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Factors associated with Rift Valley fever in south-west Saudi Arabia

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Summary

The authors undertook a study of environmental and animal risk factors associated with Rift Valley fever (RVF) in south-west Saudi Arabia. An enzyme-linked immunosorbent assay was used to detect the presence of immunoglobulin M (IgM) and immunoglobulin G (IgG) antibodies against the RVF virus in serum samples from sentinel animals. In addition, a further 32 known IgM-positive serum samples were tested using the reverse transcription polymerase chain reaction (RT-PCR) to detect the RVF virus genome.

The results were analysed using the univariate odds ratio (OR). To control for confounding, Mantel-Haenszel adjusted odds ratio (M-H OR) was used. Positive associations were found between RVF and the following factors: a dense mosquito population (OR = 4.2), high rainfall (M-H OR = 2) and the presence of lakes and/or ponds (M-H OR = 2.2). The RVF virus genome was detected in four (12.5%) serum samples, indicating an early stage of RVF. The study found that the probability of detecting the virus genome was greater in animals with a high percentage of IgM antibodies against the virus (OR = 3) and in animals who had aborted (OR = 4.3). In addition, more sheep than goats tested positive for the presence of the genome (OR = 4).

The authors conclude that the environmental and animal risk factors identified in this study can be considered good predictors for RVF and that the animal factors, in particular, should be considered when developing an efficient and cost-effective control strategy.

Keywords

Association – Confounding factor – Middle East – Reverse transcription polymerase chain reaction – Rift Valley fever – Rift Valley fever virus genome – Risk factor – Saudi Arabia – Sentinel animal.

Introduction

Rift Valley fever (RVF) is a viral disease that affects both animals and humans. The disease is caused by a mosquito-borne virus belonging to the family *Bunyaviridae*, genus *Phlebovirus* (19). In Saudi Arabia, an outbreak of RVF occurred in the period between September 2000 and April 2001. However, approximately two-thirds (64.7%) of animal cases occurred in September and October. Out of the total number of animal cases, 65.6% occurred in the Jazan region, 26.9% in Tahamat Asir and 7.5% in Tahamat Makkah. Infection rates were as follows:

- 9.7% in sheep
- 7.9% in goats
- 1.2% in cattle
- 1.3% in camels (5).

In the 2000 to 2001 outbreak, both humans and animals (primarily sheep and goats) were seriously affected (5, 12).

Drastic control measures were implemented when the outbreak began, including:
– the restriction of animal movements
– mosquito (vector) control
– active surveillance (clinical and serological)
– vaccination of livestock.

In a serological survey conducted in the Jazan region, during the rainy season of 2003, no cases of RVF were diagnosed (6). However, detecting RVF infection during inter-epizootic periods is difficult, except with specific epidemiological techniques. One effective method is to place sentinel animals in high-risk areas to follow up RVF virus activity.

The enzyme-linked immunosorbent assay (ELISA) (16) is a surrogate test which detects immunoglobulin M (IgM) and immunoglobulin G (IgG) antibodies against the RVF virus. This test was used to diagnose the infection in the animal population during the 2000 to 2001 outbreak and is still used in the serological surveillance conducted as part of the RVF control programme. Since IgM antibodies appear in the blood a few days after natural infection, and can be detected by the IgM-capture ELISA for six to twelve weeks (16) or even in the following five months (15), this test cannot distinguish between the early stage of RVF, during which the virus is present in the blood, and late-stage infection, after the clearance of the virus. However, it is possible to make this distinction using reverse transcription polymerase chain reaction (RT-PCR), a reasonably sensitive diagnostic test that detects the RVF virus genome in serum samples. No significant difference was observed between the effectiveness of RT-PCR and that of virus isolation in diagnosing the RVF virus (18). Thus, RT-PCR could reliably be used as a pathognomonic test to detect RVF virus and to distinguish between the early and late stages of RVF.

