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Seroprevalence, distribution, and risk factors of infectious bovine rhinotracheitis in eastern and southern Algeria

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Abstract

Infectious bovine rhinotracheitis (IBR), caused by Bovine Herpesvirus-1 (BoHV-1), represents a significant economic burden on the global dairy industry through reduced productivity, reproductive disorders, and abortion. This cross-sectional study estimated the seroprevalence of IBR and identified associated risk factors among cattle in Eastern and Southern Algeria. Between September and December 2023, blood samples were collected from 380 cattle across 45 unvaccinated dairy farms in thirteen provinces. Sera were tested for BoHV-1 antibodies using a competitive enzyme-linked immunosorbent assay (cELISA), and seropositive samples underwent DIVA testing (Differentiating Infected from Vaccinated Animals) to detect glycoprotein E (gE) antibodies. Multivariable logistic regression analysis assessed risk factor associations with seropositivity. The overall seroprevalence was 38.95% (148/380), with a 100% herd-level prevalence. Among seropositive animals, 66.89% (99/148) were gE-positive, indicating natural infection, while 33.11% (49/148) were gE-negative, suggesting prior vaccination or vaccination exposure. Multivariable analysis identified four significant risk factors ($p < 0.05$): exotic origin (aOR = 5.33), large herd size (aOR = 2.12), age >3 years (aOR = 1.77), and breed, with crossbreeds showing lower susceptibility (aOR = 0.15) compared to Prim'Holstein cattle. These findings demonstrate widespread circulation of IBR in Algerian cattle, predominantly through natural infection rather than vaccination. The implementation of comprehensive control strategies, including official vaccination programmes utilizing DIVA-compatible vaccines and enhanced biosecurity measures, is crucial to mitigate economic losses in Algeria's dairy sector.

Keywords

Infectious bovine rhinotracheitis, herpesvirus-1, herpesvirus-1, Seroprevalence, DIVA testing, Algeria, Cattle

Introduction

Livestock production underpins global food security, rural livelihoods, and economic stability, with cattle providing essential resources, including meat, milk, and income for millions worldwide. However, infectious diseases continue to undermine sustainable cattle production by reducing productivity and compromising animal welfare. Bovine respiratory disease (BRD) is one of the most significant health challenges, accounting for approximately 50 % of feedlot cattle mortalities and resulting in substantial economic losses through decreased growth rates, reduced milk yield, and increased treatment costs (Ostler & Jones, 2023).

Bovine herpesvirus 1 (BoHV-1), a double-stranded DNA virus belonging to the Herpesviridae family and Varicellovirus genus, ranks among the most important and widely distributed BRD pathogens (Nagy et al., 2022). This virus causes infectious bovine rhinotracheitis (IBR) and infectious pustular vulvovaginitis (IPV) (Nandi et al., 2009). A defining characteristic of BoHV-1 infection is lifelong latency establishment in sensory neurons, with potential stress-induced reactivation and viral shedding, substantially complicating eradication efforts (Ackermann & Engels, 2006). Clinical manifestations encompass a diverse range of syndromes, including respiratory, ocular, reproductive, neurological, enteric, neonatal, and cutaneous disorders, underscoring the pathogen's epidemiological and economic significance (Iscaro et al., 2021).

The World Organization for Animal Health (WOAH) lists BoHV-1 as a transboundary animal disease due to its impact on international trade and cattle health. Several European countries, including Denmark, Austria, and Switzerland, have successfully eradicated BoHV-1 through rigorous test-and-slaughter or marker vaccination programmes, demonstrating achievable eradication under robust veterinary infrastructure (Raaperi et al., 2014). Conversely, the disease remains endemic in numerous low- and middle-income countries due to inadequate surveillance, limited vaccination coverage, and lack of coordinated control strategies (Klem et al., 2015).

