

**Simultaneous infection of bovine aborted fetuses by Infectious Bovine Rhinotracheitis
and *Neospora caninum* in a dairy farm around Tehran, Iran**

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Abstract

Infectious bovine rhinotracheitis (IBR) is a predominant viral abortifacient agent and *Neospora caninum*, has been documented as a primary etiological agent of reproductive losses in dairy herds. Cattle co-infected with IBR and *N. caninum* exhibit elevated abortion rates compared to herds infected with a single pathogen. The present study aimed to investigate the concurrent infection of bovine fetuses with IBR and *N. caninum*, emphasizing the critical need for implementing control measures. A total of 23 blood samples, 23 placentas, 23 vaginal secretions and 7 fetuses from aborted cattle, were collected for the identification of *N. caninum* and IBRV. Real-time PCR developed for the detection of *N. caninum* and bovine herpesvirus 1 (BoHV-1). The presence of *N. caninum* and IBRV specific antibodies was assessed using commercially available ELISA kits. Serological analysis revealed a higher prevalence of IBRV infection compared to *N. caninum*, whereas aborted fetuses demonstrated greater frequency of *N. caninum* infection. ELISA results indicated that 60.9% and 43.5% of cattle sera tested positive for antibodies against IBRV and *N. caninum*, respectively. IBRV was detected in 34.8% of the fetuses, while *N. caninum* infection was identified in 43.5%. Concurrent infection with both pathogens was observed in 26.1% of the fetuses, and 4.3% of placental and vaginal discharge samples tested positive for both agents. All positive fetuses and the infected placental sample originated from seropositive cattle. Effective control of neosporosis and IBR infection in cattle requires vaccination and biosecurity measures. Implementation of comprehensive hygienic measures is critical which should include rigorous environmental disinfection, isolation of suspected cases, control of stray dogs (the definitive host of *Neospora* spp.), and proper disposal of reproductive tissues to effectively limit disease transmission.

Keywords: Abortion, Cattle, Dog, Infectious bovine rhinotracheitis, *Neospora caninum*

59 1. Introduction

60 Abortion is a major contributor to economic losses in the dairy cattle industry, adversely
61 impacting both production efficiency and reproductive performance. Uncontrolled abortion in
62 dairy herds can result in fetal mortality, reproductive inefficiency, diminished milk yield,
63 premature culling of affected animals, and decreased body condition (1). Globally, the
64 estimated economic cost of abortions in dairy cattle ranges from \$90 to \$1,900 (2). Among
65 abortion cases in dairy cattle, infectious agents represent the predominant etiology, attributed
66 to their high abortifacient potential, diagnostic accessibility, and zoonotic implications (3).

67 Infectious bovine rhinotracheitis (IBR) is a bovine Alphaherpesvirus type 1 (BoAHV-1), which
68 belongs to the *Varicellovirus* genus, a member of the family *Herpesviridae*, subfamily
69 *Alphaherpesvirinae* (4). IBR is recognized as a reportable disease by the World Organization
70 for Animal Health (WOAH) (5). Nevertheless, despite its economic significance and impact
71 on bovine reproduction, many nations have yet to establish standardized control programs for
72 the prevention and mitigation of the disease. IBR virus is a predominant viral abortifacient
73 agent that induces placentitis, impairing placental function and disrupting nutrient and oxygen
74 exchange between the dam and fetus (6, 7). In addition, respiratory and ocular disorders are the
75 other complication of the virus infection (8). The abortion rate associated with IBR virus varies
76 from 5% to 60%, resulting in significant economic losses every year (9). Tadege et al. (10) in
77 2021 reported a seroprevalence rate of 25.6% for IBR virus in the Dessie and Kombolcha
78 districts of Ethiopia, with all seropositive cases resulting in abortion (100% abortion
79 incidence).

80 Beyond IBR virus, multiple other abortifacient pathogens substantially compromise
81 reproductive efficiency in dairy production systems, requiring integrated control measures
82 (11,12). *Neospora caninum* (*Sarcocystidae* family), has been extensively documented as a
83 primary etiological agent of reproductive losses in dairy herds, contributing to significant
84 economic burdens (13). Canids serve as critical epidemiological reservoirs for *N. caninum*,
85 facilitating its maintenance and transmission within dairy cattle populations (14). Studies in
86 Iran have reported seropositivity ranging from 3.8% to 76.2% in cattle infected with *Neospora*,
87 highlighting widespread exposure to the parasite (15). A review study by Nayeri et al. (16) in
88 2022, reported consistent *N. caninum* identification in abortion cases through serological
89 testing, with 47% prevalence via ELISA and 45% via immunofluorescence assay (IFA). The
90 study by Kaveh et al. (17) in 2017, demonstrated that *Neospora* infection accounted for 30.47%

of bovine abortions (39/128 cases) in Qazvin province, Iran, representing the most frequently identified cause of reproductive loss. This substantial epidemiological variation demonstrates significant consequences for bovine reproductive health, necessitating immediate implementation of targeted prevention and control strategies.

