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Editorial

Insights into Bovine Viral Diarrhea Epidemiology in Moroccan Cattle Population

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Abstract

This study aimed to estimate the seroprevalence of bovine viral diarrhea virus (BVDV) in Moroccan cattle and to investigate associations with age, sex, breed, housing system, and geographic region. A total of 545 serum samples were randomly collected from cattle across various Moroccan regions between December 2023 and February 2024. Antibodies against BVDV were detected using a commercial competitive ELISA, and herd-level data were gathered via questionnaire. Overall, 25.0% (95% CI: 21.4 – 28.8) of samples tested seropositive. The highest prevalence was observed in the Tanger-Tetouan-Al Hoceima region (44.0%; 95% CI: 24.4 – 65.1), followed by Casablanca-Settat (32.6%; 95% CI: 26.1 – 39.6). Seropositivity was highest among cattle older than 12 months (37.5%) and in crossbred animals (86.1%) compared to purebreds (74.3%). Although not statistically significant, cattle in intensive systems showed higher prevalence (29.3%) than those in semi-intensive systems (23.2%). Females exhibited a higher seroprevalence (27.87%) than males (21.7%), with sex emerging as a significant risk factor. These findings highlight the widespread circulation of BVDV in Morocco and underscore the need for targeted control measures and improved herd management practices to mitigate virus transmission.

Keywords

Morocco, bovine viral diarrhea, BVDV, cattle, ELISA, seroprevalence

Introduction

Bovine Viral Diarrhea Virus (BVDV) infection is a globally recognized disease of ruminants, with significant economic implications due to its impact on cattle health and international trade. The World Organization for Animal Health (WOAH) classifies BVDV as a notifiable and priority disease because of the substantial economic losses it can cause (Mishra et al., 2011).

BVDV, the causative agent of Bovine Viral Diarrhea (BVD), belongs to the *Pestivirus* genus within the *Flaviviridae* family and is highly prevalent in many countries worldwide (Scharnböck et al., 2018). The virus is categorized into two biotypes—cytopathic (CP) and non-cytopathic (NCP)—based on their behavior in cell cultures. Genetically, BVDV is classified into three species: BVDV-1 (*Pestivirus A*), BVDV-2 (*Pestivirus B*), and BVDV-3 (*Pestivirus H* or *HoBi -like virus*) (de Oliveira et al., 2021).

BVDV is transmitted both horizontally and vertically. Horizontal transmission occurs primarily through direct contact, especially via mucosal membranes during activities such as coitus, and indirectly via secretions, excretions, blood, and fomites (Flores et al., 2005; Radostits et al., 2007). Vertical transmission occurs through the placenta and can result in persistently infected (PI) calves, weak or non-viable offspring, or fetal abortion, depending on the virus genotype and the stage of gestation (Flores et al., 2005; Radostits et al., 2007).

The clinical severity of BVDV infection varies depending on the viral strain and the host's immune status, ranging from subclinical infections to severe clinical forms. Severe cases may involve fever, anorexia, depression, gastrointestinal erosions, hemorrhages, diarrhea, and dehydration (Givens et al., 2012). While most infections are subclinical, the disease can evolve over a period of 2–3 days to several weeks. Early signs include a transient fever (40–41 °C), often subsiding before the onset of diarrhea (Brock et al., 2004). Under natural conditions, NCP BVDV is the predominant biotype and responsible for extensive damage. However, CP strains are primarily associated with mucosal disease (MD) in PI animals, which typically results from fetal exposure to NCP BVDV between 42 and 125 days of gestation (Fulton et al., 2009).

BVDV is particularly known for its immunosuppressive effects, which facilitate its spread within herds. The virus impairs both innate and adaptive immunity in a strain-dependent manner, compromising the host's ability to resist secondary infections (Deng et al., 2015). PI animals, in particular, are immunotolerant to the virus due to in utero exposure, rendering them unable to mount an effective immune response or produce significant levels of neutralizing antibodies (Evans et al., 2021). Consequently, they become lifelong shedders of the virus, acting as key sources of transmission (Flores et al., 2005; Radostits et al., 2007).

