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# MOLECULAR DETECTION AND PREVALENCE STUDY OF Neospora Caninum ISOLATED FROM BLOOD OF ABORTED COWS IN BABYLON PROVINCE OF IRAQ

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Supporting Information

ABSTRACT: Neosporosis is internationally documented as one of the most popular diseases in cattle that cause economic losses due to high levels of abortion cases. Although Neospora caninum has been recently classified as a new species, it is still sharing many features with Toxoplasma gondii. This study aimed to detect and Imaging N. caninum in the blood of aborted cows, and prevalence study of N. caninum infection based on age, region and month. Blood samples from 106 aborted cows were collected using the appropriate method. First, these samples were examined microscopically via blood smears using Giemsa dye to diagnose the N. caninum within RBC. A gPCR technique was carried out to detect accurately 18S rRNA gene accurately. The results revealed that 65% of total aborted cases were positive for 18S rRNA detection of N. caninum, although this parasite was found microscopically in 15% of blood smear samples. According to PCR results, the prevalence study showed that the highest rate of infection was signed in the Al-Qassim district (75%) followed by the Al-Mahaweel district (74%) and decreased in Western Hamza district (48%). According to study months, November recorded the peak of infection (88%), then August (71%), whereas July recorded the lowest percentage (50%). The statistical analysis revealed there was no significant difference between the subjected regions and study months based on (P<0.05). On the other hand, it was found that cows less than 3 years old were more susceptible to infection than those over 3 years old. the results revealed that 71% of infected cows were less than 3 years old, while 29% were at age over 3 years old with a significant difference (P<0.005). In conclusion, N. caninum can be detected through blood within RBC. Age and regional factors in cows play an important role in resisting infection with this pathogen.

Keywords: Cow, Neosporosis, N. caninum, Prevalence, 18S rRNA

# INTRODUCTION

Neosporosis is a parasitic disease caused by *N. caninum*. It is recognised as an intracellular protozoan parasite of livestock distributed worldwide. In cattle, it is considered one of the main causes of abortion (Wei et al., 2022). Neosporosis has been related to epizootic and sporadic abortion in dairy herds worldwide. Since the discovery of Neosporosis, some studies have been conducted to assess the prevalence and to identify factors related to the disease, Prevalence's has been estimated in ranges between 16.8% and 70% (Waldner et al., 2004). In intermediate hosts, tachyzoites and tissue cysts are the infective stages (Mahajan et al., 2019). It has been reported in many countries with different prevalence rates since the disease was recognized in 1988 (Noori et al., 2019).

Morphology for parasite tachyzoites are ovoid, crescent or spherical in shape according to the phase of division and measures  $3-7 \times 1-5 \mu m$  in size (Speer et al., 1999), bradyzoites are slightly longer, slenderer than the tachyzoites, measuring  $8.1 \times 2 \mu m$ . parasite, capable of forming tissue cysts containing up to 100 parasites and Oocysts almost rounded measuring about  $11.7 \times 11.3 \mu m$  in diameter, surrounded by a smooth, colorless, 0.6-0.8  $\mu m$  thick wall (Lindsay et al., 1999). Definitive hosts (dog, coyote, dingo) shed unsporulated oocysts in their feces, which sporulate within several days to become infectious to the intermediate host such as cow, sheep, goats or deer, water buffaloes, horse, etc. when they consume foods or water contaminated by them (Lindsay and Dubey, 2020; Venturoso et al., 2021). García et al. (2015) found that many cases of abortion in both dairy and beef cattle were caused by *N. caninum*. Cattle get infected due to feeding mostly on mixed, drinking from rivers, and existing in contact with other animals at the same farm. As observed in many reports, the second way to spread the infection is by consuming parasite oocysts or eggs contaminated food or water or grazing on contaminated pastures (Claude et al., 2017). In addition, the transmission of infection could be transplanted during pregnancy to the fetus from the infected mother (Jiménez-Pelayo, et al., 2019). Previous specific

studies showed that the higher anti-*N. caninum* antibodies were found in cattle living on farms with dogs in comparison with those without dogs, suggesting the active involvement of dogs in the transmission of parasites to cattle (Gharekhani et al., 2020). The release of oocysts of *N. caninum* through dog faces could contaminate the food and water which become the source of infection (Ahmed et al., 2021). Billions of dollars were lost annually as reported in New Zealand and the US by the infection of Neosporosis, due to loss of fetus, milk yield, gaining weight, and time for rebreeding (Reichel et al., 2013).