This study deals with the experimental use of sentinel animals to monitor RVF and investigate associations with environmental risk factors. The authors also report on employing the one-step RT-PCR test to diagnose the early stage of RVF and examine associations with animal risk factors.

Materials and methods

Sentinel animals

A total of 150 Harri sheep and 125 mountain goats were selected from Sarat Asir, a region that is considered free from RVF infection (2). These breeds were chosen because they were either similar or related to the breeds raised in the regions where they would be placed, so they could easily adapt to the new environment. Most of the animals were females and they were of the same age (approximately three to six months) at the time of placement. Before selection, these animals were clinically examined for signs of disease, and serologically tested for IgM and IgG antibodies against the RVF virus. All the animals were found to be healthy, and free from both IgM and IgG antibodies against the RVF virus.

Sites

Eleven sites were selected in all. Seven sites were chosen in seven districts in the Jazan region:
– Alarda
– Alkhoba
– Ayban
– Ahad-Almasarha
– Abu-Arish
– Baish
– Sabya.

Two sites were chosen in two districts of Tahamat Asir:
– Almagarda
– Mahayil.

Another site (Algunfoda) was chosen in Tahamat Makkah. All of these districts had been affected by the 2000 to 2001 RVF outbreak (5).

One more site (Almukhwa) was chosen in Tahamat Albaha, a surveillance region, adjacent to both Tahamat Asir and Tahamat Makkah. The 7 sites in the Jazan region were selected for their proximity to valleys, lakes and ponds or to areas with a good degree of vegetation, where the environmental conditions were ideal for mosquito breeding. The remaining 4 sites were chosen because of the absence of these factors. Twenty-five sentinel animals (15 sheep and 10 goats) were placed on each site in December 2003 or January 2004, and a local farmer looked after them. These animals were vaccinated against haemorrhagic septicaemia, enterotoxaemia, brucellosis and peste des petits ruminants within the first three months of placement.

Environmental risk factors

Information about environmental risk factors for RVF was obtained from the head office of the campaign for the control of RVF in Saudi Arabia. The risk factors investigated were:

– mosquito populations

– rainfall levels

– bodies of water

– vegetation.

Mosquito populations

Mosquitoes were captured in the period from August to October 2004 on different sites in the districts under study, using Clarke Engineering ABC Traps. Most of the mosquitoes captured were either *Culex* or *Aedes* species. The mosquito population was measured by the mean number of mosquitoes per catch in each district. The number ranged from 16 to 417, with a mean of 142 per catch per district. Using the mean as a cut-off point, mosquito populations were categorised as either dense or small. The Alarda, Abu-Arish and Alkhoba districts all had dense mosquito populations.

Rainfall levels

Rainfall levels in the districts under study ranged from 82 mm per year to 596 mm per year, with a mean of 216 mm per year. Using the mean as a cut-off point, rainfall levels were classified as high or low. The Alarda, Ayban and Alkhoba districts had a high level of rainfall.

Bodies of water

The first author estimated the number of seasonal ponds and their areas on field visits between August and October 2004. The highest numbers of ponds were observed in Alarda and Alkhoba. Alarda also has a large permanent lake (Lake Alsad), as does Abu-Arish (Lake Mushrif).

Vegetation

Agricultural activities in most of the districts in the study were similar. Most of the farmers grow crops (mainly sorghum), vegetables and fruit. However, the cultivated areas are variable. Vegetation levels were estimated by comparing the cultivated area in each district, using the map of south-west Saudi Arabia. The districts of Ahad-Almasarha, Abu-Arish, Sabya, Baish and Alkhoba were each classified as having a good degree of vegetation.

Districts not exposed to any of these environmental risk factors were:
– Mahayil and Almagarda in Tahamat Asir
– Almukhwa in Tahamat Albaha
– Algunfoda in Tahamat Makkah.