In Africa, BoHV-1 prevalence varies considerably across regions, with recent studies reporting seroprevalence rates of 21.5% in Morocco (Alali et al., 2024), 22.5% in Egypt (El-Sheikh et al., 2024), 34.7% in Ethiopia (Tesfaye et al., 2022), 31.2% in northwestern Algeria (Derrar et al., 2019), 20.9% in Kenya (Callaby et al., 2016), and 23.28% in Zambia (Mweene et al., 2003). Despite evidence of BoHV-1 circulation, comprehensive epidemiological data from Algeria remain limited, with most studies constrained by small sample sizes or restricted geographic coverage. Few investigations have systematically assessed critical transmission dynamics parameters such as herd size, management practices, animal introduction patterns, or vaccination history (Ramírez Vásquez et al., 2016; Romero-Salas et al., 2013).

Algeria maintains one of North Africa's largest cattle populations, with approximately 1.9 million head, and the livestock sector plays a vital role in national food security and economic development (MADR, 2024). However, insufficient epidemiological data on IBR impede the design of effective prevention and control programmes. This knowledge gap is particularly concerning given that uncontrolled BoHV-1 circulation may compromise animal health and productivity, as well as Algeria's participation in regional and international livestock trade. The global "One Health" emphasis further underscores the importance of controlling viral infections that can interact with other pathogens, exacerbating BRD and increasing antimicrobial usage in livestock systems (Nickell & White, 2010).

Beyond respiratory disease, BoHV-1 causes reproductive losses, decreased milk production, and immunosuppression, which predispose animals to secondary infections (Ackermann & Engels, 2006). A critical gap concerns differentiating naturally infected from vaccinated animals using DIVA tests detecting glycoprotein E (gE) antibodies, essential for monitoring control programmes (Raaperi et al., 2014). In Algeria, where dairy productivity remains suboptimal and vaccination practices are poorly documented without an official IBR control programme, determining infection versus vaccination status is crucial for assessing field virus circulation and guiding evidence-based control strategies.

This study aims to estimate the IBR seroprevalence and geographic distribution in Eastern and Southern Algerian provinces, identify herd- and animal-level risk factors associated with BoHV-1 seropositivity, differentiate naturally infected from vaccinated animals using DIVA testing to assess true field virus circulation, and propose evidence-based control strategies for future disease control policies. By generating reliable epidemiological data, this investigation contributes to the evidence base for developing tailored prevention strategies, enhancing cattle productivity, and supporting Algeria's alignment with international animal health standards.

Materials and methods

Study design and area

A cross-sectional study was conducted from September to December 2023 across 45 dairy cattle farms, housing a total of 470 cattle, in thirteen Algerian provinces: seven from Eastern Algeria and six from Southern Algeria (Table I). The Eastern region features a continental climate with hot, dry summers (mean humidity ~48%) and cold winters, situated at an average elevation of 1,025 metres above sea level. The Southern region exhibits a hot desert climate with humidity below 20% year-round and extreme diurnal temperature variations. The desert climate dominates southern Algeria, accounting for 85% of the country's total land area (Benharchache et al., 2023). Dairy cattle farming is mainly structured into three production typologies: Modern Dairy Cattle (MDC), managed under intensive systems in the northern regions; Improved Dairy Cattle (IDC), raised under semi-intensive systems in the central and eastern areas; and Local Dairy Cattle (LDC), predominantly family-based and extensive (Bousbia et al., 2024). Most farms employ manual feeding systems based on locally sourced roughage, hay, and commercial concentrates, while water supply relies primarily on local wells or municipal sources, delivered mainly through simple manual watering systems with occasional automatic drinkers. Ventilation depends exclusively on natural airflow through open doorways and windows. Farm management practices are characterised by minimal supplemental lighting, sporadic rodent control using traditional trapping methods and domestic cats, and generally absent bird-proofing measures. Cleaning protocols remain irregular in most farms, with only modern operations implementing daily manure removal and weekly disinfection. Vaccination against infectious disease follows governmental programmes, and the distribution of veterinary supplements is ensured through official veterinary services following sporadic case reports by private practitioners (Ghoulal et al., 2025).

Region	Province	farms sampled	animals sampled
East	Bourj Bou Ariridj (BBA)	08	75
	M'sila	05	45
	Constantine	04	34
	Mila	01	07
	Batna	01	04
	Setif	03	21
	Jijel	01	04
South	Biskra	01	07
	Adrar	10	95
	Laghouat	04	34
	Djelfa	03	24
	Ghardaïa	03	22
	EL-Bayadh	01	08
	Total	45	380

Table I. Distribution of sampled farms and cattle by province.