The aim of our study is to detect *N. caninum* in the blood of aborted cows using the PCR technique and to study the prevalence of this infection in the Babylon province. Furthermore, the presence of *N. caninum* in red blood cells was also observed.

## MATERIALS AND METHODS

Collection and examination processes for 106 blood samples of aborted cattle were carried out from different ages and regions of the Babylon province: (Al. Qassime, Al-Hilla, and Mahaweel Districts) as well as different periods from July 2022 to January 2023. The blood samples were collected especially from aborted cows, and 3 ml of venous blood (jugular vein) was taken in a 5 ml EDTA tube (AMEER et al., 2019).

#### **Microscopic examination**

Direct microscopic examination was performed to diagnose this parasite and to study the morphology of it. A small drop of blood was applied to the slide approximately 20 mm from one end. A spreader of another slide was placed on the blood drop at an angle of 20-30° and drawn back to another end to blood smear. After air drying, the sample was fixed with methyl alcohol for a minute and then stained with Giemsa stain for a minute again, wishing and drying were carried on after that, the samples were ready for microscopic examination (Fraser et al., 2010)

## **Molecular detection**

Genomic DNA extraction from 400  $\mu$ l blood was done using manufacturer instructions (QIA GENE KIT). The concentration of DNA was measured using a Nanodrop device at an absorbance of (260 /280) nm. PCR technique was performed on the collected samples, all PCR samples were prepared following the manufacturer protocol (1 $\mu$ l of 10 pmol forward and reverse primers, 8  $\mu$ l genomic DNA, 12.5 Mastermix, and complete volume to 25  $\mu$ l of nuclease-free water. Primers for 18S rRNA were self-designed with a predicted size (236 bp) to be used in this stage based on the NCBI database of Genbank: MT860359. The foreword primer sequence (NeoF) was (gtgtacggcgaagggactc), while the reverse primer sequence (NeoR) was (gccaagacatccattgctga). PCR programs were set according to the annealing temperature of each primer (94 °C for 5 minutes, for 40 cycles of 94 °C for 30 seconds, 50 °C for 25 seconds, 72 °C for 45 seconds, and a final extension at 72 °C for 8 minutes, with a final hold at 4 °C (THERMO-CYCLER; FISHER, GERMANY). A 1.5% agarose gel electrophoresis was prepared for checking PCR products using 1X Tris-Borate- EDTA (TBE buffer), and then the components were dissolved into 1 L of distilled H20. They were run for 60 min/ 80 volts (Hube et al., 2005). DNA bands were compared with a 1500 bp DNA ladder to confirm the specific size of the 18S rRNA gene for the subjected parasite. Imaging was carried out using a UV Trans-illuminator for DNA detection.

#### **Ethical regulation**

It was obtained from the Faculty Scientific Committee (College of Veterinary Medicine, Al-Muthanna University, Iraq) numbered 202205 – Naer Abdulbari Madlool Alkaabawi.

## RESULTS

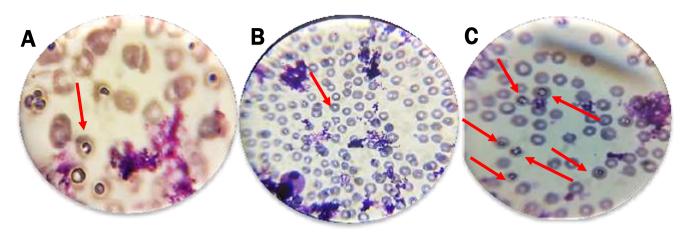
## **Direct microscopic examination**

All the collected blood samples of aborted cows were examined by direct smear method; it appeared that 15% of blood samples were suspected Neospora at the tachyzoite stage. These tachyzoites were ovoid and crescent in shape according to the phase of division and measurements of size  $(3-7 \times 1-5 \mu m)$  using an ocular micrometer lance as shown in (Figure 1).