From a serological standpoint, PI animals are persistently viremic yet fail to seroconvert in the traditional sense, as they do not produce detectable neutralizing antibodies (Evans et al., 2021). This makes their identification challenging when relying solely on antibody-based diagnostic tools, emphasizing the need for combined serological and virological testing for effective herd-level surveillance and control.

In Morocco, although BVDV vaccines are commercially available, vaccination alone is insufficient for controlling the disease if not integrated with biosecurity measures and proper risk management strategies (Makoschey and Berge, 2021). Several factors influence the prevalence and control of BVDV, including herd size, population density, production systems, environmental conditions, and the presence of PI animals (Khezri, 2015).

Only a limited number of studies have investigated BVDV seroprevalence in Morocco. An early study from 1985 reported a seroprevalence of 48.5% (Mahin et al., 1985), while later studies reported rates of 37.71% (Lucchese et al., 2016) and 56.1% (Alali et al., 2024), suggesting that BVDV remains endemic in the country.

Given the persistent circulation of BVDV in Moroccan cattle, the present study aims to estimate the current seroprevalence of BVDV and to identify associated risk factors across various regions. Specific variables under investigation include sex, breed, age group, and farming system. The findings of this study will provide critical insights for designing and implementing effective control strategies tailored to the Moroccan context.

Materials and methods

This study was conducted between December 2023 and February 2024 at the Regional Laboratory of Analysis and Research in Casablanca. A total of 545 cattle serum samples were collected from seven administrative regions of Morocco: Tangier-Tetouan-Al Hoceima, Oriental, Fès-Meknès, Rabat-Salé-Kénitra, Béni Mellal-Khénifra, Casablanca-Settat, and Marrakech-Safi (Figure 1).

These regions were selected to capture the geographic and environmental diversity of Morocco, which may influence the epidemiology of BVDV. A brief description of each region is provided below:

Tangier-Tetouan-Al Hoceima: Located in northern Morocco, this region features a Mediterranean climate with coastal plains and the Rif Mountains. It supports substantial agricultural activity, particularly livestock farming.

Oriental: Situated in the northeastern part of the country, this region encompasses both mountainous terrain and Mediterranean coastline. It exhibits a mix of semi-arid and humid climates and sustains both crop cultivation and livestock farming.

Fès-Meknès: Located in north-central Morocco, the region is characterized by plains and foothills under a semi-arid climate. It supports a combination of extensive and intensive agricultural systems.

Rabat-Salé-Kénitra: A coastal region surrounding the capital city, Rabat. It features fertile Atlantic plains and a Mediterranean climate with mild, wet winters and hot, dry summers. The area is conducive to both crop production and intensive livestock farming.

Béni Mellal-Khénifra: Located in central Morocco, this region includes mountainous areas (Middle Atlas) and agricultural plains. It has a relatively dry climate and supports diverse farming systems, including both extensive and intensive livestock operations.

Casablanca-Settat: Encompassing Morocco's largest city, this region combines significant urbanization and industrial activity with fertile plains and a Mediterranean climate. It is characterized by a high density of intensive farming enterprises.

Marrakech-Safi: Situated in the southwest, this region includes parts of the Atlas Mountains and coastal plains. It has a predominantly semi-arid to arid climate and supports widespread agricultural activity, including both crop and livestock production.

Regarding vaccination status, none of the animals sampled in these regions had been vaccinated against BVDV. All vaccinated animals were excluded from the study.

