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Epidemiology of caprine brucellosis in family farms in the south east of Algeria

Nacira Ramdani¹, Sabrina Boussena^{2*}, Farida Ghalmi³, Mohammed Hocine Benaissa⁴, Nassim Moula⁵

¹Management of Animal Health and Productions Laboratory, Institute of Veterinary Sciences, University of Frères Mentouri Constantine 1; Regional Veterinary Laboratory of El Oued, National Institute of Veterinary Medicine - DZ

²Management of Animal Health and Productions Laboratory, Institute of Veterinary Sciences, University of Frères Mentouri Constantine 1 - DZ

³Research Laboratory Management of Local Animal Resources, Higher National Veterinary School Rabie Bouchama, Algiers - DZ

⁴Scientific and Technical Research Center for Arid Regions (CRSTRA), Touggourt, Algeria. - DZ

⁵Department of Veterinary Management of Animal Resources, Faculty of Veterinary Medicine, Liège, Belgium. - BE

*Corresponding author at: Management of Animal Health and Productions Laboratory, Institute of Veterinary Sciences, University of Frères Mentouri Constantine 1 - DZ

E-mail: s_boussena@umc.edu.dz

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Abstract

This cross-sectional study aimed to estimate the seroprevalence and the potential risk factors of *Brucella* infection among goats in family farms in the southern east of Algeria. A total of 196 sera samples were randomly collected from 59 family farms and tested in parallel by Rose Bengal test (RBT) and indirect ELISA (iELISA). A structured questionnaire was used to collect information on potential risk factors. Apparent seroprevalence values were 8.7% (95% CI: 5.49-13.45) and 2.04% (95% CI: 0.8-5.13) for RBT and iELISA respectively. The estimated true prevalence values were 11.1% (95% CI: 6.87-17.42) for the RBT test and 1.58% (95% CI: 0.3-4.74) for iELISA. Dog presence in family farm was significantly associated with *Brucella* spp. seropositivity ($p=0.03$) using iELISA, with at least 38 times the odds of brucellosis seropositivity (OR: 38.55, 95% CI: 1.42-1049.17). Goats with previous history of stillbirth were significantly associated with *Brucella* spp. seropositivity ($p=0.04$) using RBT, with almost six (6) times higher odds (OR: 6.62, 95% CI: 1.06-41.55). Origin of animals reared on family farms was also significantly associated with *Brucella* spp. seropositivity ($p=0.05$) using iELISA with higher odds in foreign goats (OR: 12.99, 95% CI: 1.03-163.22) and lower odds in goats born in farms (OR: 0.08, 95% CI: 0.01-0.97). Based on these findings, further epidemiological studies related to the perception of the disease by animal owners and brucellosis in herding dogs needed to be conducted.

Keywords

Algeria, Brucellosis, Cross-sectional, Family farms, Goats, Risk factors

Introduction

Brucellosis is a significant zoonotic disease affecting both animals and humans, caused by various species of the Gram-negative coccobacillus *Brucella* (Corbel 2006). The disease is prevalent worldwide, particularly in regions such as the Middle East, the Mediterranean, sub-Saharan Africa, China, India, Peru, Mexico, and Central and Southwest Asia, although it has been eradicated in several developed countries (WOAH 2021). In humans, brucellosis typically manifests as a febrile illness with potential for severe complications if untreated, and it is primarily contracted through direct contact with infected animals or the consumption of unpasteurized dairy products (Corbel 2006). In animals, the disease leads to decreased productivity, abortion in pregnant animals and infertility, and increased veterinary costs leading to substantial economic losses in the livestock industry (Seleem *et al.* 2010; Singh *et al.* 2015).

In North Africa, brucellosis remains a significant public health and economic concern, particularly in countries like Algeria, Tunisia, Morocco, and Egypt (Musallam *et al.* 2015; Douifi *et al.* 2021). The endemic nature of the disease in

these regions is attributed to traditional farming practices, insufficient vaccination coverage among animals, and limited public health interventions (FAO 2009; Musallam *et al.* 2015).

