301.
5. Black EJ, Powell CS, Dempsey DM, Hendrickson RC, Mims LR, Lefkowitz EJ (2026) Virus taxonomy: the database of the International Committee on Taxonomy of Viruses. Nucleic Acids Res 54(D1): D776-D789. https://doi.org/10.1093/nar/gkaf1159
6. Boelaert F, Biront P, Soumare B, Dispas M, Vanopdenbosch E, Vermeersch JP, Raskin A, Dufey J, Berkvens D, Kerkhofs P (2000) Prevalence of bovine herpesvirus-1 in the Belgian cattle population. Prev Vet Med 45(3–4):285–95. https://doi.org/10.1016/s0167-5877(00)00128-8.
7. Brock J, Lange M, Guelbenzu-Gonzalo M, Meunier N, Vaz AM, Tratalos JA, Dittrich P, Gunn M, More SJ, Graham D, Thulke HH (2020) Epidemiology of age-dependent prevalence of Bovine Herpes Virus Type 1 (BoHV-1) in dairy herds with and without vaccination. Vet Res 51(1):124. https://doi.org/10.1186/s13567-020-00842-5;
8. Chandrasekhar Reddy RV, Bajibabu P, Sarangi LN, Rana SK, Surendra KSNL, Ponnanna NM, Sharma GK (2020). Shedding of bovine alphaherpesvirus-1 in bovine extended frozen semen in Indian semen stations: A longitudinal analysis. *Theriogenology* 157:467–471. https://doi.org/10.1016/j.theriogenology.2020.08.021.
9. Chandrasekhar Reddy RV, Thodangala N, Gonuguntla HN, Poojitha GUS, Chandaka KD, Gujjala M, Palamuru P, Surendra KSNL, Sarangi LN, Ponnanna NM 2025 Isolation, identification and extent of positivity of Bubaline alphaherpesvirus 1 (BuAHV1) in India. Braz J Microbiol 56(3):2045–2057. https://doi.org/10.1007/s42770-025-01670-5
10. Danu AM, Deresa AK, Dinagde CG (2024) Seroprevalence and Associated Risk Factors of Infectious Bovine Rhinotracheitis (IBR) and Animal Owners' Knowledge, Attitude and Practice (KAP) Towards the Disease in Selected Districts of East Wollega Zone, Oromia Regional State, Ethiopia. Vet Med Sci 10(6):e70043. https://doi.org/10.1002/vms3.70043;
11. Das P, Mohanty NN, Ranganatha S, Ranabijuli S, Sarangi LN, Panda HK (2014) A comparative evaluation of avidin-biotin ELISA and micro SNT for detection of antibodies to infectious bovine rhinotracheitis in cattle population of Odisha, India. Vet World 7: 548–552. https://doi.org/10.14202/vetworld.2014.548-552
12. El-Sheikh ME, Bakar L, El-Mekawy MF, Eisa MI, Abouzeid NZ, Abdelmonim MI, Yousef SG (2024) Seroprevalence and risk factors of infectious bovine rhinotracheitis in cattle in Gharbia governorate, Egypt: A comparative study of traditional and commercial production systems. Open Vet J 14(11):2960–2969. https://doi.org/10.5455/OVJ.2024.v14.i11.24
13. Fernandes LG, Denwood MJ, de Sousa Américo Batista Santos C, Alves CJ, Pituco EM, de Campos Nogueira Romaldini AH, De Stefano E, Nielsen SS, de Azevedo SS (2019) Bayesian estimation of herd-level prevalence and risk factors associated with BoHV-1 infection in cattle herds in the State of Paraíba, Brazil. Prev Vet Med 169:104705. https://doi.org/10.1016/j.prevetmed.2019.104705;