Ethical considerations

This study was conducted in accordance with Algerian Law No. 08-88 (26 January 1988) regarding domestic animal handling and treatment, and complied with international animal welfare standards outlined in the WOAH Terrestrial Animal Health Code (2018), Section 7, Article 7.5.1. Informed consent was obtained from all farm owners prior to sample collection and questionnaire administration. All blood samples were collected by qualified veterinary practitioners following standard veterinary procedures.

Sample size determination

The minimum sample size was calculated using Thrusfield's (2013) formula:

$$n = Z^2 \times P_{exp} (1 - P_{exp}) / d^2$$

where n represents required sample size, Z = 1.96 (95% confidence level), P_{exp} = 50% (expected prevalence), and d = 5% (desired absolute precision). This yielded a minimum requirement of 384 animals. A total of 380 cattle were sampled, meeting statistical requirements.

Farm selection and sampling strategy

Provinces were selected to represent contrasting agro-climatic zones (continental versus desert). Within each province, farms were randomly chosen from official veterinary lists in collaboration with local veterinary services, aiming for broad geographic coverage and inclusion of both smallholder and large-scale herds. Farms were stratified by herd size: small (≤ 10 animals) and large (> 10 animals). For farms exceeding 10 cattle, a maximum of 10 animals were randomly selected; for farms with ≤ 10 animals, all animals were sampled.

Data collection

Epidemiological data were collected using a structured questionnaire administered to farm owners, including open-ended and closed-ended questions gathering individual animal and herd-level information. Variables assessed included region (East/South), age (1-3 years/ > 3 years), sex (male/female), breed (Prim'Holstein/Montbéliard/Crossbreed), herd size (≤ 10 / > 10 animals), and origin (local/exotic).

Sample collection and processing

Blood samples (5-10 mL) were collected via jugular venipuncture using vacutainer tubes without anticoagulant. Samples were transported to the laboratory in coolers, allowed to clot at room temperature for 2-4 hours, then centrifuged at 3,000 rpm for 10 minutes. Sera were transferred aseptically into 2 mL microtubes and stored at -20°C until analysis.

Serological testing

All sera were tested for BoHV-1 antibodies using competitive ELISA targeting glycoprotein B (gB) (ID Screen® IBR gB Competition, IDvet, Grabels, France), with diagnostic specificity of 100% and sensitivity of 95% according to the manufacturer.

For DIVA testing, gB-positive sera were additionally tested for glycoprotein E (gE) antibodies using ID Screen® IBR gE Competition (IDvet, Grabels, France). Animals were classified as naturally infected (gB-positive and gE-positive), vaccinated (gB-positive and gE-negative), or seronegative (both tests negative).

Individual seroprevalence was calculated as gB-positive animals divided by total tested. Herd-level seroprevalence represented the proportion of farms with at least one seropositive animal. Vaccination coverage was estimated as the proportion of gE-negative/gB-positive animals.

Statistical analysis

Data were analysed using SPSS version 28.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics were calculated for all variables. Univariate associations between potential risk factors and BoHV-1 seropositivity were assessed using Pearson's chi-square test. Variables with $p < 0.05$ in univariate analysis were entered into multivariable binary logistic regression. Adjusted odds ratios (aOR) and 95% confidence intervals (CI) are reported. Statistical significance was set at $p < 0.05$.

Mapping

Distribution maps were created using ArcGIS Pro 2.9.0 with shapefiles from the Global Administrative Areas Project (<http://gadm.org/>).

Results

Overall BoHV-1 seroprevalence

Of 380 serum samples tested, 148 were positive for BoHV-1 antibodies, yielding an overall individual seroprevalence of 38.95% (95% CI: 34.0-43.9%). At the herd level, all 45 farms (100%) had at least one seropositive animal (Figure 1).