In Algeria, brucellosis is a notable zoonosis, with 10,198 human cases reported in 2017 (National Institute of Public Health INSP 2017). The primary sources of human infections are animals like sheep, goats, and cattle though camels and dogs also play roles in certain regions (Corbel 2006).

Since 2006, Algeria has implemented control measures, including vaccination of young small ruminants and screening-slaughtering programs for cattle (MADR 2016). Despite these efforts, uncontrolled animal movement, lack of livestock identification, low vaccination coverage (12.58% in 2014) (MADR 2016), and the absence of a comprehensive, long-term control plan tailored to socio-economic conditions continue to perpetuate the disease.

In Algeria, recent studies investigating the seroprevalence and epidemiological data of brucellosis in goats or small ruminant were conducted in the provinces of El-Bayadh (Nehari *et al.* 2014), Batna and Setif (Gabli *et al.* 2015), and on the national territory by Kardjadj *et al.* (2016). Additional serological surveys in cattle have been conducted in Tiaret (Aggad and Boukraa 2006; Abdelhadi *et al.* 2015) and Djelfa (Yahia *et al.* 2018) provinces. Conversely, the isolation and the genotypic identification of brucellae in man and animals are rare (Lounes *et al.* 2014, Lounes *et al.* 2021). However, risk factors associated with caprine brucellosis remain under-investigated.

Caprine brucellosis, specifically caused by *Brucella melitensis*, is particularly important due to its high pathogenicity. Goat farming is a vital agricultural sector in developing countries, with about 35% of the world's goat population located in Africa (Skapetas and Bampidis 2016). In Southeast Algeria, particularly in El Oued province, goat milk is a nutritious and widely consumed product. The accessibility and lower management needs of goat breeding have led to the proliferation of family goat farms in the region. According to the Health and Population Directorate of El Oued province, animal brucellosis results in nearly a hundred human cases annually, with goats responsible for the majority of transmissions (DSP El Oued 2016; DSA El Oued 2016).

Despite the significant number of family farms and associated zoonotic risks from close animal-human contact, these farms often remain unnoticed by veterinary public health authorities. Therefore, this study conducted a cross-sectional survey of caprine brucellosis seroprevalence in family goat farms to highlight the concealed zoonotic risk. The main objectives were to estimate the seroprevalence of caprine brucellosis, determine risk factors associated with *Brucella* spp. seropositivity, and raise public awareness of the risks related to brucellosis in goat populations.

Materials and methods

Study area and animal population

El Oued province is located in the South-East of Algeria (Figure 1); it occupies an area of 44,586.8 km² (about 1.87% of the Algeria land area) and divided into 30 municipalities. El Oued is located at an altitude of 88 m above sea level, latitude 33° 21' N and longitude 6° 51' E. According to the data of DSA El Oued (2016), there were about 1,156,500 of livestock at the time of the study, including 1.43% cattle, 3.46% camels, 46.69 % goats and 48.42% sheep.

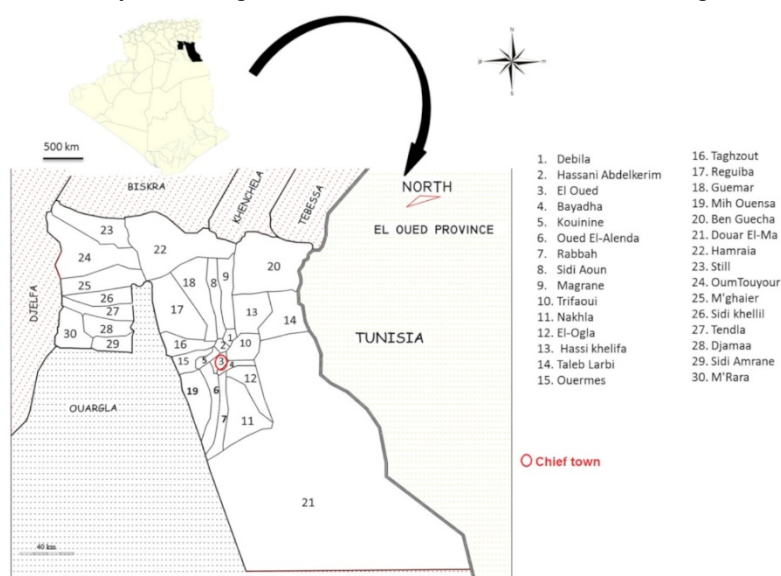


Figure 1. Administrative division chart of El Oued province (municipalities of El Oued).