14. Ghougal K, Baghezza S, Azizi A, Kerkoub H, Ghougal O, Becheur M, Haif A, Mokhtar-Rahmani M, Djokhdem L (2026) Seroprevalence, distribution, and risk factors of infectious bovine rhinotracheitis in eastern and southern Algeria. Vet Ital 62(1):1–12 https://doi.org/10.12834/VetIt.3900.38314.2.
15. Jones C (2019) Bovine Herpesvirus 1 Counteracts Immune Responses and Immune-Surveillance to Enhance Pathogenesis and Virus Transmission. Front Immunol 10:1008. doi: 10.3389/fimmu.2019.01008.
16. Kaddour A, Bouyoucef A, Fernandez G, Prieto A, Geda F, Moula N (2019) Bovine herpesvirus 1 in the northeast of Algiers, Algeria: Seroprevalence and associated risk factors in dairy herd. J Adv Vet Anim Res 6(1):60–65. https://doi.org/10.5455/javar.2019.f312.
17. Karabassova A, Kirpichenko V, Nissanova R, Turkeev M, Akylbay A, Akshalova P, Bashenova E, Tulepov B, Mamanova S, Kaimoldina S, Zhapbar A, Ikramkulova F, Kassen A, Zharmukhametova A, Abay Z, Yussupov M, Zakarya K, Rsaliyev A, Abduraimov Y, Zhetpisbay Z, Sairambekova G, Nurpeisova A and Kassenov M (2026) Serological and molecular surveillance of infectious bovine rhinotracheitis in Kazakhstan. Front Vet Sci 12:1734128. https://doi.org/10.3389/fvets.2025.1734128
18. Kipyego ES, Gitau G, Vanleeuwen J, Kimeli P, Abuom TO, Gakuya D, Muraya J, Makau D (2020) Sero-prevalence and risk factors of infectious bovine rhinotracheitis virus (type 1) in Meru County, Kenya. Prev Vet Med 175:104863. https://doi.org/10.1016/j.prevetmed.2019;
19. Kolech TA, Kebede YK, Mekonnen SA (2025) Seroprevalence and associated risk factors of bovine herpesvirus 1 in smallholder dairy farms in two districts of Gondar zones, North-West Ethiopia. Prev Vet Med 234:106367. https://doi.org/10.1016/j.prevetmed.2024.106367
20. Mahmoud H, Ali A (2022) Epidemiological investigation on Bovine alphaherpesvirus 1 and bovine viral diarrhea virus in cattle and camels in southern Egypt. Vet Ital 58(4). https://doi.org/10.12834/VetIt.2361.14459.2;
21. Martucciello A, Balestrieri A, Righi C, Cappelli G, Scoccia E, Grassi C, Brandi S, Rossi E, Galiero G, Gioia D, Fusco G, Feliziani F, De Carlo E, Petrini S (2023) Evaluation of an Immunization Protocol Using Bovine Alphaherpesvirus 1 gE-Deleted Marker Vaccines against Bubaline Alphaherpesvirus 1 in Water Buffaloes. Vaccines (Basel) 11(5):891. https://doi.org/10.3390/vaccines11050891
22. Montagnaro S, De Martinis C, Iovane V, Ciarcia R, Damiano S, Nizza S, De Martino L, Iovane G, Pagnini U (2014) Bovine herpesvirus type 1 marker vaccine induces cross-protection against bubaline herpesvirus type 1 in water buffalo. Prev Vet Med 116(1–2):56–62. https://doi.org/10.1016/j.prevetmed.2014.06.002.
23. Muylkens B, Thiry J, Kirten P, Schynts F, Thiry E (2007) Bovine herpesvirus 1 infection and infectious bovine rhinotracheitis. Vet Res 38:181–209. https://doi.org/10.1051/vetres: 20060 59;
24. Nandi S, Kumar M, Manohar M, Chauhan RS (2009) Bovine herpes virus infections in cattle. Anim Health Res Rev 10(1):85–98. https://doi.org/10.1017/S1466252309990028.
25. Naveena T, Sarangi LN, Rana SK, Prasad A, Suryaprabha T, Jhansi Reddy D, Ponnanna NM, Sharma GK (2022) Seroprevalence to common infectious abortifacient and infertility causing agents in the

dairy herds of India. Iran J Vet Res 23(3):189–195. https://doi.org/10.22099/IJVR.2022.42574.6184.

