Pathogen co-infection patterns within domestic dogs in rural environments

Djion A Holness1, Amaka Nina Ananaba2, Nicole L Gottdenker2
University of Connecticut1, Storrs CT, University of Georgia, Athens GA2

Introduction
Pathogens can interact with each other within a host, which can influence patterns of co-infection in populations by complex interactions within the host’s immune system; such as immunosuppression caused by infection with one pathogen which may influence susceptibility to infection with other pathogens.4,5 Furthermore, behavioral and environmental factors, such as habitat-associated contacts with a vector, can influence patterns of host co-infection.1,3

Objective: To study relationships of intrinsic host factors and extrinsic (environmental) factors in relation to parasite/pathogen co-infections in domestic dogs from a rural landscape.

Study system: The pathogens in this study include a mosquito borne disease (heartworm, dirofilaria), kissing bug transmitted disease (Chagas disease caused by Trypanosoma cruzi (T. cruzi) infection, sandfly transmitted diseases (leishmania), and canine distemper (directly transmitted virus) within domestic dogs within individuals, households, communities, and across communities in rural Panama.2,3

Hypotheses
- Dogs in more isolated and and more forested communities will be more likely to be infected with a higher number of species, potentially due to lack of preventative care and complex habitats supporting a diverse array of pathogens.
- Mortality due to sandfly transmitted disease prevalence will be more variable with environmental factors (community or habitat type) than co-infection interactions.
- Dogs in poor overall health (based on hematological analysis) are more likely to be co-infected with multiple pathogens.
- Animals who have been infected with/without to canine distemper (CDV) are more likely to be co-infected with multiple bloodborne pathogens, due to CDV-induced immunosuppression.

Background
- Data was collected from 275 domestic dogs from 6 communities that reside where there were distinct levels of deforestation (two replicates each of highly deforested, moderate deforestation, no deforestation), on each side of the Panama Canal.
- Intrinsic factors include dog nutritional status, sex, age, the type of pathogens co-occurring within a host, and host physiology/immune traits (e.g. red blood cell count, white blood cell count).
- Extrinsic factors include household type/dog care, community, and environmental (ecosystem, forest cover, altitude).

Methods
- Figure 1: Map of studies sites with general vegetation data on surrounding area to the east and west of the Panama Canal. Bajo Bonito and Altos de Pacora (Forested), Cañasus and Tierra Prometida (Fragmented forests), Pueblo Nuevo and Superación Campesina (Deforested).

Results
- Figure 2: Proportion of infected individuals by community for each infection type. Rate of infection is heavily dependent on community. Disease, forested, yellow, fragmented, red, deforested. The relationship between community and T cruzi infection status is statistically significant (Fisher’s exact test, p = 0.000036). Dirofilaria infection status and habitat is marginally significant (Fisher’s exact test, p = 0.06605). For the other two infection types there was no significant relationship between community and infection rate.

- Figure 3: Frequency (counts) of infected individuals in each age group. (on left). There was no significant difference between infection and sex, although samples were male-biased.

- Table 2: Types of diagnostic tests for each infection.
- General body condition was evaluated for each dog from a standardized Purina Body condition scale for dogs. Blood samples were collected from dogs for hematologic and diagnostic assays. T. cruzi, leishmania, and CDV exposure or infection were tested by a number of tests listed in Table 2 (above).

- Table 3: Co-infection test between each infection type. There was no significant association between expected and observed prevalence of different combinations of co-infecting pathogens.

- Figure 4: Lymphocyte and white blood cell count and T cruzi presence.

There was a significant difference in T. cruzi infection status, total white blood cell (WBC), and lymphocyte (lym) cell count1017 (cells μl count (WCW), p-value 0.04602, and 0.01431 respectively). T. cruzi infection status and neutrophil count (p = 0.04805), and Leishmania with hemocrit (p = 0.04456). There was no significant relationship between dirofilaria and CDV infection data and hematology results.

Contact: djion.holness@uconn.edu

References

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Table 1: Key information on each infection type studied.

Table 2: Types of diagnostic tests for each infection.

Table 3: Co-infection test between each infection type. There is no significant association between expected and observed prevalence of different combinations of co-infecting pathogens.

Figure 6: Pathogen species richness by community type (on left) and by habitat (on right). Using a generalized linear mixed model there was no significant difference between infection species richness across habitat types.

Figure 4: Lymphocyte and white blood cell count and T cruzi presence.

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