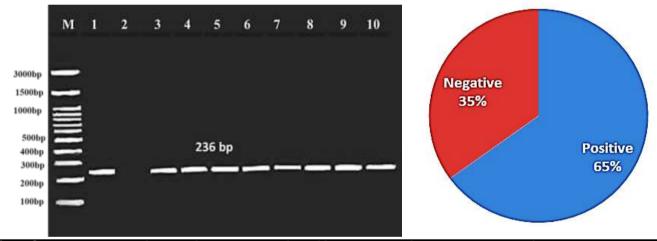
## Detection of 18S rRNA of N. caninum

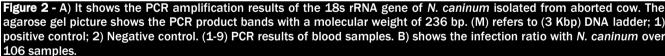
According to the results of the microscopic examination, all samples were run on PCR for 18S rRNA detection of *N. caninum* with PCR product size (236 bp). The results show that 65% of the total samples are infected with *N. caninum* (Figure 2).

Prevalence of *N. caninum* infection in aborted cows based geographical areas using PCR is at the highest rate in Al-Qassim and Al-Mahaweel districts which are 75% and 74%, respectively. Al-Hilla District records 63%. The lowest rate is in Western Hamza district which archives 48%. The statistical analysis (P>0.05) reveals that there is no significant difference (P=0.154) in the prevalence of parasites among geographical areas. These statistics are similar with no significant difference (P=0.239) to the prevalence of *N. caninum* infection according to the time of infection, although the infection rate was at the highest level during November (88%) (Figure 3). On the other hand, it is found that the *N. caninum* parasite is detected in (71%) of aborted cows aged 1-3 years group. Meanwhile, a ratio of 29% is identified in the aborted cows at age over 3 years group. This refers to a significant difference between these two groups based on statistical analysis at P<0.05 that recorded P<0.005.



**Figure 1** - Shows different stages of infection with *Neospora* caninum parasite inside the red blood cells at (40x) after dying by Giemsa stain. (A and B) pictures refer to tachyzoite phase, while (C) refers to heavy infection with *N. caninum* in red blood cells (40x)





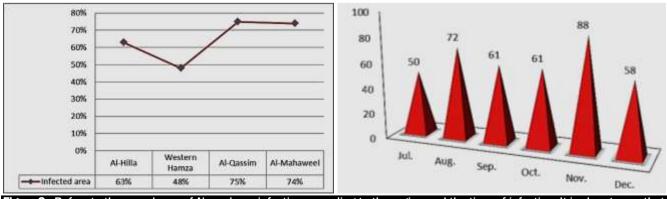


Figure 3 - Refers to the prevalence of *N. caninum* infection according to the region and the time of infection. It is clear to see that the highest ratio of infection is in Al-Qassim district, which records (75%) while November is the critical time of infection (88%).

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# DISCUSSION

Neospora caninum is the main cause of neosporosis as a polysystemic disease that is an obligated intracellular parasite that belongs to the phylum Apicomplexa (Dubey and Schares, 2011). Neosporosis was misdiagnosed as toxoplasmosis due to sharing several morphological and biological features that are closely related to *Toxoplasma gondii* (Dubey et al., 2017). In 1984 was the first recognition of *N. caninum* in Norwegian dogs (Bjerkas et al., 1984), then a significant classification was done to consider it as a separate species from *Toxoplasma gondii* since 1988 (Dubey et al., 1988; Seltmann et al., 2020).

Among diagnostic techniques, the PCR is more sensitive and specific than other tests and less likely to be affected by autolysis or postmortem changes. In addition, it can be applied for the identification of *N. caninum* DNA in blood, semen, brain, spinal cord, different fetal fluids, embryonic tissues, and even oocysts in the faeces of the final host (Kamali et al., 2014).