Study design

A cross-sectional study was carried out in El Oued province from April to June 2016. Our target population was the entire goat raised in family farms in this province. The sampling unit was the animals (goats). The number of family farms was obtained from the proportion of families raising livestock animals in their houses, which depends on the lifestyle of inhabitants in each municipality. Therefore, the number of animals was obtained by multiplying the farm number by four (4) which is the average number of goats raised on family farm (Table I).

Municipality	Number of houses*	Farms number (%)	Goats number
El Oued	27921	1675 (6)	6700
Kouinine	2756	165 (6)	660
Reguiba	6773	2031 (30)	8124
Hamraia	1526	610 (40)	2440
Guemar	9335	933 (10)	3732
Taghzout	2919	437 (15)	1748
Ouermes	1778	177 (10)	708
Debila	5062	1518 (30)	6072
Hassani Abdelkerim	4458	1337 (30)	5348
Hassi khelifa	5493	2197 (40)	8788
Trifaoui	1840	736 (40)	2944
Magrane	4386	657 (15)	2628
Sidi Aoun	3231	1453 (45)	5812
Rabbah	4212	1053 (25)	4212
Nakhla	2908	1017 (35)	4068
El-Ogla	1561	546 (35)	2184
Bayadha	6999	1049 (15)	4196
Taleb Larbi	1722	1377 (80)	5508
Ben Guecha	1178	942 (80)	3768
Douar El-Ma	1873	1498 (80)	5992
Mih Ouensa	3928	1374 (35)	5496
Oued El-Alenda	1909	668 (35)	2672
M'ghaier	9056	2716 (30)	10864
Sidi khellil	1791	537 (30)	2148
Still	1144	343 (30)	1372
OumTouyour	2293	687 (30)	2748
Djamaa	9491	2847 (30)	11388
Sidi Amrane	5086	1525 (30)	6100
M'Rara	1821	546 (30)	2184
Tendla	1998	599 (30)	2396
Total	136448	33250	133000

* Directorate of programming and budget monitoring of El Oued province (2015).

Table I. Estimation of the total number of goats raised on family farms per municipality.

Sampling strategy and sample size

The sample size (n) was calculated according to simple random sampling formula (Thrusfield 2007) as follows:

$$n = \frac{1.96^2 \times P_{exp} (1 - P_{exp})}{d^2}$$

The expected prevalence (P_{exp}) was 13.4% (Lounes and Bouyoucef 2008) with a desired absolute precision (d) of 5% and associated 95% confidence interval of the estimate. Five municipalities from thirty (El Oued, Sidi Aoun, Ben Guecha, Taghzout and Tendla) were sampled systematically using the inclusion probability. The number of goats to be sampled in each municipality was distributed proportionally to the size. The number of herds to be sampled was obtained by dividing animals' number of the sample by the average number of family farms. Afterward, herds and animals in each herd were selected randomly. Only animals more than six months of age and which stayed more than one year in the herd were sampled. Newly introduced animals were excluded due to lack of vaccination history to avoid diagnostic interference.

Samples and data collection

Selected family farms owners were informed about the purpose of this study and their agreement was obtained verbally. One hundred and ninety-six goat blood samples were withdrawn from jugular vein by venipuncture in 5 ml labeled vacutainer tubes. Sera were collected after centrifugation at 3000 rpm for 5 min, and stored in 2 ml labeled Eppendorf tubes at -20 °C until their testing at the Scientific and Technical Research Center on Arid Regions (CRSTRA), Touggourt, Algeria.

In parallel with blood collecting, a structured questionnaire was administered regarding animals and farms. For each sampled animal, biodata such as age, sex, production system, parity, pregnancy, origin and reproductive disorders (abortion, mastitis and stillbirth) were recorded. Information on farm localization, recent entry of animals, presence of others species on the farm, and veterinary service was also detailed.