26. Nickell JS, White BJ (2010) Metaphylactic antimicrobial therapy for bovine respiratory disease in stocker and feedlot cattle. Vet Clin North Am Food Anim Pract 26(2):285–301. https://doi.org/10.1016/j.cvfa.2010.04.006.;
27. Ortiz-González AD, Buitrago HAL, Bulla-Castañeda DM, Lancheros-Buitrago DJ, Garcia-Corredor DJ, Díaz-Anaya AM, Tobón-Torreglosa JC, Ortiz-Ortega D, Pulido-Medellín MO (2022) Seroprevalence and risk factors associated with bovine herpesvirus 1 in dairy herds of Colombia. Vet World 15(6):1550–1556. https://doi.org/10.14202/vetworld.2022.1550-1556;
28. Patil SS, Suresh KP, Velankar A, Shivaranjini C, Hemadri D, Hiremath J, Jacob SS (2022) Seroprevalence of Infectious bovine rhinotracheitis (IBR) in India: A 5-year study. Vet Ital 58(3):339–345 https://doi.org/10.12834/VetIt.2433.16160.1;
29. Paudel S, Subedi D, Shrestha S, Acharya M, Chandran D, Dhama K (2022) Seroprevalence and risk factors of infectious bovine rhinotracheitis in dairy cattle of Chitwan, Nawalpur and Rupandehi Districts of Nepal. J Exp Biol Agric Sci 10:1100–1108. https://doi.org/10.18006/2022.10(5).1100.1108
30. Raaperi K, Orro T, Viltrop A (2014) Epidemiology and control of bovine herpesvirus 1 infection in Europe. Vet J 201(3):249–56. https://doi.org/10.1016/j.tvjl.2014.05.040;
31. Rehman H, Rabbani M, Ghafoor A, Riaz A, Awan FN, Raza S (2020) First isolation and genetic characterization of Bovine herpesvirus 1 from cattle in Pakistan. Pak Vet J 41:163–165. https://doi.org/10.29261/pakvetj/2020.092
32. Renukaradhya GJ, Rajasekhar M, Raghavan R (1996) Prevalence of infectious bovine rhinotracheitis in southern India. Rev Sci Tech 15(3):1021–8. https://doi.org/10.20506/rst.15.3.970;
33. Rimayanti R, Khairullah AR, Lestari TD, Moses IB, Utama S, Damayanti R, Mulyati S, Raharjo HM, Kusala MKJ, Raissa R, Wibowo S, Abdila SR, Fauzia KA, Yanestria SM, Fauziah I, Siregar JE (2024) Infectious bovine rhinotracheitis: Unveiling the hidden threat to livestock productivity and global trade. Open Vet J 14(10):2525–2538. https://doi.org/10.5455/OVJ.2024.v14.i10.3;
34. Sandhyarani M, Chandrasekhar Reddy RV, Ponnanna NM, Sarangi LN (2025) Optimizing surveillance: feasibility of pooled sample testing for bovine alphaherpesvirus 1 detection by real–time PCR. Virus Dis 36(3):518–523. https://doi.org/10.1007/s13337-025-00934-w
35. Sarangi LN, Rana SK, Dash SK, Bhattacharya K, Naveena T, Shroff AI, Reddy RVC, Prasad A, Surendra KSNL, Bahekar VS, Ponnanna NM and Sharma GK (2020) Pilot Control of Infectious Bovine Rhinotracheitis through inactivated marker vaccine: a field study in India. IDF Animal Health Report. 14: 15–17. (https://store.fil-idf.org/product/idf-animal-health-report-n-14/)
36. Sarangi LN, Reddy RVC, Rana SK, Naveena T, Ponnanna NM, Sharma GK (2021b) Sero-diagnostic efficacy of various ELISA kits for diagnosis of infectious bovine rhinotracheitis (IBR) in cattle and buffaloes in India. Vet Immunol Immunopathol 241:110324. https://doi.org/10.1016/j.vetimm.2021.110324.

37. Sarangi LN, Tharani N, Polapally S, Rana SK, Thodangala N, Bahekar VS, Prasad A, Chandrasekhar Reddy RV, Surendra KSNL, Gonuguntla HN, Ponnanna NM, Sharma GK. (2021a) Infectious bovine abortions: observations from an organized dairy herd. Braz J Microbiol 52(1):439–448. https://doi.org/10.1007/s42770-020-00414-x.
38. Saravanajayam M, Kumanan K, Balasubramaniam A (2015) Seroepidemiology of infectious bovine rhinotracheitis infection in unvaccinated cattle. Vet World 8(12):1416–9. doi: 10.14202/vetworld.2015.1416-1419;
39. Segura-Correa JC, Zapata-Campos CC, Jasso-Obregón JO, Martinez-Burnes J, López-Zavala R. (2016) Seroprevalence and risk factors associated with bovine herpesvirus 1 and bovine viral diarrhea virus in North-Eastern Mexico. Open Vet J 6(2):143–9. https://doi.org/10.4314/ovj.v6i2.12;
40. Sergeant, ESG (2017) Epitools epidemiological calculators. Retrieved from http://epitools.ausvet.com.au/.
41. Sibhat B, Ayelet G, Skjerve E, Gebremedhin EZ, Asmare K. (2018) Bovine herpesvirus-1 in three major milk sheds of Ethiopia: Serostatus and association with reproductive disorders in dairy cattle. Prev Vet Med 150:126–132. https://doi.org/10.1016/j.prevetmed.2017.12.019;
42. Tejaswi G, Reddy RVC, Ponnanna NM, Sarangi LN (2023) Molecular detection of bovine alphaherpesvirus-1 in cases of reproductive disorders among cattle and buffaloes in Gujarat. Virus Dis 34:526–530. https://doi.org/10.1007/s13337-023-00851-w
43. The jamovi project (2025) jamovi (Version 2.7) [Computer software]. Available at: https://www.jamovi.org
44. Trangadia B, Rana SK, Mukherjee F, Srinivasan VA (2010) Prevalence of brucellosis and infectious bovine rhinotracheitis in organized dairy farms in India. Trop Anim Health Prod 42(2):203–7. https://doi.org/10.1007/s11250-009-9407-7;
45. Verma AK, Kumar A, Sahzad, Reddy NC, Shende AN (2014) Seroprevalence of infectious bovine rhinotracheitis in dairy animals with reproductive disorders in Uttar Pradesh, India. Pak J Biol Sci 17(5):720–4. https://doi.org/10.3923/pjbs.2014.720.724
46. Waldeck HWF, van Duijn L, van den Heuvel-van den Broek K, Mars MH, Santman-Berends IMGA, Biesheuvel MM, van Schaik G (2021) Risk Factors for Introduction of Bovine Herpesvirus 1 (BoHV-1) Into Cattle Herds: A Systematic European Literature Review. Front Vet Sci 8:688935. https://doi.org/10.3389/fvets.2021.688935;