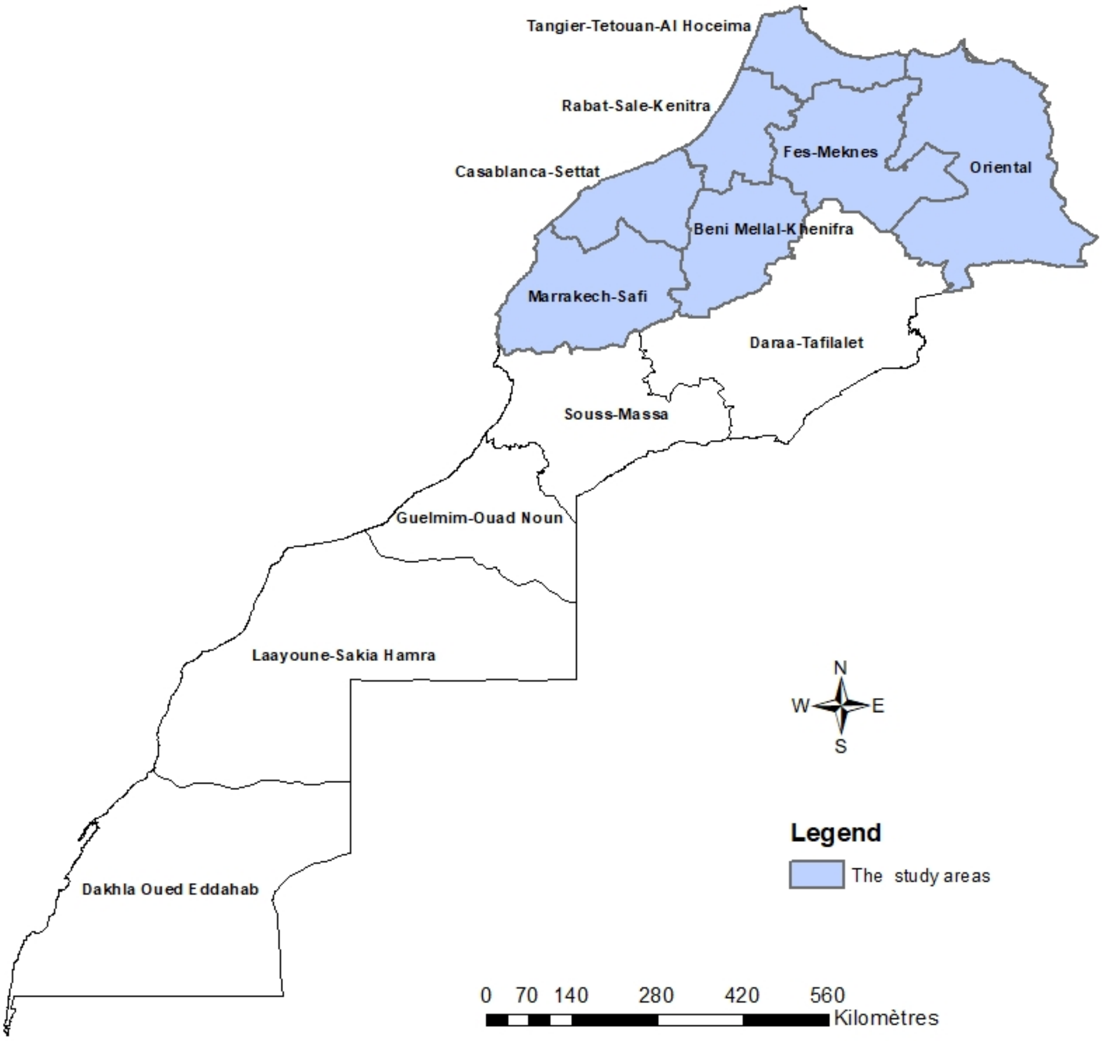

Figure 1. Map of Morocco that shows the study area

Methodology

A total of 545 cattle, all unvaccinated against BVDV, were randomly selected from various regions of Morocco. The sampled animals varied in age (108 were <6 months, 405 were between 6–12 months, and 32 were >12 months), sex (258 males and 287 females), breed (509 crossbred and 36 purebred), and farming system (388 from intensive and 157 from semi-intensive systems). Sample collection followed standard procedures to minimize stress and ensure animal welfare.

A significant number of animals were excluded during sampling due to prior vaccination against BVDV. This explains

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the relatively low number of purebred cattle and animals older than 12 months included in the study.

Five milliliters of blood were collected from the jugular vein of each animal using vacutainer tubes without anticoagulant (EDTA). Serum was separated by centrifugation at 3,000 rpm (1008 × g) for 10 minutes and stored at −20 °C until analysis.

Serological testing for BVDV antibodies was conducted using a commercially available competitive enzyme-linked immunosorbent assay (ELISA), following the manufacturer's instructions. The assay used was the ID Screen® BVD p80 Antibody ELISA (ID Vet, France; Lot K93), designed for the in vitro detection of antibodies against BVDV.