Study design

To investigate possible associations between RVF and environmental risk factors, the study was designed in a prospective cohort fashion. Sentinel animals were classified, according to their exposure to each risk factor, into 'exposed' and 'not-exposed' groups. The exposed group consisted of animals placed on sites (in the Jazan region) which possessed the risk factor under investigation. The 'not-exposed' group comprised animals placed on sites in the remaining regions, which did not have the risk factor being examined. All sentinel animals were monitored for IgM and IgG antibodies against the RVF virus at least twice, both before and during or after the rainy season, which extends from July to October. The exposed and not-exposed groups were also followed up through clinical examination and serological testing. If either IgM or IgG antibodies against the RVF virus were detected in the serum of a sentinel animal a case of RVF was diagnosed – the results obtained from all individual animals, exposed or not exposed, were included in the statistical analysis.

Immunoglobulin M-positive serum samples

As well as monitoring sentinel herds to identify environmental risk factors, thirty-two IgM-positive serum samples were examined by one-step RT-PCR to examine animal risk factors for RVF. Of these 32 samples, 22 came from an epidemiological surveillance programme (conducted from 21 August to 31 October 2004) which the authors describe elsewhere in this issue of the *Review*. The remaining samples were diagnosed between November 2004 and January 2005. These samples tested positive for IgM antibodies against RVF virus by IgM-capture ELISA (16) and were considered naturally infected with RVF. On 2 March 2005, these serum samples were subjected to testing by one-step RT-PCR to detect the RVF virus genome. Information about the 32 animals from which these serum samples were taken, and the results of the IgM-capture ELISA, were obtained from the head office of the campaign for the control of RVF in Saudi Arabia.

Laboratory diagnosis

All serum samples were tested by the Jazan Veterinary Diagnostic Laboratory. The IgM-capture and IgG-sandwich ELISA techniques used in this study have been fully described elsewhere (16). The one-step RT-PCR procedure is described below.

Extraction method

Nucleic acids were extracted from serum samples with the MagNa Pure LC Total Nucleic Acid Isolation Kit and the MagNa Pure LC instrument (Roche).

Reverse transcription polymerase chain reaction

The one-step RT-PCR was performed using the LightCycler RNA Amplification Kit, SYBR Green 1, and the LightCycler instrument (Roche).

Primers

The primer sequences used in the one-step RT-PCR are shown in Table I. The primers were obtained from TIB MOLBIOL Synthoselabor, GmbH.

Master mix

The preparation of the master mix is shown in Table II.

Table I
Oligonucleotide primer sequences used in the one-step reverse transcription polymerase chain reaction to detect Rift Valley fever virus ribonucleic acid genome in serum samples

Primer	Nucleotide sequence	Length
TIB-566360-RVFVF	GGAATGATGACATTAGAAGGGA	22-mer
TIB-566361-RVFVA	CTCTTTTGCTGCTTGCAGAA	20-mer

Table II
Preparation of the master mix used in the one-step reverse transcription polymerase chain reaction (RT-PCR) to detect Rift Valley fever virus ribonucleic acid genome in serum samples

Component	Volume	Final concentration
PCR-grade water	7.2 µl	
LightCycler RT-PCR reaction mix (SYBR green)	4 µl	1 ×
Magnesium chloride	2.4 µl	6 mM
Primer 1 (RVFVF)	2 µl	0.5 mM
Primer 2 (RVFVA)	2 µl	0.5 mM
LightCycler RT- PCR enzyme mix	0.4 µl	
Sample	2 µl	
Total volume	20 µl	

mM: millimolar

Controls

A complementary deoxyribonucleic acid (cDNA) segment of the RVF virus, obtained from the Regional Laboratory Centre, Ministry of Health, Jeddah, Saudi Arabia, and the live attenuated RVF Smithburn strain vaccine (RSA Registered No. G 0119) were used as positive controls. PCR-grade water was used as a negative control.

Experimental protocols

The following procedures were performed according to the Roche instruction manual (17):

– reverse transcription of the template ribonucleic acid (RNA)
– denaturation of the cDNA/RNA hybrid
– amplification of the cDNA
– melting curve analysis for product identification
– cooling the rotor and the thermal chamber.