Figures

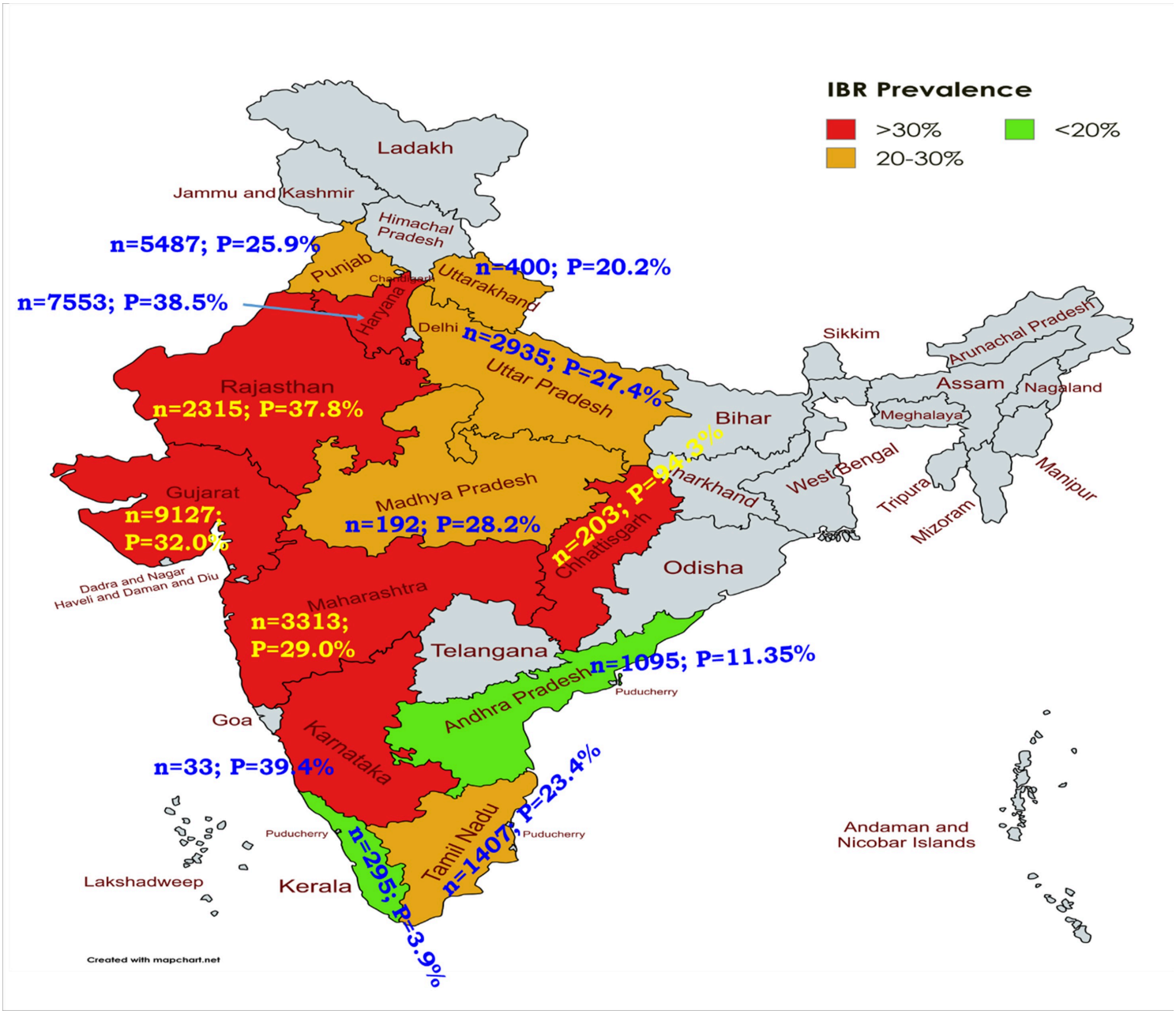


Figure 1

State-wise distribution of true seroprevalence of infectious bovine rhinotracheitis (IBR) in Indian bovines showing sample size and prevalence estimates