The prevalence of N. caninum infections was the highest in the Al-Qassim and Al-Mahaweel districts which were 75% and 74.07% respectively, while in the Al-Hilla District was 63.33% and the lowest rate was in Western Hamza district which was 48%. The statistical analysis reveals that there was no significant difference in the prevalence of parasites among geographical areas (P>0.05). Globally, several various studies were carried out to detect the prevalence of bovine N. caninum, using different diagnostic tests that revealed significant variation in their prevalence between countries, regions as well as between herds as Semango et al. (2019) discuss in their paper. The results of this study were higher than those reported by Al-Gharban et al. (2017) that were (12.36%). However, it was nearly close to the findings of Japa et al. (2019), they found the diversity of N. caninum infection rates (16-50 %) in different districts of Phayao province in Thailand using PCR for placental samples of beef cattle. This success in the detection of DNA was expected because the blood was confirmed to be a transport factor for Neospora tachyzoites between body tissues (Okeoma et al., 2004). Neosporosis has a wide range of infection rates with the presence of contrast between the study's districts. This finding might be attributed to the inequality of applied techniques and/or their cut-off origin of evaluated herds and the probability of frequent exposure to sources of infection (Moura et al., 2011). As well as, the increase in N. caninum prevalence could occur because discrepancy of animal housing or poor hygienic management, herds that are involved in a study, increasing exposure to definitive host or intermediate hosts, and the contact, directly or indirectly, to adjacent endemic areas (Celik et al., 2013; Llano et al., 2018).

The prevalence of *N. caninum* infections was at a high rate within 1-3 year's old group which was 71%, while the lower rate of infection was at the age over 3 years old group, which was 29%. The statistical analysis using the T-test parameter showed that there was a significant difference between age groups (P<0.05). Furthermore, the results of the present study showed that the lowest per cent was in the age group years old which may be due to the fact that cows in this age ( >3 years) have good resistance and immunity against *N.caninum*. These results agreed with Noori et al., (2019), who discussed that the vertical transmission of *N. caninum* might be the reason for increasing the infection in cows under 3 years old more than those increasing over 3 years based on his seroprevalence study. However, the results of Metwally et al. (2023) revealed that those aged (3-5) years old were more exposed to the infection with seropositive version, due to horizontal transmission. Moreover, the results of Razmi et al. (2006) and Mallah et al. (2012) also disagreed with the present data, when they announced that there is no significant difference between age groups (P>0.05). The age effect might be influenced by management practices such as replacement rate, and the cattle may be exposed to horizontal transmission, or by selective culling of seropositive animals (Bartels et al., 2006).

On the other hand, the results of this study revealed that the prevalence of *N. caninum* infection based on the time recorded that the highest rate of infection was in November (88 %) followed by 72% in August, while the lower prevalence was in July which was 50% (figure 3). The statistical analysis reveals no significant difference at (P>0.05) in aborted cows among studied months (figure 3). Distribution of *N. caninum* infection takes place all year round, the peak of infection was observed in Nov. with a percentage of 88%, this result was in agreement with (Ibrahim et al. 2012) who found the peak of Neospora infection in autumn and winter California. However, this result was in disagreement with Pitel et al. (2001) in France, who found the peak of Neospora infection in March-June. These differences in infection may be due to seasonal differences in parasite exposure and/or oocyst survival by providing suitable environmental conditions (temperature and humidity) Because of its close relationship with *T. gondii* it is assumed that the environmental resistance of *N. caninum* oocysts is similar to *T. gondii* oocysts that the degree of suitable temperatures for sporulation of oocysts was ranged between (22-30) C° (Dubey, 2007).

## CONCLUSION

Overall, despite, that there are many sources to isolate *N. caninum* from the infected body, blood is the main linker to spread the pathogens into other body organs, and apparently, it is the best source for early diagnosis of infection. We can also conclude that the age factor plays a crucial role in resisting the infection, especially over 3 years old cows. However, the region and time factors do not make any difference in spreading the infection of *N. caninum* in the Babylon province of Iraq.

# DECLARATIONS

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## Authors' contribution

Nawras Abdul bari Madlol Alkabi did the study conception, design, and monitored the experiments. Ra'afat Sabbar Abbas Al-Rikaby did all the preparations for sample collection, and the laboratory works involving the molecular part. Naer Abdulbari Alkaabawi prepared and read the molecular part of the laboratory work, interpreted the data and revised the final version of this paper.

