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Paper



Serological evidence of hidden circulation of three arthropod-borne diseases (Rift Valley fever, West Nile fever, and Crimean-Congo haemorrhagic fever) in dromedary camels from the Eastern Algerian Sahara

Nacer Eddine Messahel^{1*}, Soraya Nadia Younes Bouacida², Aissam Hachid³, Mohammed Hocine Benaissa⁴, Ahmed Fayez Khardine⁵, Abdelhakim Kimouche⁶, Djilali Degui⁷, Ahcène Hakem⁸, Idir Bitam⁸, Ismail Lafri⁹

¹Laboratory for the Improvement and Development of Plant and Animal Production (LADPVA), Faculty of Nature and Life Sciences, University Ferhat Abbas Setif 1, 19000, Algeria - DZ

²Ecole Nationale Supérieure Vétérinaire d'Alger, 16000 Alger, Algérie - DZ

³Faculté de Pharmacie, Université des Sciences médicales, 16000 Alger, Algérie, Laboratoire des Arbovirus et Virus Émergents, Institut Pasteur d'Algérie, 16000 Algiers, Algérie - DZ

⁴Centre de recherche scientifique et technique sur les régions arides (CRSTRA), 30002 Touggourt, Algérie. - DZ

⁵Laboratoire des Arbovirus et Virus Émergents, Institut Pasteur d'Algérie, 16000 Algiers, Algérie - DZ

⁶Direction des Services Agricoles de la Wilaya d'Illizi, 33000 Illizi, Algérie - DZ

⁷Faculté de Médecine, Université Alger 1, 16000 Alger, Algérie. Laboratoire des Biotechnologies Liées à la Reproduction Animale (LBRA), Institut des Sciences Vétérinaires, Université de Blida 1, 09000 Blida, Algeria - DZ

⁸Centre de Recherche en Agropastoralisme (CRAPast) Djelfa, 17000 Djelfa, Algeria - DZ

⁹Institut des Sciences Veterinaires, Université Blida 1, 09000 Blida, Algérie, Laboratoire de Bactériologie Vétérinaire. Département de Microbiologie et Pathologie Vétérinaire, Institut Pasteur d'Algérie, Algérie - DZ

*Corresponding author at: Laboratory for the Improvement and Development of Plant and Animal Production (LADPVA), Faculty of Nature and Life Sciences, University Ferhat Abbas Setif 1, 19000, Algeria - DZ

E-mail: nacermessahel1@gmail.com

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Abstract

Several arthropod vectors, including ticks, sand flies, and mosquitoes, play a prominent role in the introduction and spread of numerous viral diseases. Despite Algeria being at high risk of arbovirus emergence, data on the circulation of arboviruses remain limited, except for some reports on West Nile virus (WNV). Therefore, the aim of this study was to investigate the seroprevalence of antibodies against three arboviruses in several regions of the Algerian Sahara in order to document previous viral exposure. Serum samples collected from dromedaries between May and November 2023 were tested for IgG antibodies against the mosquito-borne viruses Rift Valley fever virus (RVFV) and West Nile virus (WNV), as well as the tick-borne Crimean-Congo haemorrhagic fever virus (CCHFV), using commercial ELISA kits. A total of 224, 79, and 73 serum samples were tested for RVFV, WNV, and CCHFV, respectively. The seroprevalence of IgG antibodies was 2.68% for RVFV, 50.63% for WNV, and 75.34% for CCHFV. Co-seropositivity was most frequently observed for WNV and CCHFV (20.55%, 15/73). Place of residence and sex were significantly associated with CCHFV seropositivity in dromedaries ($p < 0.05$). Overall, the findings suggest widespread circulation of the studied arboviruses in the eastern Algerian Sahara and indicate the possible presence of these pathogens in camels from previously unexplored regions of the country. The results also highlight the imminent risk facing Algeria, particularly from haemorrhagic viruses, and underscore the importance of strengthening arbovirus surveillance and expanding diagnostic panels to include additional arboviruses.

Keywords

Seroprevalence, West Nile virus, Rift Valley fever virus, Crimean Congo haemorrhagic fever virus, Algeria, Camels

Introduction

Arboviruses are a diverse group of RNA viruses maintained in nature through transmission cycles involving vertebrate hosts and arthropod vectors. These viruses require replication within the vector before transmission to a susceptible host and typically persist in enzootic cycles involving wildlife reservoirs (Zhu et al., 2019; AlSaiari et al., 2026). Although most arboviral infections are asymptomatic and symptomatic cases often present as influenza-like illnesses, a proportion of infected individuals may develop severe or life-threatening complications (Weaver and Reisen, 2010). Globally, arboviral diseases are estimated to cause approximately 360 million infections each year. The risk posed by these diseases is expected to increase considerably as climate change, human mobility, urbanisation, and other ecological and socio-environmental factors facilitate their spread beyond traditional endemic regions and alter their epidemiology (Erazo et al., 2024; Sant'Anna et al., 2025).