Statistical analysis

Field data collected using individual data sheets were entered into a Microsoft Excel spreadsheet (MS Office 2016) and organized for subsequent analysis. The dataset was then imported into IBM SPSS Statistics version 29.0.2.0 for statistical evaluation. All analyses were based on the results of the ELISA serological tests.

Seroprevalence was calculated by dividing the number of ELISA-positive samples by the total number of samples tested. A structured questionnaire was also administered to collect information on general animal characteristics, herd history, and individual animal records.

Associations between categorical variables (e.g., age, sex, breed, housing system, region) and BVDV seropositivity were assessed using the Pearson chi-square test. A p-value of less than 0.05 was considered statistically significant. The statistical results were summarized and presented in tabular form.

Results

The study revealed an overall BVDV seroprevalence of 25.0% (95% CI: 21.4 – 28.8), with 136 out of 545 serum samples testing positive (Table I). Since none of the sampled cattle had been vaccinated against BVDV, the observed seropositivity is attributed to natural infection. The highest regional prevalence was recorded in Tangier-Tetouan-Al Hoceima (44.0%; 95% CI: 24.4 – 65.1), followed by Casablanca-Settat (32.6%; 95% CI: 26.1 – 39.6). In contrast, the lowest prevalence was observed in the Marrakech-Safi region (13.4%; 95% CI: 5.0 – 26.8). Analysis by farming system showed that BVDV was present in both intensive and semi-intensive systems. A higher proportion of seropositive animals was found in intensive systems (29.3%) compared to semi-intensive systems (23.2%). However, this difference was not statistically significant (Table II). With respect to breed, crossbred cattle exhibited a higher seroprevalence (25.7%) than purebred cattle (13.9%), although the association between breed and seropositivity was not statistically significant (Table II). A statistically significant association was observed between BVDV seropositivity and sex ($p < 0.05$), with females showing a higher prevalence (27.87%) than males (21.7%). Although no statistically significant association was found between age group and seropositivity, cattle older than 12 months exhibited a higher prevalence (37.5%) compared to younger age groups (Table II).

Region in Morocco	No. of samples tested	No. of positives	**Prevalence (95% CI)**
Beni Mellal- Khenifra	66	19	**28 . 8% (18 . 2 – 40 . 9)**
Casablanca – Settat	193	63	**32.6% (26.9 -39.4)**
Fes –Meknes	78	13	**16.7% (9.0-25.6)**
Oriental	54	10	**18.51% (7.4-29.6)**
Marrakech-Safi	45	6	**13.4% (4.5-25.0)**
Tangier - Tetouan - Al Hoceima	25	11	**44.0% (23.2-61.5)**
Rabat - Sale – Kenitra	84	14	**16.7% (9.6-25.3)**
Total	545	136	**25.0% (14.2-35.3)**

Table I. Region wise cattle serum samples tested for BVD (December 2023 - February 2024).

Variable	Category	No. of samples tested	No. of positives	Prevalence	P-value
Sex	Male	258	56	**10.28 %**	**0,004**
	Female	287	80	**14.68 %**	
Farming system	Intentive	157	46	**29.3 %**	**0.135**
	Semi-intensive	388	90	**23.2 %**	
Breed	Crossbreed	509	131	**25.7%**	**0.112**
	Purebreed	36	5	**13.9%**	
Age	< 6 months	108	28	**25.9%**	**0.214**
	6-12 months	405	96	**23.7%**	
	>12 months	32	12	**37.5**	

Table II. Association of different categorical variables in the prevalence of BVDV in cattle (December 2023 - February 2024).

Discussions

The observed variations in BVDV seroprevalence across regions in this study can be attributed to multiple epidemiological factors. These include cattle density, housing conditions, breeding practices, shared pastures and water sources, overstocking, trade dynamics, and environmental variables such as temperature and humidity. Additional influences—such as immunosuppression, stress, inconsistent vaccination policies, inadequate biosecurity, and the absence of structured control or eradication programs—may further contribute to the spread of the virus (Brodersen, 2014). Previous studies by Talafha et al. (2009) and Saa et al. (2012) have similarly noted the roles of farm management, herd size, animal age, and the presence of persistently infected (PI) animals in explaining regional differences in BVDV prevalence.