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#### Conflict of interest

The authors have not declared any conflict of interest.

## **Consent to publish**

We, give our consent for the publication of identifiable details, which can include photograph(s) and details within the text to be published in the OJAFR.

## REFERENCES

- Ahmed F, Cappai MG, Morrone S, Cavallo L, Berlinguer F, Dessì G, et al. (2021). Raw meat based diet (RMBD) for household pets as potential door opener to parasitic load of domestic and urban environment. Revival of understated zoonotic hazards? A review. One health, 13: 100327. <u>https://doi.org/10.1016/j.onehlt.2021.100327</u>
- Al-Gharban HA, Al-Eodawee EM and Al-Shabbani AH (2017). Seroepidemiological and molecular identification of *Neospora caninum* in cattle in Wasit province. Basrah Journal of Veterinary Research, 16(2): 172-183. https://www.cabdirect.org/cabdirect/20183043305
- Ameer QJ. Madlol NA, and Kaabawi, NA (2019). Detection of Theileriaannulata isolated from cattle using Real-Time PCR. International Journal of Pharmaceutical Research (09752366), 11(2). <u>Google Scholar</u>
- Bartels CJ, van Schaik G, Veldhuisen JP, van den Borne BH, Wouda W, and Dijkstra T (2006). Effect of Neospora caninum-serostatus on culling, reproductive performance and milk production in Dutch dairy herds with and without a history of *Neospora caninum-associated abortion epidemics*. Preventive Veterinary Medicine, 77(3-4): 186-198. <u>https://doi.org/10.1016/j.prevetmed.2006.07.003</u>
- Bjerkas I. Mohn SF, and Presthus J (1984). Unidentified cyst-forming sporozoon causing encephalomyelitis and myositis in dogs. Zeitschrift für Parasitenkunde, 70(2): 271-274. Google Scholar
- Celik HA, Kozan E, Mustafa Eser, Yilmaz O, Birdane MK, and Sarimehmetoğlu HO (2013). A research on seroprevalence of *Neospora* caninum in cattle. Ankara Üniversitesi Veteriner Fakültesi Dergisi, 60(2): 99-102. <u>http://vetjournal.ankara.edu.tr/en/download/article-file/659795</u>
- Dubey JP, and Schares G (2011). Neosporosis in animals—the last five years. Veterinary parasitology, 180(1-2): 90-108. https://doi.org/10.1016/j.vetpar.2011.05.031
- Dubey JP, Carpenter JL, Speer CA, Topper MJ, and Uggla, ANDA (1988). Newly recognized fatal protozoan disease of dogs. Journal of the American Veterinary Medical Association, 192(9): 1269-1285. <u>https://europepmc.org/article/med/3391851</u>
- Dubey JP, Hemphill A, Calero-Bernal R, and Schares G (2017). Neosporosis in Animals (1st ed.). CRC Press. https://doi.org/10.1201/9781315152561
- Dubey JP, Schares G, and Ortega-Mora L (2007). Epidemiology and control of neosporosis and Neospora caninum. Clinical microbiology reviews, 20(2): 323-367. <u>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1865591/</u>
- Fraser ST, Isern J, and Baron MH (2010). Use of transgenic fluorescent reporter mouse lines to monitor hematopoietic and erythroid development during embryogenesis. In Methods in enzymology. 476: 403-427. Academic Press, Elsevier Inc. <u>https://doi.org/10.1016/S0076-6879(10)76022-5</u>
- García-Ispierto I, Serrano-Pérez B, Almería S, Martínez-Bello D, Tchimbou AF, et al. (2015). Effects of crossbreeding on endocrine patterns determined in pregnant beef/dairy cows naturally infected with *Neospora caninum*. Theriogenology, 83(4): 491-496. https://doi.org/10.1016/j.theriogenology.2014.10.013
- Gharekhani J, Yakhchali, M, and Berahmat R (2020). Neospora caninum infection in Iran (2004–2020): A review. Journal of Parasitic Diseases, 44: 671-686. <u>https://doi.org/10.1007/s12639-020-01266-w</u>
- Claude LH, Lavado A, Rivera D, Talloni MN, West CH (2017). Seroprevalence and risk factors for *Neospora caninum* in small dairy farms in central Chile. Revista MVZ Córdoba, 22(1): 5666-5673. <u>http://www.scielo.org.co/scielo.php?pid=S0122-02682017000105666&andscript=sci\_arttext</u>
- Hube F, Reverdiau P, lochmann S, and Gruel Y (2005). Improved PCR method for amplification of GC-rich DNA sequences. Molecular biotechnology, 31: 81-84. <a href="https://doi.org/10.1385/MB:31:1:081">https://doi.org/10.1385/MB:31:1:081</a>
- Ibrahim AME, Elfahal AM, and El Hussein ARM (2012). First report of *Neospora caninum* infection in cattle in Sudan. Tropical Animal Health and Production, 44(4): 769-772. <u>https://doi.org/10.1007/s11250-011-9963-5</u>