One-step RT-PCR was conducted in LightCycler capillaries for:

a) one cycle at 55°C for 30 min

b) one cycle at 95°C for 30 s

c) 45 cycles at 95°C for 5 s, 55°C for 10 s and 72°C for 10 s.

Analysis

Analysis consisted of a quantification program that displayed the fluorescence values versus the cycle number, and a melting curve program that assessed the specificity of the amplified PCR product by performing a melting curve analysis.

Statistical analysis

For each risk factor, the data were displayed in a two-by-two contingency table. Univariate analysis was performed, using the odds ratio (OR) statistic to determine the strength of the epidemiological association between RVF and each risk factor. The OR is a basic statistic that measures epidemiological association, independent of sample size (13). Calculation of the OR is quite simple and it is referred to as the cross-products ratio (ad/bc) (13). In the case of environmental risk factors, to control for confounding factors, the Mantel-Haenszel (M-H) statistical method for calculating an adjusted OR (M-H OR) was used (9).

The risk factor of the mosquito population was considered the confounding factor. Both the OR and M-H OR were calculated according to the procedures and examples given in a previous publication (13).

Results

Sentinel animals

Out of the 175 sentinel animals placed in the Jazan region, 35 (20%) died before testing for IgM and IgG antibodies against the RVF virus occurred. Out of the 100 animals placed in the other regions, only ten (10%) animals died. Most of the deaths occurred within the first three months of placement, i.e. before vaccination was complete.

In May 2004, approximately five or six months after placement, the sentinel animals were tested for IgM and IgG antibodies against the RVF virus. All animals were found to test negative for both types of antibodies.

In the period from August 2004 to January 2005, the animals were tested again and four serological cases of RVF were diagnosed in three of the sentinel herds. Two herds were in the Jazan region (two cases in the Alarda district and one in Alkhoba) and one came from the Mahayil district in the region of Tahamat Asir (Table III). These four cases included two which tested positive for the presence of IgM antibodies only, and two which tested positive for IgG antibodies only. One of the animals which tested positive for IgG antibodies suffered an abortion.

Table III
Districts in Saudi Arabia which were exposed or not exposed to each environmental risk factor and the number of Rift Valley fever cases which occurred in each one, August 2004 to January 2005
The univariate odds ratio and Mantel-Haenszel adjusted odds ratio measure the association between Rift Valley fever and each risk factor

Risk factor	Districts exposed to risk factor (number of RVF cases)	Districts not exposed to any risk factor (number of RVF cases)	Univariate odds ratio	Mantel-Haenszel odds ratio
Dense mosquito population	Alarda (2) Abu-Arish (0) Alkhoba (1)	Algunfoda (0) Almagarda (0) Almukhwa (0) Mahayil (1)*	4.2	Not applicable
High rainfall level	Alarda (2) Alkhoba (1) Ayban (0)	Algunfoda (0) Almagarda (0) Almukhwa (0) Mahayil (1) *	5	2
Presence of lakes and/or ponds	Alarda (2) Abu-Arish (0) Alkhoba (1)	Algunfoda (0) Almagarda (0) Almukhwa (0) Mahayil (1) *	4.2	2.2
Good vegetation	Ahad-Almasarha (0) Abu-Arish (0) Baish (0) Sabya (0) Alkhoba (1)	Algunfoda (0) Almagarda (0) Almukhwa (0) Mahayil (1) *	2	1.1

RVF: Rift Valley fever
* The occurrence of one case in the district of Mahayil could be due to risk factors that were not investigated in this study or to interactions between the investigated environmental risk factors. Multivariate statistical analysis to investigate the interactions between risk factors was not conducted in this study

Positive associations were found between RVF and each of the following factors:

– a dense mosquito population (OR = 4.2)

– high rainfall (M-H OR = 2)

– the presence of lakes and/or ponds (M-H OR = 2.2).