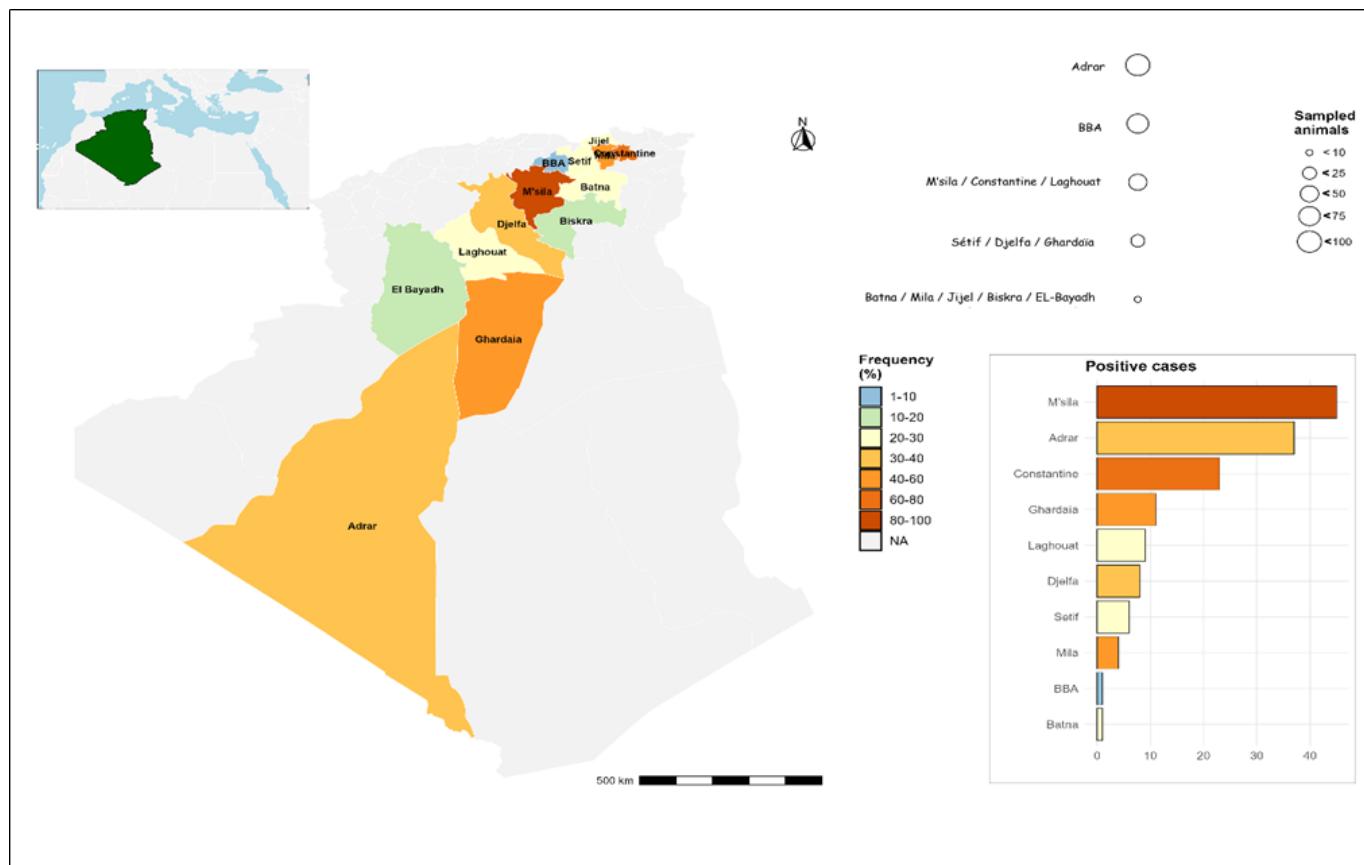


Figure 1. Geographical distribution of IBR antibody-positive sera in thirteen Algerian provinces (created using ArcGIS).

DIVA test results

Among 148 seropositive samples, 99 (66.89%) tested positive for gE antibodies, indicating natural infection, while 49 (33.11%) were gE-negative, suggesting vaccination (Table II). Vaccinated animal distribution differed between regions: 47.76% (32/67) in Southern provinces versus 20.99% (17/81) in Eastern provinces.