- Japa O, Nuangmek A, Prakhammin K, and Flynn RJ (2019). Prevalence of vertically transmitted *Neospora caninum* amongst beef cattle in Phayao, Thailand. Parasitology international, 70: 98-101. <u>https://doi.org/10.1016/j.parint.2019.02.008</u>
- Jiménez-Pelayo L, García-Sánchez M, Vázquez P, Regidor-Cerrillo J, Horcajo P, et al. (2019). Early Neospora caninum infection dynamics in cattle after inoculation at mid-gestation with high (Nc-Spain7)-or low (Nc-Spain1H)-virulence isolates. Veterinary research, 50: 1-14. <u>https://doi.org/10.1186/s13567-019-0691-6</u>
- Kamali A, Seifi HA, Movassaghi AR, Razmi GR, and Naseri Z (2014). Histopathological and molecular study of *Neospora caninum* infection in bovine aborted fetuses. Asian Pacific Journal of Tropical Biomedicine, 4(12): 990-994. <u>https://doi.org/10.12980/APJTB.4.201414B378</u>
- Lindsay DS, and Dubey JP (2020). Neosporosis, toxoplasmosis, and sarcocystosis in ruminants: an update. Veterinary Clinics: Food Animal Practice, 36(1): 205-222. <a href="https://doi.org/10.1016/j.cvfa.2019.11.004">https://doi.org/10.1016/j.cvfa.2019.11.004</a>
- Lindsay DS, Upton SJ, and Dubey JP (1999). A structural study of the *Neospora caninum* oocyst. International journal for parasitology, 29(10): 1521-1523. <u>https://doi.org/10.1016/s0020-7519(99)00121-6</u>
- Llano HAB, Guimarães MS, Soares RM, Polo G, and da Silva AC (2018). Seroprevalence and risk factors for *Neospora caninum* infection in cattle from the eastern Antioquia, Colombia. Veterinary and Animal Science, 6: 69-74. <u>https://doi.org/10.1016/j.vas.2018.03.001</u>
- Mahajan V, Banga HS, and Filia G (2019). Patho-epidemiological and risk factor studies for detection of Neospora-associated abortion in cattle and buffaloes in Punjab, India. Revue Scientifique et Technique (International Office of Epizootics), 38(3): 801-808. https://europepmc.org/article/med/32286566
- Mallah MO, Dawood KA, and Alrodhan MA (2012). Seroepidemiological study for the prevalence of *Neospora caninum* in Dairy and Beef cattle in some Iraqi provinces. Al-Qadisiya Journal of Veterinary Medical Science, 11(1): 103-110. https://www.iasj.net/iasj/download/67f498f704052c5b
- Metwally S, Hamada R, Sobhy K, Frey CF, and Fereig RM (2023). Seroprevalence and risk factors analysis of *Neospora caninum* and Toxoplasma gondii in cattle of Beheira, Egypt. Frontiers in veterinary science, 10: 1122092. <u>https://doi.org/10.3389/fvets.2023.1122092</u>
- Moura AB, Souza AP, Sartor AA, Bellato V, Pisetta GM, Teixeira EB, and Heusser Junior A (2011). *Neospora caninum* antibodies and risk factors in dogs from Lages and Balneário Camboriú, SC. Arquivo Brasileiro de Medicina Veterinária e Zootecnia, 63: 262-265. https://www.scielo.br/j/abmvz/a/ch8NS5ymf9Wx3Pxcqq5zDMw/?lang=en&andformat=pdf
- Noori M, Rasekh M, Ganjali M, and Nourollahi Fard SR (2019). Seroprevalence of *Neospora caninum* Infection and Associated Risk Factors in Cattle of Sistan Areas, Southeastern Iran in 2016. Iranian journal of parasitology, 14(2): 340–346. <u>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6737369/</u>