Almost no association was found between RVF and vegetation (M-H OR = 1.1) (Table III).

Immunoglobulin M-positive serum samples

Out of the 32 serum samples which had tested positive for IgM antibodies in the separate surveillance programmes, four (12.5%) tested positive for the RVF virus genome by one-step RT-PCR (Table IV). Positive associations were found between the RVF virus genome and each of the following characteristics:

– a high percentage positivity (PP) of IgM antibodies (OR = 3)

– the tested animal was a sheep (OR = 4)

– abortion (OR = 4.3).

Details of these variables are shown in Table IV.

Discussion

It has been reported that RVF outbreaks usually occur in seasons of high rainfall with an over-abundance of mosquitoes (19). The period from January to the end of May in the regions under study is a dry season and the mosquito population is small. The absence of IgM and IgG antibodies against the RVF virus in the serum samples from the sentinel animals indicates that no RVF infection had occurred in the regions under study during that time.

Table IV
Characteristics of the 4 out of 32 animals whose IgM-positive serum samples tested positive for Rift Valley fever virus genome

Positive sample	Percentage positivity for immunoglobulin M antibodies [a]	Type of animal [b]	Abortion [c]
Animal 1	NA	Sheep	Yes
Animal 2	High	Sheep	No
Animal 3	High	Sheep	No
Animal 4	Low	Goat	No

a) Out of the 32 serum samples 10 had a high percentage positivity and 13 had a low percentage positivity, data were not available for the remaining 9 samples
b) Out of the 32 animals 15 were sheep and 17 were goats
c) Only one of the 32 animals aborted
NA: not available

The transmission of RVF occurs during the course of the clinical disease when the virus is present in the blood as well as in the other body fluids of the diseased animal (1, 18, 19). Thus, RVF control programmes should be directed towards avoiding the occurrence or reducing the frequency of clinical disease. There are a range of possible control strategies, including:

– monitoring and surveillance

– restriction of animal movements

– quarantine

– vaccination only

– vaccination and stamping out of clinically diseased animals

– vaccination and stamping out of the entire affected herd.

To choose the appropriate control strategy, it is necessary to know the epidemiology of RVF in the affected region (including the stage of infection) and the environmental and animal risk factors associated with the disease.

The results of this study confirm the occurrence of four serological cases of RVF (including one clinical case) in sentinel animals placed in several districts in south-west Saudi Arabia. These cases demonstrate that there is continuing RVF virus activity in the regions of Jazan and Tahamat Asir.

Previous studies have mentioned some relationship between RVF and mosquitoes (7, 8, 10, 11), rainfall (4), lakes (14, 20) and vegetation (3). However, none of these studies has quantified the relationship through a proper study design and appropriate statistical analysis which accounts for confounding. Confounding occurs when a confounding variable is associated with the independent variable and the dependent variable under investigation. This confounding variable, if ignored, can distort the observed association (13). A control for confounding shows the unbiased association of each independent variable with the dependent variable in the presence of the confounding variable.

It would have been appropriate to investigate more risk factors, such as temperature, humidity, wind speed and type of soil in the sites where the sentinel animals were located. Unfortunately, information about these factors was not available. However, the mosquito population risk factor probably reflects variations in these conditions. Their effect is in the way in which they contribute to creating the right breeding conditions for mosquitoes; they are unlikely to have a direct impact on the prevalence of disease.

Statistical analysis of the data collected from the sentinel animals demonstrates that there is a positive and strong association between RVF and a dense mosquito population (OR = 4.2). This finding is consistent with the results of several previous studies, which confirmed the important biological role of mosquitoes as vectors for the transmission of RVF (7, 8, 10, 11).