Numerous arboviruses have been reported to significantly affect humans and other vertebrates, including members of the families *Bunyaviridae* and *Flaviviridae*, which are responsible for diseases such as Rift Valley fever and West Nile fever. These zoonotic infections have attracted increasing attention as emerging and re-emerging threats during the 21st century, posing major challenges to both veterinary medicine and public health worldwide (Khan and Smith, 2016; Marino et al., 2025). RVFV is a mosquito-borne virus classified within the genus *Phlebovirus*; however, human infections most commonly occur through contact with the blood or tissues of infected animals (WHO, 2024). The virus is responsible for high abortion rates and neonatal mortality in domestic animals, including camels and small ruminants, and can cause a broad spectrum of clinical manifestations in humans, ranging from acute febrile illness to severe complications such as encephalitis, retinitis, and haemorrhagic syndromes (Saadet et al., 2026). Major outbreaks associated with RVFV have occurred periodically over the past decades and are frequently linked to rainfall patterns (Barry et al., 2025).

West Nile virus, a member of the genus *Flavivirus*, is another mosquito-borne virus with a broad host range that primarily affects birds and is transmitted mainly by mosquitoes of the genus *Culex*. In humans, infection is usually asymptomatic or results in mild disease; however, in a small proportion of cases, it may progress to severe and potentially fatal neuroinvasive disease (Marino et al., 2025). The virus has been responsible for numerous outbreaks affecting both humans and animals across several continents (Sejvar, 2003).

Classified by the World Health Organization (WHO) as one of the priority emerging diseases, Crimean-Congo haemorrhagic fever is a severe tick-borne zoonosis with a case-fatality rate that can reach 40% in humans (WHO, 2025). The causative agent, CCHFV, belongs to the family *Nairoviridae* and infects a wide range of domestic and wild animals, including cattle, sheep, and goats, which generally remain asymptomatic and act as reservoirs that facilitate silent viral circulation (Nasirian, 2020). Although human infection may occur following the bite of infected hard ticks of the genus *Hyalomma* (family *Ixodidae*), direct contact with the blood or bodily fluids of infected animals or humans also represents a major route of transmission (WHO, 2025). As the most geographically widespread tick-borne viral disease, CCHF has shown an increasing trend in reported human cases and associated mortality over recent decades, accompanied by geographic expansion into regions where the disease was previously rare or absent (WHO, 2025; Khafaji et al., 2026).

In Algeria, the largest country in Africa, the risk of arboviral infections and their potential for spread should not be overlooked, given the favourable ecological conditions and the diversity of vectors and hosts that support their transmission. Several serological surveys, although limited in number, have demonstrated the presence of antibodies against multiple arboviruses, including WNV (Hachid et al., 2019; Medrouh et al., 2020; Laabassi et al., 2023), RVFV (Di Nardo et al., 2014; Trabelsi et al., 2023), and CCHFV (Guidoum et al., 2023; Degui et al., 2024), in different regions of the country. Despite these findings, many areas remain poorly documented or completely unexplored because of difficult field conditions and limited accessibility, particularly in the Sahara, which shares extensive borders with countries where these arboviruses are endemic. Therefore, the present study aimed to assess the seroprevalence of selected arboviruses (WNV, RVFV, and CCHFV) in dromedary camels from several regions of the Algerian Sahara, with particular emphasis on RVFV.

Materials and methods

Study areas

This cross-sectional seroepidemiological study was conducted using samples collected from six municipalities across four provinces in south-eastern Algeria (Figure 1): Djanet (24.27° N, 9.47° E; 968 m a.s.l.), Bordj El Haouas (24.95° N, 8.57° E; 800 m a.s.l.), Illizi (26.48° N, 8.47° E; 543 m a.s.l.), Debdeb (29.43° N, 7.55° E; 350 m a.s.l.), Ouargla (31.95° N, 5.32° E; 141 m a.s.l.), and El Oued (33.37° N, 6.86° E; 61 m a.s.l.). The selected regions are characterised by a typical Saharan desert climate, marked by extremely high temperatures during summer and relatively mild to warm conditions in winter (Peel et al., 2007).