Serological tests

The Rose Bengal test (antigen prepared from *B. abortus*, strain 99) was performed as per standard procedure (Morgan *et al.* 1969) and the manufacturer protocol (Lillidale Diagnostics, Dorset, United Kingdom). A multi-species indirect ELISA (iELISA) Kit for the detection of antibodies against *B. abortus*, *B. melitensis* or *B. suis* was used. The protocol was conducted according to manufacturer instructions (ID-VET®, Montpellier, France). All serum samples were subjected to both RBT and iELISA tests.

Data analysis

Apparent (AP) and true (TP) seroprevalences and their confidence intervals (CI) were computed using the online Epitools Calculator (Sergeant 2018). Apparent prevalence (the proportion of the goats that tests positive using a diagnostic method) was calculated as follows:

$$AP = \text{Positive animals} / \text{Total screened animals}$$

Wilson method was used to calculate confidence intervals for the apparent prevalence as described by Brown *et al.* (2001). True prevalence (the proportion of truly infected goats) was calculated using the Rogan and Gladen (1978) equation. The formula for the calculation is:

$$TP = (AP + Sp - 1) / (Se + Sp - 1)$$

Blaker method was used to estimate 95% confidence intervals of the true prevalence as described by Reiczigel *et al.* (2010). Sensitivity (Se, ability of the test to detect true positives) and specificity (Sp, ability of the test to detect true negatives) for RBT are 75.8%, 99.7% respectively, and 98.2, 99.5% for iELISA, respectively (Minas *et al.* 2007). Seroprevalence of parallel interpretation was calculated considering animals that tested positive to at least one serological test. Comparison between seroprevalences estimates of RBT and iELISA has been achieved by McNemar test using IBM SPSS Statistics 25 (IBM Corp., New York, USA).

Initially, a univariate explanatory analysis of assumed risk exposure factors was performed by simple logistic regression. Variables whose *P*-value ≤ 0.25 as well as biologically plausible factors were selected for the multivariate analysis. Collinearity between the selected variables was evaluated by Cramer V test. Variables were considered strongly correlated if V coefficient was higher than 0.15 and only the most biologically plausible to brucellosis would be kept for the multivariate analysis.

Binary logistic regression models for RBT and iELISA were performed, using a backward stepwise likelihood ratio test procedure with cut-off 0.05 for entry and 0.1 for removal at each step. The goodness of fit of the models was assessed by Hosmer and Lemeshow test and Omnibus test. Confounding factors were detected if there was a change in regression coefficients by a factor of 20% when removed. Possible interaction effect was checked for significance ($p < 0.05$). Variables with $p < 0.05$ at the final step were considered statistically significant.

All relevant analyses were performed using IBM SPSS Statistics 25 (IBM Corp., New York, USA).

Results

Seroprevalence

Apparent seroprevalence values were 8.7% (95% CI: 5.49-13.45) and 2.04% (95% CI: 0.8-5.13) with RBT and iELISA, respectively. True prevalence using RBT was 11.1% (95% CI: 6.87-17.42) and 1.58% (95% CI: 0.3-4.74) using iELISA. Seroprevalence of parallel testing was 9.18% (95% CI: 5.89-14.05). A significant difference ($p = 0.001$) of seroprevalences estimates of RBT and iELISA was found as a result of McNemar test (Table II).

	RBT+	RBT-	P-value McNemar's test
i ELISA+	3	1	0.001
i ELISA-	14	178	

Table II. Comparison of RBT and iELISA results used for *Brucella* spp. infection diagnosis in family farms goats.

Risk factors

Rose Bengal test results

Four variables (origin, stillbirth history, newly purchased animals, nulliparity) of $p \leq 0.25$ at the univariate analysis were included into the multivariate logistic regression (table III). Municipality was excluded due to collinearity with stillbirth history. Other variables such as age, reproductive disorders and multiparity were added to the multivariate model for biological plausibility to brucellosis. The final logistic regression model showed only a statistically significant association between stillbirth occurrence and goats seropositivity ($p=0.04$), with higher odds (OR: 6.62, 95% CI: 1.06-41.55) as shown in table IV. The Hosmer and Lemeshow goodness of fit test showed a non-significant result ($p=0.3$), indicating that the model fitted well the data. Additionally, the results of Omnibus test ($p=0.04$) demonstrated an improvement of the predictive power of the final model.