A positive association was also found between RVF and a high rainfall (M-H OR = 2). In fact, the eastern districts of the Jazan region (Alarda, Alkhoba and Ayban) are characterised by the highest rainfalls in south-west Saudi Arabia. Agricultural fields in these districts are flooded by rainwater, forming field dams for future irrigation. These field dams are also a good habitat for mosquito breeding. The relationship between high rainfall and a dense mosquito population may explain why, after control for confounding, the OR sharply decreased from 5 in the univariate analysis to 2 in the M-H analysis. This sharp decrease demonstrates the importance of controlling for confounding factors to obtain an unbiased measure of association.

The environment in the Alarda and Abu-Arish districts is very much affected by the presence of large, permanent lakes (Lake Alsad and Lake Mushrif), formed by the construction of the Wadi (a seasonal river) Jazan dam. This study indicates that RVF is associated with the presence of lakes and/or ponds (M-H OR = 2.2). The association is consistent with the results of previous studies, which have also observed some relationship between RVF and lakes (14, 20).

A previous study, which used satellite imaging and a normalised difference vegetation index, has linked outbreaks of RVF with vegetation density (3). In the current study, almost no association was found between RVF and vegetation (M-H OR = 1.1). A large amount of vegetation was observed in the districts of Ahad-Almasarha, Baish and Sabya. These districts have low rainfalls, so farmers rely on underground water for irrigation. Thus, there are few field dams and consequently the population of mosquitoes is small. This may explain the absence of an association between RVF and vegetation. However, the mosquito population confounded the relationship between RVF and vegetation, as seen in the decrease of the OR from 2 in the univariate analysis to 1.1 in the M-H analysis.

In this study, when serum samples which had tested positive for IgM antibodies were tested by one-step RT-PCR, the RVF virus genome was detected in only a low percentage of the samples. This may be explained by the fact that these serum samples were taken during the inter-epizootic phase of the disease, when virus activity is low. Another explanation is that most of these samples were probably taken from animals after they had recovered from the disease and the RVF virus had cleared from the blood.

Degradation of the RNA during sample transportation and storage could be another explanation.

However, the percentage of RVF virus genome observed in this study (12.5%) is more than double the percentage of a previous study, which detected the RVF virus genome in only 5% of the serum samples testing positive for IgM antibodies (18). Nevertheless, detection of the RVF virus genome indicates the presence of RVF virus (18). A suitable control strategy should thus be implemented to prevent transmission of the virus.

Positive associations were found between the RVF virus genome and each of the following characteristics:

– a high percentage positivity (PP) of IgM antibodies (OR = 3)

– the tested animal was a sheep (OR = 4)

– abortion (OR = 4.3).

These results are consistent with those of a previous study that reported a higher prevalence of RVF in sheep (5), and also with another study, which reported isolating the RVF virus from aborted sheep foetuses (1).

The authors recommend employing both tests (IgM-capture ELISA and one-step RT-PCR) to screen serum samples for IgM antibodies and subsequently identify the RVF virus genome in the IgM-positive samples. As RT-PCR is often considered laborious and expensive, testing only IgM-positive samples from clinically suspected herds effectively limits the use of this test.

As Saudi Arabia continues its campaign to control RVF, developing and implementing an efficient and cost-effective control strategy is crucial. The environmental and animal risk factors identified in this study as being associated with RVF should be carefully considered as part of this process. ■

Facteurs associés à la présence de la fièvre de la Vallée du Rift dans le sud-ouest de l'Arabie saoudite

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Résumé

Les auteurs ont entrepris une étude des facteurs de risque, liés à l'environnement et aux animaux, pouvant être associés à la présence de la fièvre de la Vallée du Rift dans le sud-ouest de l'Arabie saoudite. Les anticorps IgM et IgG dirigés contre le virus de la fièvre de la Vallée du Rift ont été recherchés par une méthode immuno-enzymatique dans les sérums d'animaux sentinelles. En outre, 32 sérums possédant des IgM ont été soumis à la technique d'amplification en chaîne par la polymérase après transcription inverse (RT-PCR) en vue de détecter le génome du virus de la fièvre de la Vallée du Rift.