Some sampling municipalities are located along international borders, including Djanet near the Libyan border to the east and the Nigerien border to the south, Illizi and Debdeb near the Libyan border to the east, while Bordj El Haouas, Ouargla, and El Oued are interior sites within Algeria. Multiple criteria were considered in selecting the study areas, including proximity to countries where arboviruses are reported or endemic, transboundary livestock movements for grazing, and high camel density. Camel samples were collected from two different sources. In the municipality of El Oued, due to field-related logistical constraints, samples were obtained exclusively from a local slaughterhouse. In the remaining study municipalities, samples were collected from camels belonging to nomadic pastoral herds managed under extensive traditional husbandry systems. These herds move seasonally across the Sahara, including across international borders, in search of grazing areas and water resources. Sampling was conducted at locations where the herds were temporarily present during the study period.

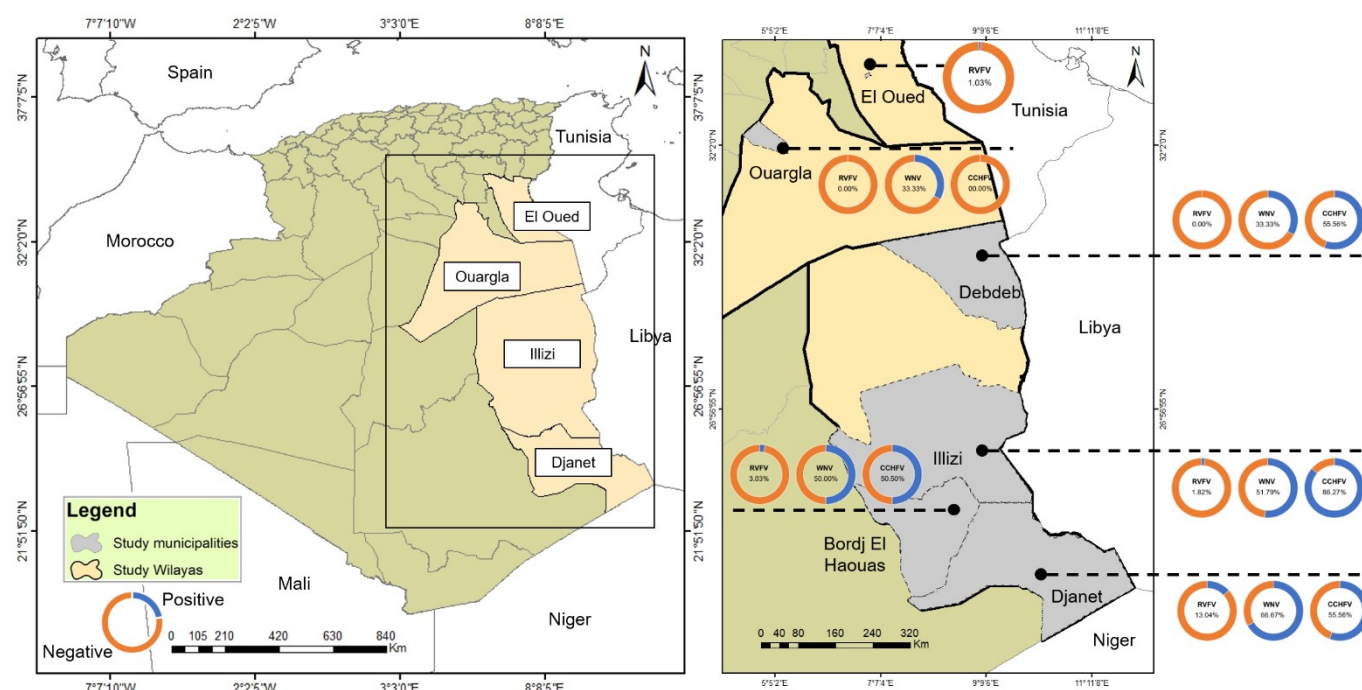


Figure 1. Map of Algeria showing the geographical locations of the study areas and the seroprevalence of the investigated arboviruses. The seropositivity rate of each virus is represented in blue and expressed as percentages within the indicated circles.

Sample collection

Samples were collected from May to November 2023. All animals were clinically healthy at the time of sampling. For each animal, 5 mL of blood was aseptically drawn from the jugular vein. Sera were separated by centrifugation and stored at -20 °C until laboratory analysis for the detection of virus-specific IgG antibodies. Notably, blood collection was conducted by trained personnel, with camels safely restrained in a recumbent position with the assistance of three to four handlers.