Variable	Category	RBT		iELISA	
		No. Positive (total)	P-value	No. Positive (total)	P-value
Sex	Female	16 (185)	0.96	4 (185)	0.99
	Male	1 (11)		0 (11)	
Age	≥ 2 years	15 (174)	0.94	4 (174)	0.99
	6 months to 2 years	2 (22)		0 (22)	
	Milk	16 (184)		4 (184)	
Type of production	Meat	1 (7)	0.88	0 (7)	1
	Reproduction	0 (5)		0 (5)	
Origin	Foreign	7 (49)	0.11*	3 (49)	0.05*
	Born in farm	10 (147)		1 (147)	
Pregnancy	Yes	0 (13)	0.99	0 (13)	0.99
	No	17 (183)		4 (183)	
Abortion	Yes	0 (11)	0.99	0 (11)	0.99
	No	17 (185)		4 (185)	
Mastitis	Yes	1 (8)	0.69	0 (8)	0.99
	No	16 (188)		4 (188)	
Stillbirth	Yes	2 (6)	0.05*	0 (6)	0.99
	No	15 (190)		4 (190)	
Nulliparous	Yes	3 (18)	0.21*	0 (18)	0.99
	No	14 (178)		4 (178)	
Primiparous	Yes	3 (53)	0.36	2 (53)	0.31
	No	14 (143)		2 (143)	
Pluriparous	Yes	10 (114)	0.95	2 (114)	0.73
	No	7 (82)		2 (82)	
Municipality	El Oued	13 (63)	0.16*	3 (63)	0.99
	Ben guecha	0 (38)		1 (38)	
	Sidi Aoun	1 (55)		0 (55)	
	Tendla	3 (24)		0 (24)	
Sheep	Taghzout	0 (16)	0.59	0 (16)	0.99
	Yes	2 (32)		0 (32)	
Dog	No	15 (164)	0.99	4 (164)	0.99
	Yes	0 (6)		1 (06)	
Pigeon	No	17 (190)	0.36	3 (190)	0.04*
	Yes	1 (26)		0 (26)	
Newly purchased animals	No	16 (170)	0.21*	4 (170)	0.99
	Yes	2 (48)		0 (48)	
Veterinary services	No	15 (148)	0.90	4 (148)	0.99
	Yes	10 (118)		0 (118)	
	No	7 (78)		4 (78)	0.67

*Variables showing statistical value of significance $p \leq 0.25$ were included into multivariate analysis.

Table III. Results of univariate analysis of potential risk factors associated with *Brucella* spp. seropositivity in goats' family farm.

Indirect ELISA results

Variables with a p value ≤ 0.25 at the explanatory analysis: origin of animals and presence of dogs in family farms (Table III), as well as the same variables biologically plausible added in the first model were included into the binary logistic model with iELISA test results as the dichotomous dependent variable. The final model revealed that the presence of dogs in family farms increased at least 38 times the odds of *Brucella* seropositivity with iELISA ($p=0.03$) (OR: 38.55, 95% CI: 1.42-1049.17) (Table IV). It also showed that foreign origin of animals increased about 12 times the odds of *Brucella* seropositivity ($p=0.05$) (OR: 12.99, 95% CI: 1.03-163.22) compared to animals born in farms, and

the later are 92 % less likely to being seropositive compared to animals of external origin (OR: 0.08, 95% CI: 0.01-0.97).

The model fitted well the data with a p -value of Hosmer and Lemeshow test equal to 0.72, and showed a significant improvement of predictability of independent variables via Omnibus test results ($p=0.03$).