Les résultats ainsi obtenus ont été analysés en utilisant l'odds ratio (OR) à une variable. Pour le contrôle de confusion on a eu recours au odds ratio ajusté Mantel-Haenszel (M-H OR). Des associations positives ont été trouvées entre la présence de la fièvre de la Vallée du Rift et les facteurs suivants : forte concentration de moustiques (OR = 4,2) ; pluviométrie élevée (M-H OR = 2) ; présence de lacs ou d'étangs (M-H OR = 2,2). Le génome du virus de la fièvre de la Vallée du Rift a été détecté dans quatre sérums (12,5 %), indiquant que la maladie se trouve en phase initiale. L'étude a révélé que la probabilité de détecter le génome du virus est plus élevée chez les animaux possédant un fort pourcentage d'anticorps IgM vis-à-vis de ce virus (OR = 3), ainsi que chez les animaux ayant avorté (OR = 4,3). En outre, le génome du virus a été détecté chez un plus grand nombre d'ovins que de caprins (OR = 4).

Les auteurs estiment que les facteurs de risque, liés à l'environnement et aux animaux, identifiés dans cette étude peuvent être considérés comme de bons signes avant-coureurs de la maladie ; en particulier, les facteurs liés aux animaux devront être pris en compte au moment de concevoir une stratégie de prophylaxie qui soit à la fois efficace et rentable.

Mots-clés
Amplification en chaîne par la polymérase après transcription inverse – Animal sentinelle – Arabie saoudite – Association – Facteur de confusion – Facteur de risque – Fièvre de la Vallée du Rift – Génome du virus de la fièvre de la Vallée du Rift – Moyen-Orient.

Factores asociados a la fiebre del Valle del Rift en el sudoeste de Arabia Saudí

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Resumen
Los autores llevaron a cabo un estudio de los factores de riesgo de origen ambiental o animal asociados a la fiebre del Valle del Rift (FVR) en la zona sudoeste de Arabia Saudí. Para detectar la presencia de inmunoglobulinas M (IgM) y G contra el virus de la enfermedad se aplicó un ensayo inmunoenzimático a muestras séricas procedentes de animales centinela. Además, se sometieron a prueba otras 32 muestras séricas en las que se había detectado IgM en un ensayo anterior, y se les aplicó la técnica de reacción en cadena de la polimerasa acoplada a transcripción inversa (RT-PCR) con el fin de detectar el genoma del virus.
Los resultados fueron analizados empleando un cociente de posibilidades a una variable (*odds ratio* : OR). Para controlar los factores de confusión fue utilizado el modelo Mantel-Haenszel odds ratio (M-H OR) ajustado. Se observó una asociación positiva entre la FVR y los siguientes factores: densa población de mosquitos (OR = 4.2); elevada pluviosidad (M-H OR = 2); y presencia de lagos y/o estanques (M-H OR = 2.2). Se detectó el genoma vírico en cuatro muestras de suero (un 12,5%), hecho indicativo de la presencia de FVR en una fase temprana de su evolución. Con el estudio se descubrió que había más probabilidades de detectar el genoma vírico en ejemplares con un porcentaje elevado de IgM contra el virus (OR = 3) y en hembras que habían abortado (OR = 4,3). Además, hubo más ovinos que caprinos que resultaron positivos a las pruebas de detección del genoma (OR = 4).
Los autores concluyen que los factores de riesgo de origen ambiental o animal encontrados en el estudio son buenos predictores de la FVR, y que a la hora de elaborar una estrategia de control eficaz y rentable conviene tener en cuenta, en particular, los factores animales.

Palabras clave
Animal centinela – Arabia Saudí – Asociación – Factor de confusión – Factor de riesgo – Fiebre del Valle del Rift – Genoma del virus de la fiebre del Valle del Rift – Oriente Medio – Reacción en cadena de la polimerasa acoplada a transcripción inversa.

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