Region	Province	Samples verified	gB-positive n (%)	gE-positive/gB positive n (%)	gE-negative / gB-positive n (%)
	Bourj Bou Ariridj (BBA)	75	1(1.33)	1(100)	0
East					
	M'sila	45	45(100)	45(100)	0
	Constantine	34	23(67.64)	17(73.91)	6(26.09)
	Mila	7	4(57.14)	0	4(100)
	Batna	4	1(25)	1(100)	0
	Setif	21	6(28.57)	0	6(100)
	Jijel	4	1(25)	0	1(100)
	Biskra	7	1(14.29)	0	1(100)
	Adrar	95	37(38.95)	17(45.95)	20(54.05)
South	Laghouat	34	09(26.47)	7(77.77)	2(22.23)
	Djelfa	24	8(33.33)	6(75)	2(8.33)
	Ghardaïa	22	11(11)	4(36.36)	7(63.63)
	EL-Bayadh	8	1(12.50)	1(100)	0
Total		380	148 (38.95)	99 (66.89)	49 (33.11)

Table II. Seroprevalence of BoHV-1 and distribution of naturally infected and vaccinated cattle by region and province. Footnotes: gB+: animals positive for antibodies against glycoprotein B (total BoHV-1 seropositive); percentages calculated from total animals tested per province. gE+/gB+: animals positive for antibodies against glycoprotein E among gB+ animals; (natural infection); percentages calculated from gB+ animals per province. gE-/gB+: animals negative for antibodies against glycoprotein E among gB+ animals; (vaccinated animals); percentages calculated from gB+ animals per province

Risk factor analysis

Variable	Univariate Analysis			Multivariable Analysis			
	n (%)	χ^2	p-value	aOR	95% CI	p-value	Wald χ^2
Region		2.08	0.149	Not included			
East	81/190 (42.6)						
South	67/190 (35.3)						
Sex		0.03	0.863	Not included			
Female	124/320 (38.8)						
Male	24/60 (40.0)						
Age		4.08	0.043				
1-3 years	109/300 (36.3)			1.00	Reference		
>3 years	39/80 (48.8)			1.765	1.101-2.829	0.018	5.56
Breed		39.47	<0.001				
Prim'Holstein	80/150 (53.3)			1.00	Reference		
Montbéliard	48/100 (48.0)			0.808	0.486-1.342	0.410	0.68
Crossbreed	20/130 (15.4)			0.151	0.086-0.265	<0.001	42.9
Herd size		9.85	0.002				
≤10	22/90 (24.4)			1.00	Reference		
>10	126/290 (43.4)			2.119	1.202-3.738	0.009	6.76
Origin		41.67	<0.001				
Local	20/130 (15.4)			1.00	Reference		
Exotic	128/250 (51.2)			5.329	3.025-9.383	<0.001	33.5

Multivariable Model: Overall model $\chi^2 = 89.5$ (df = 5), $p < 0.001$; Nagelkerke $R^2 = 0.124$; Model accuracy = 62.8%; Hosmer-Lemeshow goodness-of-fit test: $\chi^2 = 12.4$ (df = 8), $p = 0.134$

Abbreviations: aOR, adjusted odds ratio; CI, confidence interval; n, number; χ^2 , chi-square statistic.

Footnotes: Variables with $p \geq 0.05$ in univariate analysis were not included in the multivariable model.

Table III. Univariate and multivariable logistic regression analysis of risk factors associated with BoHV-1 seropositivity.

Univariate Analysis: Univariate logistic regression (Table III) identified significant risk factors ($p < 0.05$), including breed, age, herd size, and animal origin. Prim'Holstein (53.3%, 80/150) and Montbéliard (48.0%, 48/100) breeds

exhibited significantly higher seroprevalence compared to crossbreeds (15.4%, 20/130) ($p < 0.001$). Seroprevalence did not differ significantly between regions (East: 42.6%, 81/190; South: 35.3%, 67/190; $p = 0.14$) or sexes (females: 38.8%, 124/320; males: 40.0%, 24/60; $p = 0.80$).