The sample size was determined by the availability and accessibility of camels, as well as logistical constraints encountered at the study sites during the sampling period. Consequently, no formal sample size calculation was performed prior to sample collection. In total, 224 serum samples were included in the study. Of these, 97 were obtained from slaughterhouses and 127 were obtained from nomadic pastoral herds managed under extensive traditional husbandry systems. All 224 samples were tested for RVFV, whereas a smaller subset was analysed for the

other targeted arboviruses, including CCHFV (n = 73) and WNV (n = 79). This sampling strategy reflects the primary focus of the study on RVFV, for which a larger number of samples were prioritised, as well as diagnostic test availability for the other assays.

For the analysis of co-seropositivity, only the subset of 73 samples that had been tested for all three arboviruses (RVFV, CCHFV, and WNV) was included. This approach was adopted to ensure consistency and comparability across infections.

Serological assays

Serological analyses were performed at the Pasteur Institute of Algeria, within the Laboratory of Arboviruses and Emerging Viruses. Serum samples were screened for antibodies against the aforementioned arboviruses using commercial ELISA kits: the ID Screen® West Nile Virus Competition Multi-species kits, the ID Screen® CCHF Double Antigen Multi-species, and the ID Screen® Rift Valley Fever Competition Multi-species (IDvet, Grabels, France), following the manufacturer's recommendations. The assay for WNV detects antibodies directed against an epitope of the pr-E envelope protein of flaviviruses, whereas the assays for CCHFV and RVFV are designed to detect antibodies targeting the viral nucleocapsid protein (NP). Optical density values were measured at a wavelength of 450 nm using an ELISA microplate reader. Interpretation of the ELISA results was performed according to the criteria specified by the assay manufacturers. For WNV and RVFV, samples were considered positive when the residual binding ratio (S/N%) was $\leq 40\%$, doubtful when it was between 40% and 50%, and negative when $> 50\%$. For CCHFV, results were expressed as the S/P% ratio (OD sample/OD positive control), with values greater than 30% being considered positive. All samples were tested in duplicate to ensure the reliability and reproducibility of the results.

Data analysis and mapping

Data analysis was performed using XLSTAT software (version 2016). Potential risk factors for arbovirus seroprevalence, including sex, age, and geographical origin, were assessed using Pearson's chi-square (χ^2) test to evaluate associations between groups. These factors were selected because age may reflect cumulative exposure to arboviruses over time, sex may be associated with differences in management practices and animal movement patterns, and geographical origin may influence exposure through differences in microenvironmental and ecological conditions that affect vector distribution. A p-value of less than 0.05 was considered statistically significant for arbovirus seropositivity. Ninety-five per cent confidence intervals (95% CI) were also calculated.

To generate maps depicting the geographic locations of the surveyed study areas and to visualise the distribution of arbovirus seroprevalence among camels in each investigated region, ArcMap version 10.8 was used. This approach provides a clear spatial representation of the epidemiological data.

Results

Overall seroprevalence

Anti-CCHFV IgG antibodies were detected in 75.34% (55/73; 95% CI: 63.8%-84.7%) of the tested dromedary samples. The second most prevalent virus was WNV, with a seropositivity rate of 50.63% (40/79; 95% CI: 39.1%-62.1%). On the other hand, only 2.68% (6/224; 95% CI: 1.0%-5.7%) of dromedary samples tested positive for anti-RVFV IgG antibodies (Table I, Figure 1).

