protocols.io

Molecular and serological surveys of canine distemper virus: a meta-analysis of cross-sectional studies 🔗

📖 PLOS One

Vivaldo Costa[1], Marielena Saivish[2], Roger Rodrigues[2], Rebeca de Lima Silva[2], Marcos Moreli[2], Ricardo Krüger[1]

[1]University of Brasilia, [2]Federal University of Goiás

👤 Vivaldo Costa ⚡

ABSTRACT

Background: Although studies have been conducted on the frequency and risk factors associated with canine distemper virus (CDV) infection, there are no comprehensive data on the current epidemiological magnitude in the domestic dog population at regional and national levels. Therefore, we conducted a cross-sectional study and included our results in a meta-analysis to summarize and combine available data on the frequency and potential risk factors associated with CDV infection.

Methods: For the cross-sectional study, biological samples from dogs suspected to have canine distemper (CD) were collected and screened for viral RNA. Briefly, the PRISMA protocol was used for the meta-analysis, and data analyses were performed using STATA IC 13.1 software.

Conclusion: Considering the high frequency of CDV positivity associated with almost all the variables analyzed in dogs, it is necessary to immediately and continuously plan mitigation strategies to reduce the CDV prevalence, especially in determined endemic localities.

EXTERNAL LINK

https://doi.org/10.1371/journal.pone.0217594

1 Literature search

This protocol conforms to the Preferred Reporting Items for Systematic Review and Meta-analysis protocols (PRISMA-P) guidelines for reporting a protocol for a systematic review and meta-analysis [1].

Articles in the English, Spanish and Portuguese languages were screened in the PubMed, SciELO and ScienceDirect databases from July to October 2018. The following subject headings and keywords were used for each electronic databases: ("*canine distemper virus*," "*canine distemper*," "*viruses in dogs*," "*dogs*," "*domestic dogs*," "*canis familiaris*," and "*canis lupus familiaris*"). We also sought additional studies by examining the reference lists of the articles and published reviews.

Four independent investigators (Vivaldo Costa, Roger Rodrigues, Marielena Saivish and Rebeca de Lima Silva) reviewed the study titles, abstracts and methods. Ambiguous or controversial articles were assessed by reading the full text. Disagreements were resolved by a consensus meeting.

2 Inclusion criteria:

1) Original articles published in scientific journals that contained information on serological and molecular surveys for the detection of CDV in domestic dogs;

2) Studies containing data related to the proportion/rate of CDV infection by laboratory tests;

3) Seroepidemiological surveys for the detection of anti-CDV antibodies that included data concerning groups of animals not vaccinated against CDV;

4) Data secondary to CDV positivity to analyze risk factors such as gender, age, vaccine status, breed, coinfection and lifestyle (free-ranging dogs versus non-free-ranging dogs);

5) studies that used the most conventional ante-mortem detection tests.

Exclusion criteria:

1) Absence or confusing specification of the outcome of interest regarding the CDV positivity of laboratory tests;

2) Revisions, book chapters, and seroprevalence studies not involving domestic dogs;

3) Small scale studies with a sample size <50.

3 Data extraction:
Collected data: first author, year of publication, place of study, baseline characteristics of the studies including mean age, sex percentage, dog lifestyle, method of diagnosis, number of dogs investigated for CDV infection, proportion of positive animals, and clinical sign of CD and vaccine status.

4 Risk bias

A modified Joanna Briggs Institute and Strengthening the Reporting of Observational Studies in Epidemiology checklist [2].

5 Statistical analysis

For all of the meta-analysis procedures, STATA IC/64 version 13.1 software was used (Stata Corporation, College Station, TX, USA). The metaprop, metafunnel and metaninf commands were used for data analysis. To ensure proportionate weight distribution to

studies presenting extreme frequency (near 0 or 1), we applied the Freeman-Tukey arcsine methodology [3,4]. The dichotomous data of the selected studies were extracted and plotted in a 2x2 table to obtain individual and combined odds ratios (ORs). The I^2 test was also used to assess the existence of heterogeneity between studies (I^2=75-100%, p<0.05) [5]. In addition, we evaluated the existence of publication bias by visual inspection of Begg's funnel plot as well as by Egger's test calculations [6,7].

6

References

1. Moher D, Shamseer L, Clarke M, Ghersi D, Liberati A, Petticrew M, et al. Preferred reporting items for systematic review and meta-analysis protocols (PRISMA-P) 2015 statement. Systematic reviews. 2015;4:1. http://doi.org/10.1186/2046-4053-4-1.

2. Vandenbroucke JP, von Elm E, Altman DG, Gøtzsche PC, Mulrow CD, Pocock SJ, et al. Strengthening the reporting of observational studies in epidemiology (STROBE): explanation and elaboration. PLoS Medicine 2007; 4: e297. https://doi.org/10.1371/journal.pmed.0040297

3. Freeman MF, Tukey JW. Transformations related to the angular and the square root. Ann Math Statist. 1950;21:607-11.

4. Nyaga VN, ArbynM, Aerts M. Metaprop: a Stata command to perform meta-analysis of binomial data. Arch Public Health. 2014;72(1):39. https://doi.org/10.1186/2049-3258-72-39.

5. Higgins JP, Thompson SG. Quantifying heterogeneity in a meta-analysis. Stat Med. 2002;21:1539-58. https://doi.org/10.1002/sim.1186

6. Egger M, Davey Smith G, Schneider M, Minder C. Bias in meta-analysis detected by a simple, graphical test. BMJ. 1997;315:629-34. https://doi.org/10.1136/bmj.315.7109.629.

7. Begg CB, Mazumdar M. Operating characteristics of a rank correlation test for publication bias. Biometrics. 1994;50:1088-101. https://doi.org/10.2307/2533446