Multivariable Analysis: The multivariable logistic regression model (Table III) identified four independent risk factors significantly associated with BoHV-1 seropositivity: exotic origin ($aOR = 5.33$, 95% CI: 3.03-9.38, $p < 0.001$), large herd size >10 animals ($aOR = 2.12$, 95% CI: 1.20-3.74, $p = 0.009$), age >3 years ($aOR = 1.77$, 95% CI: 1.10-2.83, $p = 0.018$), and breed, with crossbreeds showing significantly lower odds ($aOR = 0.15$, 95% CI: 0.09-0.27, $p < 0.001$) compared to Prim'Holstein cattle. Model fit statistics: Overall model $\chi^2 = 89.5$ (df = 5), $p < 0.001$; Nagelkerke $R^2 = 0.124$; accuracy = 62.8%; Hosmer-Lemeshow test: $\chi^2 = 12.4$ (df = 8), $p = 0.134$.

Discussion

This study estimated BoHV-1 seroprevalence among Algerian dairy cattle and identified associated risk factors. The overall individual seroprevalence of 38.95% obtained using cELISA is comparable to findings from other studies employing identical diagnostic methodology. This prevalence is lower than reported in Turkey (43.5%; Ozturk et al., 2012), Ethiopia (55.4%; Asmare et al., 2018), and South Africa (74.47%; Njiro et al., 2011), yet substantially higher than the 14.16% previously reported in Northeastern Algeria (Kaddour et al., 2019). This discrepancy likely reflects differences in study populations, sampling periods, geographic regions, or temporal changes in herd management practices and disease control measures.

BoHV-1 is endemic worldwide, with notable exceptions including Finland, Switzerland, Austria, Denmark, parts of Italy, and the Czech Republic, which achieved disease freedom through systematic eradication programmes (Iscaro et al., 2021). Global prevalence varies substantially, from 0.1% in Slovenia due to ongoing eradication programmes (Hostnik et al., 2021) to 99.92% in certain Spanish regions (Dias et al., 2013). A Chinese meta-analysis estimated pooled seroprevalence at 40% (Chen et al., 2018), remarkably similar to our findings. Other studies reported 57.5% in Colombia (Ortiz-González et al., 2022), 71.3% in Brazil (Abad-Zavaleta et al., 2016), and 76.32% in Mexico (Posado et al., 2013). Such variations may be attributed to differences in diagnostic test type and sensitivity, production systems (dairy versus beef), herd size and management practices, biosecurity measures, vaccination strategies, animal movement patterns, and environmental or climatic factors influencing virus transmission and survival.

Regional seroprevalence differences were observed (East: 42.6%; South: 35.3%) but were not statistically significant ($p = 0.14$), suggesting relatively homogeneous BoHV-1 distribution across study areas. This may reflect variations in environmental conditions, management practices, altitude, and climatic factors (Danu et al., 2024). The lack of significant regional variation suggests widespread virus circulation, highlighting the need for national control strategies across different production systems.

Breed and animal origin

Breed and animal origin emerged as significant seropositivity predictors in multivariable analysis. Prim'Holstein cattle exhibited higher infection odds compared to Montbéliard, while crossbreeds showed significantly lower susceptibility than purebreds. These findings align with El-Sheikh et al. (2024) and Ortiz-González et al. (2022), who reported highest seroprevalence in Holstein cattle. Similarly, Saravanajayam et al. (2015) observed that native breeds were less susceptible than Jersey and Holstein crossbreeds.

Several mechanisms may explain higher Holstein seroprevalence. First, Holsteins are predominantly raised in intensive dairy systems characterised by high stocking densities, facilitating direct contact transmission and aerosol spread. Second, physiological stress associated with high milk production may compromise immune function, increasing infection susceptibility (Sordillo & Aitken, 2009) and promoting viral reactivation in latently infected animals (Ostler & Jones, 2023). Third, frequent animal movements for breeding and replacement stock acquisition in commercial operations create multiple opportunities for virus introduction and spread (Van Schaik et al., 2002; Cailleau et al., 2021). Finally, differences in herd health management, biosecurity measures, and vaccination coverage between production systems may contribute to observed breed variation (Ackermann & Engels, 2006).

Age and herd size

Both age and herd size emerged as significant independent predictors ($p < 0.05$). Animals >3 years had 1.77-fold higher seropositivity odds compared to younger animals, while cattle in larger herds had 2.12-fold higher odds compared to smaller herds. The positive age association is consistent with previous studies (Brock et al., 2020; Danu et al., 2024), attributable to cumulative lifetime exposure, repeated subclinical infections maintaining antibody levels, and age-related immunosenescence combined with lactation-associated physiological stress compromising immune surveillance and facilitating viral reactivation (Singh & Sinha, 2006; Farooq et al., 2021).