Variable	RVFV-IgG			WNV-IgG			CCHFV-IgG		
Age (Years)	Seroprevalence (n of positive samples/n of tested samples)	p-value/Khi2	% (95 % CI)	Seroprevalence (n of positive samples/n of tested samples)	p-value/Khi2	% (95 % CI)	Seroprevalence (n of positive samples/n of tested samples)	p-value/Khi2	% (95 % CI)
< 5	4.55% (1/22)	P>0.05 Khi2=4.06	0.00-13.25	37.50% (3/8)	P>0.05 Khi2=2.65	3.95-71.05	75.00% (6/8)	P>0.05 Khi2=0.07	45.00-100.00
5-10	0.79% (1/127)		0.00-2.33	47.17% (25/35)		33.73-60.61	74.47% (35/47)		62.00-86.93
>10	5.33% (4/75)		0.25-10.42	66.67% (12/18)		44.89-88.44	77.78% (14/18)		58.57-96.98
Sex									
Male	2.13% (1/47)	P>0.05 Khi2=0.06	0.00-6.25	38.89% (7/18)	P>0.05 Khi2=1.28	16.37-61.41	33.33% (6/18)	P<0.05* Khi2=22.69	13.78-61.22
Female	2.82% (5/177)		0.38-5.27	54.10% (33/61)		41.59-66.60	89.09% (49/55)		76.95-94.98
Municipality									
Illizi	1.82% (1/55)	P>0.05 Khi2=10.54	0.00-5.35	51.79% (29/56)	P>0.05 Khi2=2.39	38.70-64.87	86.27% (44/51)	P<0.05* Khi2=13.89	76.83-95.72
Djanet	13.04% (3/23)		0.00-25.73	66.67% (6/9)		35.87-97.47	55.56% (5/9)		23.09-88.02
Bordj El Haouas	3.03% (1/33)		0.00-8.88	50.00% (1/2)		0.00-100.00	50.00% (1/2)		0.00-100.00
Ouargla	0.00% (0/7)		0.00-0.00	33.33% (1/3)		0.00-86.68	00.00% (0/2)		0.00-0.00
El Oued	1.03% (1/97)		0.00-3.04	/		/	/		/
Debdeb	0.00% (0/9)		0.00-0.00	33.33% (3/9)		2.54-64.13	55.56% (5/9)		23.10-88.02

Table 1. Seropositivity of the investigated arboviruses according to dromedary age, sex, and sampling site. CI: Confidence Interval. * Statistically significant (p<0.05).

Seropositivity for multiple viruses

Among the 73 camels tested for all three viruses, 20 samples (27.40%) exhibited co-seropositivity. Co-seropositivity was most frequently observed for WNV and CCHFV (20.55%, 15/73), followed by RVFV and CCHFV (4.11%, 3/73). Only two samples (2.74%, 2/73) showed co-seropositivity for RVFV and WNV. Notably, no samples (0.0%) exhibited triple seropositivity (Figure 2).

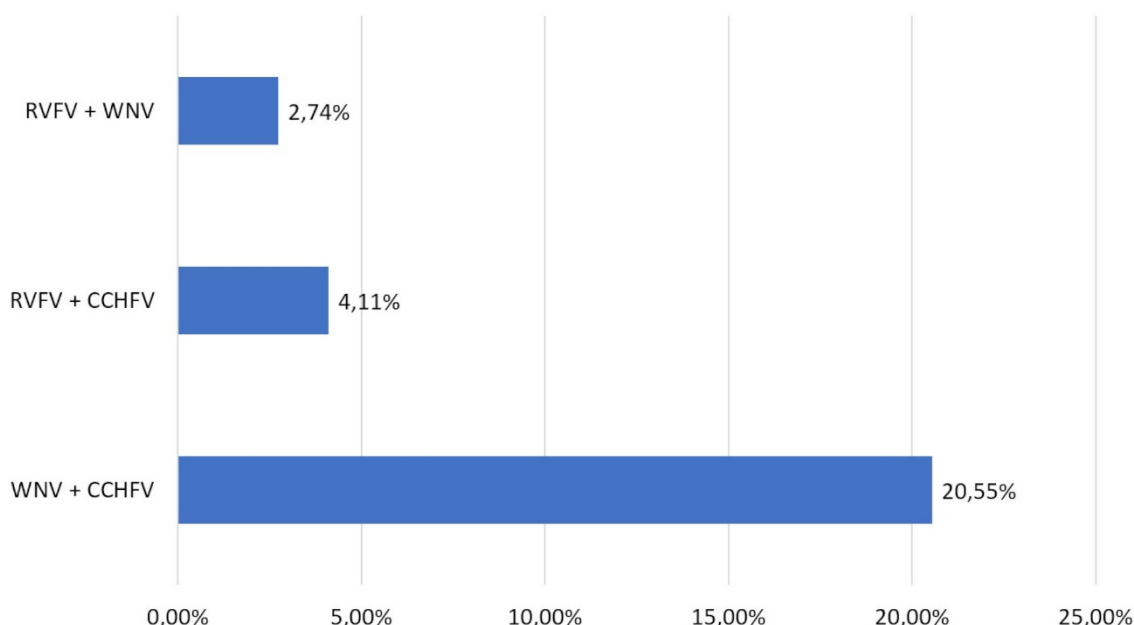


Figure 2. Samples positive for antibodies reactive to multiple viruses.

Association between seropositivity and other factors

Seroprevalence was assessed based on camel characteristics, including sex and age (Table I). Female camels consistently exhibited higher seropositivity for both CCHFV and WNV than males, with CCHFV IgG detected in 89.09% versus 33.33%, and WNV IgG in 54.10% versus 38.89%, respectively, although these differences were only statistically significant for CCHFV ($p < 0.05$). In contrast, RVFV seropositivity was quite similar between both sexes (2.82% in females vs. 2.13% in males, $p > 0.05$).