Serological test	Variable	B	SE	Wald	OR	CI 95% OR	P-value
RBT *	Stillbirth (yes)	1.89	0.94	4.07	6.62	1.06-41.55	0.04
iELISA **	Dog's presence (yes)	3.65	1.69	4.69	38.55	1.42-1049.17	0.03
	Foreign origin	2.56	1.29	3.94	12.99	1.03-163.22	0.05
	Born in farm	-2.56	1.29	3.94	0.08	0.01-0.97	

*-2 Log likelihood: 105.64

** -2 Log likelihood: 30.46

B: Log-odds, SE: Standard Error, OR: Odds Ratio, CI 95% OR: Confidence interval of Odds Ratio.

Table IV. Results of multivariate logistic regression modeling on goats' serological status in family farms against *Brucella* spp.

Discussion

The occurrence, propagation and persistence of the disease are influenced by various factors related to the characteristics of the animal, pathogen and environment (Thrusfield 2007). Identification of these determinants is crucial for stakeholders, including animal keepers, veterinarians, and policy-makers. To our knowledge, this is the first study in goats that defines risk factors associated with *Brucella* infection in family farms in Algeria.

The results of this study revealed a high caprine brucellosis seroprevalence estimate in family farms, indicating a crucial risk for these families. Smallholder farms constitute an invisible reservoir of the disease, maintained by a category of people who are often unfamiliar with the risks of infectious diseases, control measures and vaccination. Therefore, control and eradication programs should target this breeding system. Our results obtained by RBT (8.7%) were notably higher than estimates reported in small ruminants in various regions of Algeria ((3.33%) Kardjadj *et al.* 2016, (3%) Nehari *et al.* 2014, (0.98%) Gabli *et al.* 2015). However, these studies employed different study designs and serological tests.

Compared to Middle-eastern and African countries, our RBT seroprevalence estimates were also higher than rates reported in Arabian Gulf region (0.78%) (Ebid *et al.* 2020), Cameroun (1.3%) (Kamga *et al.* 2020), Nigeria (5.08%) (Buhari *et al.* 2020) and in Ethiopia (6.3%) (Tulu *et al.* 2020). On the other hand, studies from Libya (33.4%) (Al-Griwi *et al.* 2017) and Egypt (20%) (Gwida *et al.* 2020) reported higher estimates. A recent study in Egypt (El-Diasty *et al.* 2021) reported a seroprevalence estimate of 7.2%, slightly lower than our results.

Using iELISA, the seroprevalence (2.04%) was significantly lower than brucellosis prevalence reported in Egypt (20%) (Gwida *et al.* 2020) and Saudi Arabia (8.8%) (Shabana and Krimly 2020). However, our findings indicate a slightly higher seroprevalence compared to studies conducted in Cameroon (1.1%) by Kamga *et al.* (2020) and Uganda (0.3%) by Nguna *et al.* (2019). In comparison to the study conducted in Egypt by Gwida *et al.* (2020), which reported a seroprevalence of 20%, our current study found a notably lower seroprevalence value of 9.18% using parallel testing. These differences in brucellosis seroprevalence are likely not solely attributable to variations in the incidence of brucellosis. Instead, they may reflect disparities in the performance of various serological tests used in research and screening, as noted by Nielsen (2002), Minas *et al.* (2007), Rahman *et al.* (2013), and Shenoy (2016). Additionally, discrepancies in results could be influenced by differences in environmental and management conditions, as well as the methodologies employed in the studies.

Although both tests are conditionally dependent, as they both detect antibodies against the-lipopolysaccharide (S-LPS) (Gardner *et al.* 2000, Shenoy *et al.* 2016), the current study revealed a significant difference between the results obtained from RBT and iELISA ($p<0.001$). This discrepancy aligns with previous findings reported by Delgado *et al.* (1995) ($p<0.01$), Minas *et al.* (2007) ($p<0.001$) and Minas *et al.* (2008) ($p<0.01$).