Cattle co-infected with different pathogens exhibit elevated abortion rates compared to herds infected with a single agent, despite their distinct pathogenic mechanisms (1). Epidemiological investigations, including studies conducted in *Brucella*-free Algerian dairy herds, demonstrate that concurrent seropositivity for IBR virus and other abortifacient agents including *N. caninum* is significantly associated with increased abortion incidence (18). The present study aimed to investigate the concurrent infection of bovine fetuses with IBR and *N. caninum*, emphasizing the critical need for implementing control measures to address their high prevalence and associated reproductive and economic impacts.

2. Materials and methods

2.1. Study design and sample collection

Samples comprising 23 placentas and vaginal secretions, as well as 7 aborted fetuses, were collected for the identification of *N. caninum* and IBRV using real-time PCR. The samples were transported to the laboratory under cold chain conditions. Additionally, 23 blood samples were collected via jugular venipuncture from the aborted cattle using sterile syringes and transferred into EDTA-free tubes to preserve serum integrity.

2.2. Real-time PCR

DNA and RNA were extracted from homogenized tissue samples and swabs using SinaClon extraction kit according to the manufacturer's protocol. A Real-time PCR developed to amplify region of the Nc5 gene (GenBank accession: X84238.10) for the detection of *N. caninum*. Custom-designed primers and a probe were employed for amplification: forward primer (5'-CTGTGCTCGCTGGGACTTC-3'), reverse primer (5'-CGATTTACGACATACGGTGTTC-3'), and a FAM-BHQ1-labeled probe (5'-[FAM]CATCGGAGGACATCGCTCACTGACTG[BHQ1]-3').

Reactions were performed in a total volume of 25 µl, containing 400 nM of each primer, 120 nM of probe, and 5 µL of extracted nucleic acid template. Amplifications were conducted with the following thermal profile: initial denaturation at 95°C for 10 min, followed by 40 cycles of

95°C for 15 s and 60°C for 45 s. All reactions were performed in triplicate to ensure reproducibility.

A real-time RT-PCR assay was then performed to detect bovine herpesvirus 1 (BoHV-1) by targeting a highly conserved region of the glycoprotein B gene. The oligonucleotide sequences used were as follows: Forward primer (gB-F): 5'-TGT GGA CCT AAA CCT CAC GGT-3' , Reverse primer (gB-R): 5'-GTA GTC GAG CAG ACC CGT GTC-3' , TaqMan probe: 5'-AGGACCGCGAGTTCTTGCCGC-3'. The real-time RT-PCR reaction was set up in a final volume of 25 µl containing 12.5 µl of 2× Platinum Quantitative PCR SuperMix-UDG (Invitrogen), 1 µl each of forward and reverse primers (final concentration 80 nM), 1 µl of a TaqMan probe (final concentration 120 nM) labeled with FAM at the 5' end and TAMRA at the 3' end, 4 µl of nuclease-free water, and 5 µl of the extracted DNA.

Negative controls using nuclease-free water were included at all stages, while positive controls were provided by standardized BoHV-1 DNA. Amplification was carried out on a Rotor-Gene Q Series (QIAGEN) under the following cycling conditions: an initial UDG activation at 50°C for 2 minutes, a denaturation step at 95°C for 10 minutes, followed by 45 cycles of 15 seconds at 95°C and 45 seconds at 60°C for annealing and extension.

2.3. Enzyme-Linked Immunosorbent Assay (ELISA)

The presence of *N. caninum* and IBRV specific antibodies was assessed using commercially available ELISA kits (IDVET, Grabels, France) in strict accordance with the manufacturer's protocol. Optical density values were measured at 450 nm using an automated ELISA reader, with reference filters set at 620 nm.

3. Results:

The results of *N. caninum* and IBRV detection in different samples are shown in Table 1. Serological analysis revealed a higher prevalence of IBRV infection compared to *N. caninum*, whereas aborted fetuses demonstrated greater frequency of *N. caninum* infection. All the positive fetuses and the placenta sample were belonged to the seropositive cattle.

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153 **Table 1. The frequency of IBRV and *N. caninum* detection in the aborted materials and serum samples**

Sample type	Sample (N)	IBRV (N)	IBRV (%)	<i>N. caninum</i> (N)	<i>N. caninum</i> (%)	Co-Infection (N)	Co-Infection (%)
Fetus	23	8	34.8%	10	43.5%	6	26.1%
Placenta	23	1	4.3%	1	4.3%	1	100%
Vaginal Discharge	23	1	4.3%	1	4.3%	1	100%
Serum	23	14	60.9%	10	43.5%	7	30.4%

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156 **4. Discussion:**

157 It is evident that *N. caninum* and IBRV are endemic in Iranian cattle populations and play a
 158 significant role in bovine abortion (19,20). Notably, the current results demonstrated a high
 159 prevalence of these pathogens, with molecular analysis revealing IBRV and *N. caninum*
 160 infection rates of 34.8% and 43.5% among aborted fetuses, respectively (Table 1). These
 161 findings are consistent with those reported by Ansari-Lari (21) in 2021, who identified *N.*
 162 *caninum* in 34.8% of bovine fetuses collected across nine Iranian provinces. A recent study in
 163 Khorasan Razavi, Iran detected *N. caninum* in 24.76% of bovine fetuses, with 100%
 164 seropositivity among aborted cattle, suggesting endemic parasite transmission in the region
 165 (15). The serological results from this study demonstrated a high seroprevalence of both
 166 pathogens. All the samples that tested positive via molecular methods were derived from
 167 seropositive cattle.