Although camels older than 10 years exhibited higher seroprevalence rates than other groups, these differences were not statistically significant ($p > 0.05$).

CCHFV exhibited the greatest geographic disparity, with seroprevalence ranging from 0.00% in Ouargla to 86.27% in Illizi. Notably, CCHFV seroprevalence differed significantly across municipalities ($p < 0.05$), whereas no significant differences were observed for the other viruses. Detailed seropositivity rates for all six municipalities are provided in Table I and Figure 1.

Discussion

Camels, along with other livestock species, are key components of the transmission dynamics of several zoonotic viruses, as their close interactions with humans can facilitate cross-species transmission (Zhu et al., 2019). Given its vast and ecologically diverse landscape, Algeria harbours a wide range of tick, sandfly and mosquito species that are recognised as efficient vectors of several pathogens, thereby creating favourable conditions for the persistence and ongoing transmission of arboviruses among animal hosts (Manseur et al., 2022; Boubidi et al., 2024; Temani et al., 2025). To date, in Algeria, the seroepidemiological status of many arbovirus infections that threaten both animal and human health remains poorly investigated. In this context, the present study assessed the seroprevalence of CCHFV, WNV, and RVFV in camels across multiple sites in the Algerian Sahara.

Dromedaries were selected in the present study because they represent one of the most important livestock species in the Algerian Sahara, where they are continuously exposed to haematophagous arthropods, including mosquitoes and ticks, which are vectors of several arboviruses. Their long lifespan, extensive movements, and close interaction with both nomadic populations and desert ecosystems make them particularly relevant for seroepidemiological surveillance studies.

According to a recent continent-wide meta-analysis, the overall pooled seroprevalence of RVFV in camels across Africa was estimated at approximately 17.25% (Saadet et al., 2026). Our analysis revealed low circulation of RVFV antibodies among the surveyed animals. Indeed, only 2.68% of the camels tested seropositive. In comparison, RVFV seroprevalence reported in camels from other countries varies widely, ranging from 3.17% in Egypt (Abdallah et al., 2016) and 9.6% in Sudan (Mroz et al., 2017) to moderate levels in Tunisia (34%) (Selmi et al., 2020) and Niger (36.56%) (Kadja et al., 2025). Very high RVFV seroprevalence ($>80\%$) has rarely been reported in camels; however, such levels were observed in specific subpopulations, such as older camels in Tanzania, where seropositivity reached 84.6%, reflecting cumulative exposure in endemic pastoral systems (Swai and Sindato, 2015). Our findings differ markedly from an earlier investigation conducted in southwestern Algeria, which reported a moderate overall RVFV seroprevalence of 26.7% (Trabelsi et al., 2023). In that study, seropositivity reached 35.8% among imported camels, whereas no antibodies against RVFV were detected in locally raised animals. In our study, the detection of IgG antibodies against RVFV, particularly in animals younger than five years, suggests that the virus has likely circulated, at least sporadically, within the region. Even in the absence of reported outbreaks, these serological traces may indicate silent or low-level transmission.

According to a global meta-analysis, the overall pooled prevalence of CCHFV in animals was estimated at about 4.5% for acute infections and 12.0% for past infections (IgG seroprevalence) (Belobo et al., 2021). In our study, we found that CCHFV was predominant, with a high seroprevalence that surpassed 75%. This is consistent with some reports from neighbouring countries in Northern Africa, where seropositivity in camels typically ranges from 89.7% to 90.5% in Tunisia and Mauritania (Bouaicha et al., 2021; El Ghassem et al., 2023). In contrast, lower rates (5.3%-21.3%) were reported in certain regions of several other African and Middle Eastern countries, including Niger, Central Sudan, and Iran (Mariner et al., 1995; Champour et al., 2016; Suliman et al., 2017). Regional differences in CCHFV seroprevalence worldwide likely reflect variations in geography, climate, camel breeds and density, as well as management and husbandry practices (Esser et al., 2019; Blanco-Penedo et al., 2021; O'Neill et al., 2025).