- Okeoma CM, Williamson NB, Pomroy WE, Stowell KM, and Gillespie L (2004). The use of PCR to detect *Neospora caninum* DNA in the blood of naturally infected cows. Veterinary parasitology, 122(4): 307-315. https://doi.org/10.1016/j.vetpar.2004.06.001
- Pitel PH, Pronost S, Chatagnon G, Tainturier D, Fortier G, and Ballet JJ (2001). Neosporosis in bovine dairy herds from the west of France: detection of Neospora caninum DNA in aborted fetuses, seroepidemiology of *N. caninum* in cattle and dogs. Veterinary Parasitology, 102(4): 269-277. https://doi.org/10.1016/S0304-4017(01)00544-1
- Reichel MP, Ayanegui-Alcérreca MA, Gondim LF, and Ellis JT (2013). What is the global economic impact of *Neospora caninum* in cattlethe billion dollar question? International journal for parasitology, 43(2): 133-142. <u>https://doi.org/10.1016/j.ijpara.2012.10.022</u>
- Razmi GR, Mohammadi GR, Garrosi T, Farzaneh N, Fallah AH, and Maleki M (2006). Seroepidemiology of *Neospora caninum* infection in dairy cattle herds in Mashhad area, Iran. Veterinary Parasitology, 135(2): 187-189. <u>https://doi.org/10.1016/j.vetpar.2005.09.004</u>
- Seltmann A, Schares G, Aschenborn OH, Heinrich SK, Thalwitzer S, Wachter B, and Czirják GÁ (2020). Species-specific differences in Toxoplasma gondii, *Neospora caninum* and *Besnoitia besnoiti* seroprevalence in Namibian wildlife. Parasites & vectors, 13(1): 1-12. https://doi.org/10.1186/s13071-019-3871-3
- Semango G, Hamilton CM, Kreppel K, Katzer F, Kibona T, Lankester F, et al. (2019). The Sero-epidemiology of *Neospora caninum* in Cattle in Northern Tanzania. Frontiers in veterinary science, 6: 327. <u>https://doi.org/10.3389/fvets.2019.00327</u>
- Speer CA, Dubey JP, McAllister MM, and Blixt JA (1999). Comparative ultrastructure of tachyzoites, bradyzoites, and tissue cysts of *Neospora caninum* and Toxoplasma gondii. International journal for parasitology, 29(10): 1509-1519. <u>https://doi.org/10.1016/s0020-7519(99)00132-0</u>
- Venturoso PD, Venturoso OJ, Silva GG, Maia MO, Witter R, Aguiar DM, et al. (2021). Risk factor analysis associated with *Neospora caninum* in dairy cattle in Western Brazilian Amazon. Revista Brasileira de Parasitologia Veterinária, 30: e023020-e023020. https://doi.org/10.1590/S1984-296120201088
- Waldner C, Wildman BK, Hill BW, Fenton RK, Pittman TJ, Schunicht OC, et al. (2004). Determination of the seroprevalence of *Neospora* caninum in feedlot steers in Alberta. The Canadian Veterinary Journal, 45(3): 218. <u>https://europepmc.org/article/med/9731264</u>
- Wei XY, An Q, Xue NY, Chen Y, Chen YY, Zhang Y, et al. (2022). Seroprevalence and risk factors of *Neospora caninum* infection in cattle in China from 2011 to 2020: A systematic review and meta-analysis. Preventive Veterinary Medicine, 203: 105620. https://doi.org/10.1016/j.prevetmed.2022.105620