168 Most studies investigating *N. caninum* in Iranian cattle populations have relied on sero-
 169 epidemiological approaches, primarily using ELISA to detect antibodies against the parasite
 170 (16). Reported seroprevalence rates vary widely, ranging from 3.8% to 76.2%, highlighting
 171 significant variability in infection levels across studies (15). This variation may be due to
 172 factors beyond those examined, such as climatic and weather changes, breed, size of herd and
 173 test type (22). The molecular investigation conducted in the present study provides a more

reliable approach for determining the parasite involvement in fetal abortion compared to serological methods, which merely indicates prior exposure to the pathogen.

IBRV have been identified as a leading cause of bovine abortion in numerous regions of Iran, particularly in dairy farms lacking a structured vaccination program (9, 23, 24). High number of seropositive aborted cattle (60.9%) in the current study was in accordance with the study of Khaneabad et al.(23) in 2023, which showed 96.7% of pregnant cattle of Shahrekord, Iran were seropositive for the virus. Another research conducted in Khorasan Razavi, Iran detected IBRV in 84 out of 618 aborted fetuses using conventional PCR (9). Previous studies have determined BHV-1 in Iran to be 58.74% at the individual level and 82.93% at the herd level. Furthermore, intra-herd prevalence exhibited considerable variation, ranging from 16.70% to 100% (24).

In contrast to the high prevalence of the studied pathogens in aborted fetuses and serum samples, only one out of 23 placental and vaginal secretion samples (4.3%) tested positive for each pathogen. This discrepancy may be attributed to both environmental contaminations of placental and vaginal samples and limited pathogen shedding in vaginal discharges, potentially resulting in lower detection rates compared to other sample types.

The current study identified co-infection rates involving Bovine Herpesvirus-1 (BoHV-1) and *Neospora caninum* ranging from 4.3% in placental and vaginal swab samples to 26.1% in aborted fetuses and 30.4% in sera from the affected cattle. Recurrent abortions, reduced herd productivity, and economic losses are significant consequences of co-infections (25, 26). Multiple studies have reported co-infections involving various abortifacient pathogens, including bovine viral diarrhea virus (BVDV) and IBRV, as well as *N. caninum* and BVDV, along with other viral and bacterial agents (27). However, the present study represents the first documented detection of concurrent IBRV and *N. caninum* infections in bovine aborted fetuses, demonstrating a notably high frequency of co-infection (Table 1). While Bovine Herpesvirus-1 (BoHV-1) induces necrotizing placentitis, *N. caninum* triggers inflammatory responses and tissue damage (28, 29). The independent immunosuppressive effects of *N. caninum* and IBRV create a permissive environment for both latent infection recrudescence and new pathogen establishment (28, 29). Further investigation is required to establish causal relationships and characterize the precise pathophysiological mechanisms underlying the possible synergistic effect of IBRV and *Neospora*.

Effective control of neosporosis and IBR infection in cattle requires a multipath approach among which vaccination and biosecurity measures have a significant role (4). Available

vaccines against IBRV provide clinical protection to cattle upon infection and significantly reduce subsequent shedding of the field virus (4). Although vaccination may not prevent field virus infection in individual animals, it effectively limits the transmission of wild-type virus within infected herds (5). While vaccination and eradication programs remain important components of disease management, implementation of comprehensive hygienic measures is equally critical. These should include rigorous environmental disinfection, isolation of suspected cases, control of stray dogs (the definitive host of *Neospora* spp.), and proper disposal of reproductive tissues to effectively limit disease transmission.

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6. Authors contribution:

Study concept and design: M. H.

Acquisition of data: M. H., S. V.

Analysis and interpretation of data: M. H.

Drafting of the manuscript: S. V., A. L. G.

Critical revision of the manuscript for important intellectual content: A. M., P. B.

Administrative, technical, and material support: M. H.

Study supervision: A. M., P. B.

7. Ethics

Mona Hamed, Saber Vahedi, Amirabbas Lak Ghasemabadi, Alireza Mortazavinia and Parimah BourBour confirm that the manuscript has been read and approved by all named authors and that there are no other persons who satisfied the criteria for authorship but are not listed. We further confirm that the order of authors listed in the manuscript has been approved by all of us.

8. Conflict of interest and Data availability

Mona Hamedi, Saber Vahedi, Amirabbas Lak Ghasemabadi, Alireza Mortazavinia and Parimah BourBour confirm that there are no known conflicts of interest associated with this publication.

All data and supplementary information would be available upon request from the corresponding author.

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10. Reference

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