CCHFV IgG antibodies were identified in camels from all surveyed regions, with seroprevalence rates exceeding 55% in most areas, whereas no evidence of infection was detected in Ouargla. Similarly high seroprevalence levels have

been reported in previous studies conducted in Algeria, including some of the areas examined in the present study, with reported estimates ranging from 75.5% to 95.7% in northeastern and southwestern regions (Guidoum et al., 2023; Degui et al., 2024). In addition, recent molecular surveillance targeting CCHFV in ticks collected from camels in southeastern Algeria (Ouargla, Illizi, and Djanet) detected viral RNA in one out of 138 analysed tick pools, highlighting ongoing viral circulation in the region. Genetic analysis showed that the detected strain clustered within the Africa 1 genotype lineage. Additionally, the tick fauna associated with camels was overwhelmingly dominated by *Hy. dromedarii*, which accounted for 83.81% of the collected specimens (Temani et al., 2023). This tick species, previously identified as a competent vector of CCHFV, has also been reported as the predominant species in multiple entomological surveys conducted on camels in Algeria (Djerbouh et al., 2012; Hamlili et al., 2022; Chaibi et al., 2024). Collectively, these findings suggest the presence of competent CCHFV vectors that may contribute to the maintenance and circulation of CCHFV transmission cycle in the Sahara region.

Antibodies against WNV were detected in 50.63% of our samples. Comparable serosurveys conducted in Qatar, Ethiopia, and Mauritania have reported seroprevalence rates of 23.3%, 69%, and 92%, respectively (Cosseddu et al., 2021; Megenas et al., 2025; AISaiari et al., 2026). Furthermore, the first isolation of WNV from a dromedary camel was reported in the United Arab Emirates, providing additional evidence of the susceptibility of this species to WNV infection (Joseph et al., 2016). Of note, epidemiological data on WNV infection in camels remain scarce, and their potential role in the transmission dynamics of WNV, particularly with regard to human infection, has yet to be clearly established and warrants further investigation. Nevertheless, the detection of WNV-specific antibodies in the camels included in the study provides evidence of previous viral exposure and indicates active or past circulation of the virus within the surveyed areas. In addition, our findings suggest that camels may serve as valuable sentinel animals for monitoring the local circulation of arboviruses in endemic ecosystems. Despite the limited number of investigations conducted in Algeria, available studies indicate that the virus is already present in multiple regions of the country. Notably, in the Djanet area, the virus has been isolated from *Culex* mosquitoes, and serological evidence has also been reported in the local human population (Hachid et al., 2019).

The geographic expansion of arboviruses is an increasing global concern, largely driven not only by climate change, which influences vector density and distribution, but also by the growing movement and trade of livestock (Napp et al., 2018; O'Neill et al., 2025). Although CCHFV seroprevalence differed significantly among municipalities, the observed heterogeneity is unlikely to reflect true spatial or ecological variation. Rather, it is more likely to result from variations in sampling effort. In addition, the transhumant movement of camels across regions in search of grazing areas complicates the accurate determination of their geographical origin and the identification of areas most affected by the viruses being investigated. Consequently, larger and better-designed studies are required to more accurately assess the factors influencing exposure and to better understand the dynamics of virus circulation within and between regions.

Camels play a central role in the socio-economic life and cultural traditions of local Saharan populations, particularly through seasonal transhumance. These movements, whether within national boundaries or across borders, can increase contact between animals, infected hosts, and competent vectors, thereby enhancing opportunities for virus transmission. In parallel, the nomadic practices of local communities may further facilitate the cross-border introduction of zoonotic viruses, notably CCHFV and RVFV, from neighbouring endemic regions. Driven mainly by the search for pasture during periods of resource scarcity, these recurrent movements likely contribute to the silent introduction and spread of multiple viral pathogens. On the other hand, the smuggling of animals, particularly camels, from neighbouring countries represents an undeniable risk, as it may contribute to the introduction and spread of these viruses in Algeria.

In our study areas, ecological, climatic, and entomological conditions favour the emergence and circulation of multiple arboviruses. Serological and molecular investigations conducted in neighbouring regions or border areas of Algeria have reported variable prevalence levels, reflecting both past exposure and, in some cases, recent infections with the viruses under study (Zivcec et al., 2014; Maiga et al., 2017; Bouaicha et al., 2021; Schulz et al., 2021; Mencattelli et al., 2022; Adesola et al., 2025; Barhoumi et al., 2025; Kadja et al., 2025; Saadet et al., 2026). These findings support the likelihood of silent transboundary circulation of these viruses within Algeria and between Algeria and neighbouring countries such as Libya and Tunisia, as well as those of Sahel area including Mauritania, Mali and Niger. In a recent meta-analysis, Saadet and colleagues reported that the highest RVFV seroprevalence rates in dromedary camels in Africa were observed in Somalia, Niger, and Mauritania (Saadet et al., 2026). The spread of arboviruses is influenced by several factors, particularly animal movements. In fact, both legal and illegal livestock trade and transportation, as well as the natural migration of wildlife, play pivotal roles in the geographic spread of pathogens such as CCHFV and RVFV (Napp et al., 2018; Spengler et al., 2019). Notably, camels appear to be particularly important in this context, as their transboundary movement has been implicated in the introduction and dissemination of these viruses in several countries, including Egypt (Abd El-Rahim et al., 1999), the Arabian Peninsula (Balkhy and Memish, 2003), and

Mauritania (El Mamy et al., 2011).