In the present study, the overall seroprevalence of BVDV at the animal level was 25%. This figure is consistent with findings reported in Mali (23.28%) (Djeneba Sy et al., 2022), Antioquia–Colombia (22.7%) (Cristian C. et al., 2023), and Kenya (19.8%) (Callaby et al., 2016). However, it is markedly lower than rates previously reported in Morocco: 37.71% (Lucchese et al., 2016) and 56.1% (Alali et al., 2024). These results may suggest a recent decline in BVDV circulation in Morocco, potentially influenced by improved on-farm biosecurity, even in the absence of a national control or mandatory vaccination program.

When compared internationally, the 25% seroprevalence observed here is higher than that reported in Central Ethiopia (15.4%) (Birhanu et al., 2024), Egypt (10.4%) (Soltan et al., 2015), Sudan (10.7%) (Saeed et al., 2015), and Nepal (9.70%) (Gautam et al., 2022). Conversely, it is lower than rates recorded in Malaysia (33.2%) (Daves et al., 2016), Bangladesh (51.1%) (Uddine et al., 2017), Colombia (36%) (Ortega et al., 2020), Belgium (32.9%) (Sarrazin et al., 2013), China (58.09%) (Deng et al., 2016), and Australia/New Zealand (80%) (Reichal et al., 2018), highlighting regional variability in BVDV epidemiology.

This study also identified a significantly higher seroprevalence in females compared to males—a finding aligned with previous reports from Morocco (Alali et al., 2024) and Ethiopia (Endeshaw et al., 2021). In contrast, other studies conducted in Egypt and the United States (Selim et al., 2018; Wilson et al., 2016) found no significant difference between sexes. The higher female prevalence may be partially explained by production practices, as male calves are typically removed from the herd early for veal production, thereby reducing their exposure risk (Bello et al., 2016).

With regard to breed, crossbred cattle exhibited a higher seroprevalence than purebred cattle, in line with findings from Endeshaw et al. (2021), who reported a 25.9% prevalence in crossbreeds. Although this may suggest a possible genetic component in susceptibility, the relatively small number of purebred animals in this study limits the strength of this interpretation.

Differences in farming systems also appeared to influence seroprevalence. A higher percentage of positive cases was observed in intensive systems, likely due to higher stocking densities and increased animal-to-animal contact. Similar trends have been reported in Morocco (Alali et al., 2024) and Ethiopia (Birhanu et al., 2024).

Age-related trends showed that older animals had higher seroprevalence rates, likely due to increased cumulative exposure over time. This observation is consistent with previous research (Alali et al., 2024; Maher et al., 2023;

Aragaw et al., 2018). However, the limited number of animals >12 months in this study constrains the interpretability of age-related associations.

Overall, the study confirms that BVDV remains widespread in Moroccan cattle populations. Notably, sex was identified as a statistically significant risk factor for seropositivity, while no significant associations were observed with age, breed, or farming system. Despite this, the relatively high seroprevalence observed underscores the ongoing epidemiological importance of BVDV and raises concerns about its potential expansion in the absence of national control measures.

To reduce BVDV transmission, it is recommended that farmers adopt stringent hygiene practices, routine screening for PI animals, and enforce stricter biosecurity protocols. Countries that have implemented structured BVDV control or eradication programs offer valuable models for Morocco. Finally, further virological studies are warranted to characterize the BVDV genotypes currently circulating in the country, a critical step for the design of effective and regionally tailored vaccines and control strategies.

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Ethical approval

All data are available upon request to the corresponding author.

Conflict of interest

The authors declare that they have no conflict of interest.

Author Contributions

Conceptualization: H.K, F.E.M and H.A; Methodology: H.K, F.E.M, H.A; Formal analysis: H.K, F.E.M, H.A, Y.E and O.K; Investigation: H.K, F.E.M, H.A, Y.E and O.K; Writing original draft preparation: H.K, F.E.M, H.A; Writing, review and editing: H.K, F.E.M and H.A ; Visualization: HK, FE, HA; Supervision: HK, FE, HA; Project administration: H.K, F.E.M and H.A; Funding acquisition: H.K, F.E.M, H.A. All authors have read and agreed to the published version of the manuscript.

Data availability

All data are available upon request to the corresponding author.

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