The observed difference in performance between these serological tests can be attributed to the specific antibody isotypes they are designed to detect. The RBT is capable of detecting both IgM and IgG antibodies, which correspond to different stages of the disease, thereby reflecting a broader range of the immune response. In contrast, iELISA predominantly detects IgG antibodies, focusing more on a specific stage of infection (Godfroid *et al.* 2010; Diaz *et al.* 2011). Furthermore, as noted by Minas *et al.* (2008), the efficacy of a diagnostic test can be influenced by several factors, including the *Brucella* infection status, age, stage of pregnancy, overall health status, and the stage of infection

In our study, family farms housing dogs were found to be associated with significantly higher odds to brucellosis seropositivity using iELISA. On these farms, most dogs are kept as pets; however, they may still act as active or passive carriers of various diseases, including brucellosis. Indeed, *B. melitensis* and *B. abortus* have been isolated and identified in dogs across various regions globally (Alamian and Dadar 2020; Anyaoha *et al.* 2020; Bernardino *et al.* 2021). Moreover, the biological role of cats and dogs in the transmission of *Brucella* spp. was confirmed by a study conducted by Wareth *et al.* (2017), where *Brucella abortus* bv 1 was isolated from the uterine discharge of an apparently healthy bitch and queen, both of whom had open pyometra and were housed on a cattle farm. Additionally, dogs may serve as mechanical vectors of brucellosis, particularly when allowed to roam freely, potentially spreading the pathogen among susceptible animals (Aparicio 2013).

Abortion, mastitis and stillbirth are characteristic signs of *Brucella* infection, and their occurrence within flocks serves as a critical marker of the disease's presence (Saeed *et al.* 2019; Behera *et al.* 2020; Edao *et al.* 2020; Shakeel *et al.* 2020; Alemayehu *et al.* 2021). In our study, the history of stillbirth encompassed cases where offspring were either born dead or died shortly after birth. Female goats with stillbirth history were more likely to be seropositive for *Brucella* spp. with notably higher odds. These findings are consistent with those reported by Tadege *et al.* (2015), while Zewdie (2020) observed some discrepancies. Furthermore, a significant association between a history of abortions and the prevalence of brucellosis has been documented in previous studies (Saeed *et al.* 2019; Behera *et al.* 2020; Edao *et al.* 2020; Shakeel *et al.* 2020), reinforcing the importance of these reproductive complications as indicators of infection.

The introduction of infected animals is a primary source of contamination for previously disease-free farms, underscoring the necessity for rigorous biosafety measures to prevent the spread of *Brucella* infections. Our study corroborates this, revealing that the foreign origin of animals during farm renewal is significantly associated with a higher likelihood of seropositivity for *Brucella* using iELISA ($p=0.05$). In contrast, animals born and raised on the farm exhibited a lower risk of infection. These findings align with those reported by Mikolon *et al.* (1998), suggesting that the increased risk may be due to the unknown health status of the original herd and the potential for contamination during commercial exchanges, such as at animal markets or during transport. However, it is noteworthy that Gombo *et al.* (2021) observed no significant correlation between the origin of small ruminants and *Brucella* infection, highlighting the complexity of factors influencing disease transmission.

The persistence of brucellosis in developing countries is driven by multiple risk factors, as outlined by Hikal *et al.* (2023), including poor disposal of aborted materials, lack of cooperation between policymakers and health professionals, insufficient government compensation for infected animals, and public reluctance to vaccinate. Open borders and uncontrolled animal movements exacerbate the spread of the disease, while inadequate diagnostic tools hinder effective surveillance and control.

Conclusions

Family farms at El Oued province are at high risk of brucellosis according to our results. The difference in performance between RBT and iELISA underscores the critical importance of selecting appropriate serological tests for the diagnosis, screening, and control of brucellosis. Additionally, implementing specific control measures such as quarantine, self-reproduction practices, and stringent health and management protocols emerges as vital strategies for brucellosis prevention in this region.

Moreover, this study highlights the significant role of dogs in the transmission and persistence of brucellosis, a factor that is often underappreciated and largely overlooked in epidemiological investigations of human cases. The lack of recognition of canine brucellosis as a contributor to the disease cycle calls for its inclusion in future studies. Comprehensive research involving all susceptible species is essential to gain a deeper understanding of the dynamics of brucellosis transmission in Algeria. Such efforts will be instrumental in developing more effective and targeted control strategies.

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