Furthermore, migratory birds along the Trans-Saharan Flyway, particularly those carrying *Hyalomma* spp. ticks, are increasingly recognised as important drivers of the intercontinental dispersal of CCHFV between Africa and Europe (Palomar et al., 2013; Keve et al., 2025). Recent findings from southeastern Algeria further support this hypothesis, suggesting that migratory birds may facilitate the introduction of CCHFV from endemic regions. Notably, the detection of the Africa 1 lineage in *Hyalomma* ticks, closely related to strains reported in Corsica (France) and Senegal, reinforces the role of bird-mediated movement in viral spread (Temani et al., 2025). Collectively, these observations underscore a persistent risk of CCHFV dissemination across Algeria and neighbouring North African countries.

In our study, although higher seropositivity was observed in older camels, the differences between age groups were not statistically significant. However, several age-stratified studies from other regions have reported a significantly higher likelihood of IgG seropositivity in older animals (Saadet et al., 2026; Schulz et al., 2021), suggesting the likely persistence of long-term detectable antibodies. Despite this, there is still almost no longitudinal evidence characterising the durability and decline of arbovirus-specific IgG responses in camels. The serological distribution of IgG antibodies by sex revealed significant differences for CCHFV, suggesting that this variable may influence the infection pattern of the virus under study. However, these findings are inconsistent with several previously published studies reporting no significant sex-related differences for the investigated arboviruses, suggesting that sex is generally not a significant risk factor (Schulz et al., 2021; Trabelsi et al., 2023; Degui et al., 2024; Saadet et al., 2026). This is likely because males and females often share the same environment under similar management systems, and exposure is more strongly influenced by tick contact, ecological factors, and age rather than by sex.

The interpretation of our findings should consider several methodological limitations. First, the exclusive use of IgG ELISA detects only past exposure and does not reflect active infections, limiting the assessment of ongoing viral circulation. Incorporating IgM assays or molecular techniques such as RT-PCR would improve the detection of current infections. Although ELISA is sensitive, confirmatory tests such as virus neutralisation assays would strengthen the evaluation of exposure and immunity. Additionally, uneven regional sampling may explain variability in seroprevalence, and the relatively small sample size highlights the need for larger, more comprehensive studies using diverse and more specific diagnostic methods.

Despite these limitations, this study provides serological evidence from southeastern Algeria of camel exposure to multiple zoonotic viruses. It helps fill an important epidemiological gap in North Africa and establishes a baseline for future surveillance and risk assessment.

Conclusion

This study highlights the exposure of camels in the eastern Algerian Sahara to three major zoonotic viruses (RVFV, WNV, and CCHFV), providing new epidemiological insights into Algeria. Our findings provide the first evidence of arbovirus exposure in some of the investigated regions. However, since the study assessed only serological evidence of past infection, future research should focus on detecting active infections in both animal hosts and vectors to better characterise viral circulation and transmission dynamics. Moreover, incorporating advanced serological and molecular diagnostic approaches, along with long-term studies and expanded surveillance across regions and host species, is essential to improve livestock disease control and reduce the risk of zoonotic transmission to humans in close contact with animals.

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Ethical approval

The procedures involving animals were carried out under authorisation granted to the Pasteur Institute of Algeria by the Algerian Ministry of Health and the Algerian Ministry of Agriculture to perform blood sampling on live animals. The study protocol was reviewed and approved by the Institutional Animal Care and Use Committee of the Pasteur Institute of Algeria. Prior to sample collection, verbal informed consent was obtained from animal owners, as well as from the administration of the El Oued Abattoir.

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

Conceptualisation: AK, IL; Methodology: NEM, IL; Formal analysis: SNYB, DD, AH; Investigation: IL; Writing original draft preparation: NEM; Writing, review and editing: NEM, MHB, AFK, AH, IB, IL; Visualisation: IB, NEM, SNYB; Supervision: IL, IB, AH; Project administration: AH, IB, IL.

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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