The association between larger herd size and increased seropositivity aligns with previous studies (Van Schaik et al., 2002; Raaperi et al., 2014). This relationship reflects higher stocking densities increasing contact rates and facilitating aerosol transmission (Mars et al., 1999), elevated replacement rates increasing infected animal introduction risk (Cailleau et al., 2021), and more complex biosecurity challenges in larger operations (Ackermann & Engels, 2006). These findings emphasise the need for enhanced biosecurity protocols and strategic vaccination programmes in larger commercial dairy herds.

Sex

The seroprevalence showed no significant sex differences (females: 38.8%; males: 40.0%; $p = 0.80$), aligning with the findings of Zewde et al. (2021) and Danu et al. (2024). This suggests equal susceptibility under the examined management conditions. However, transmission routes may differ by sex. In females, infection can occur through natural mating with infected bulls or artificial insemination with contaminated semen, potentially causing endometritis and infertility. Following initial infection, the virus establishes latency in the sacral ganglia and may reactivate during periods of stress or immunosuppression (Graham, 2013). Females may experience increased exposure during oestrus, post-abortion, or postpartum periods when viral shedding in genital discharges is elevated (Dias et al., 2013; Gould et al., 2013).

Control measures and eradication strategies

Effective IBR prevention and control rely on comprehensive biosecurity measures minimising viral introduction and transmission (Nandi et al., 2009). Key strategies include quarantining newly purchased animals for 2-3 weeks, vaccinating susceptible cattle, and implementing strict import restrictions on animals and genetic materials (Jones & Chowdhury, 2007).

Control measures in European IBR eradication programmes include prohibiting infected animal purchases and implementing marker/DIVA vaccines combined with seropositive animal culling, enabling differentiation between infected and vaccinated cattle. However, vaccines have limitations: they reduce disease transmission and incidence but do not prevent wild-type virus infection, so outbreaks may still occur if vaccination stops. While vaccines are valuable in initial high-seroprevalence stages, complete eradication requires removing apparently healthy but seropositive animals (Ackermann & Engels, 2006).

In Algeria, where no national control programme currently exists, our findings of moderate prevalence (38.95%) indicate that disease control remains feasible. A combined strategy incorporating surveillance, marker vaccination, and biosecurity measures should be implemented before the disease becomes more widely endemic.

Conclusion

This study revealed widespread IBR among dairy cattle in Eastern and Southern Algeria, with an estimated seroprevalence of 38.95%, providing the first comprehensive baseline for the national dairy sector. These findings highlight the urgent need for structured disease surveillance and further research on BoHV-1 to understand infection dynamics, including latent carrier roles, subclinical cases, and risk factor interactions, crucial for designing effective interventions.

Based on these results, we recommend implementing a marker vaccine programme using DIVA technology alongside regular serological testing to differentiate naturally infected from vaccinated animals, facilitating progressive IBR eradication. Strengthening biosecurity measures, including quarantine protocols for new animals, controlling animal movements, and monitoring herd management practices, is essential to mitigate transmission risk from latent BoHV-1 carriers. Additionally, ensuring certified IBR-free semen use in artificial insemination programmes should be prioritized.

Study limitations include sampling restricted to 13 of 58 provinces, potentially affecting national representativeness. Nevertheless, these findings provide crucial baseline data for protecting Algeria's dairy industry from economic losses, improving herd health, and establishing a foundation for national IBR control and eventual eradication programmes.

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Ethical approval

All applicable international, national, and institutional guidelines for animal care and use were followed. This article contains no studies with human participants.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Author Contributions

Conceptualization: KG, OG, and SB; Methodology: KG, OG, and SB; Formal analysis: AA, HA, and MM-R; Writing original draft preparation: KG, MB, LD, and HK; Writing, review and editing: KG, AA, SB, and HK; Visualization: AA. All authors have read and agreed to the published version of the manuscript.

Data availability

Data are available upon request from the corresponding author.

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