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Parasites
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MEETING REPORT

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Quantitative factors proposed to influence the prevalence of canine tick-borne disease agents in the United States

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Abstract

The Companion Animal Parasite Council hosted a meeting to identify quantifiable factors that can influence the prevalence of tick-borne disease agents among dogs in North America. This report summarizes the approach used and the factors identified for further analysis with mathematical models of canine exposure to tick-borne pathogens.

Keywords: *Anaplasma, Ehrlichia, Borrelia burgdorferi*, Tick-borne infections, Prevalence map factors, Ticks, Ixodidae, Prostriata, Metastriata

Background

Dogs in the United States (USA) are hosts to a diverse range of ixodid ticks and can become infected with many of the pathogens transmitted by these vectors. Advances in diagnostic test and recording technologies have led to the creation of a monthly dataset containing county-by-county canine test results from across the USA. The Companion Animal Parasite Council (CAPC) has assembled large datasets of such results from commercial laboratories that provide diagnostic tests for canine exposure to *Borrelia burgdorferi*, *Ehrlichia* spp. and *Anaplasma* spp. [1]. These monthly, county-level CAPC prevalence maps generated interest in the utility of the datasets for assessing seroprevalence norms, forecasting future seroprevalence rates and for identifying trends in canine exposure to this array of tick-borne disease agents. A group of vector ecologists, parasitologists, other biologists and statistical modelers met in Atlanta, GA (June 9–10, 2012) to identify factors that could enhance the accuracy of these predictive models. This report narrates the results of the meeting.

Canine diagnostic test results for exposure to tick-borne pathogens, including *B. burgdorferi*, *Ehrlichia* spp. and *Anaplasma* spp., are of significant interest, not only because canine health is important to pet owners and veterinarians, but also because of the public health importance of many of these infectious disease agents. These tick-borne pathogens are transmitted by two phylogenetically distinct groups of ixodid ticks. Members of the ixodid subfamily Prostriata (*Ixodes* spp.) transmit agents of granulocytic anaplasmosis (*Anaplasma phagocytophilum*) and Lyme borreliosis (*B. burgdoferi*) and are likely to include vectors of a more recently described *Ehrlichia muris*-like agent in the USA. Members of the subfamily Metastriata (*e.g.,* the genera *Amblyomma, Dermacentor* and *Rhipicephalus*) transmit agents of canine and human ehrlichiosis (*e.g., E. canis, E. chaffeensis* and *E. ewingii*), canine anaplasmosis (*A. platys*) and spotted-fever group rickettsiosis (*i.e., Rickettsia rickettsii, R. conorii* and related *Rickettsia* spp.).

Large datasets have been assembled from reports of diagnostic test results for canine exposure to *B. burgdorferi, Anaplasma* spp. and *Ehrlichia* spp. in the USA. For example, from reports submitted nationwide from 2010–2012, 509,195 (7.2%) of 6,996,197 canine samples were seropositive for *B. burgdorferi*, 270,168 (4.4%) of 6,192,268 samples were seropositive for *Anaplasma*,

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and 111,673 (1.1%) of 6,994,683 samples were sero-positive for *Ehrlichia* [2]. A previous national survey, spanning 2001–2007, reported results from 982,336 diagnostic tests for canine exposure to *B. burgdorferi* and *Ehrlichia* spp., and 479,640 tests for canine antibodies to *Anaplasma* spp., with 5.1%, 0.6% and 4.7% of these samples testing seropositive for *B. burgdorferi*, *Ehrlichia* and *Anaplasma*, respectively [3]. Interestingly, when the canine seroprevalence of *B. burgdorferi* in the 2001–2007 study was compared to the subsequent prevalence of human Lyme disease, the most commonly reported human vector-borne illness in the USA, canine seroprevalence of *B. burgdorferi* ≥5.1% was predictive of emergent human Lyme disease in low-incidence counties; a low canine seroprevalence (≤1.0%) was associated with minimal risk for emergent human Lyme disease [4]. A subsequent report, however, underscored the importance of other variables, such as the distribution of competent vector species, for accurate interpretation of these canine diagnostic test data [5].

The overall objective of this CAPC-sponsored workshop was to identify factors that are likely to influence the seroprevalence of canine exposure to tick-borne disease agents in the USA, specifically focusing on the factors and the pathogens for which sufficient data are available, so that these factors could be evaluated for incorporation in mathematical models designed to monitor and to predict spatial and temporal seroprevalence patterns. These preliminary factors provided statisticians some of the critical information needed to begin their model-building procedures.

Approach

Two teams of researchers, from various areas of tick and tick-borne pathogen biology, were assembled and tasked with rational identification of factors thought to be relevant to the canine seroprevalence of pathogens transmitted by prostriate (eight team members) or metastriate (seven team members) ticks (Figure 1). Members of each team were selected based upon diverse areas of expertise in tick biology, tick-borne disease, vector ecology or statistics. Each panel was asked to identify and to rank ten key factors that they considered most likely to affect pathogen seroprevalence, and these preliminary factors were then presented to all of the meeting participants for further discussion. It was understood that the relevance of these factors would be subsequently assessed with mathematical models, and that these models would be adjusted with data that continue to be generated. Thus, the utility of different factors would be continually assessed as the mathematical models are refined over time.

The working groups for both ixodid subfamilies began by discussing variables categorized as (1) vector, (2) host, (3) abiotic, (4) habitat or (5) social. Both groups independently identified numerous factors. The majority of factors were thought to be associated with canine exposure to pathogens vectored by either ixodid subfamily; however, several factors specifically associated with the different ixodid subfamilies also emerged. Variables were also discussed for which there is little or inconsistent supporting data, but these factors could become useful if the data became available. However, in accordance with the workshop objectives, factors for which sufficient data are currently available were chosen for ranking by consensus of each working group.

The variables independently identified by each panel were categorized into the five groups previously indicated (i.e., vector, host, abiotic, habitat and social). Factors regarding exposure to infectious agents transmitted by prostriate ticks were heavily influenced by the preponderance of research on the phenology of *Ixodes scapularis* and *I. pacificus*, which are considered the primary vectors of *B. burgdorferi* and *A. phagocytophilum* in North America (Table 1). For metastriate-borne pathogens, host biology and human behavior were second only to vector distribution with regard to factors considered likely to influence seroprevalence (Table 2). Brief explanations and comments regarding these factors are described below.

Vector factors

Distribution

The geographic distribution of prostriate ticks was focused on the *Ixodes* spp. thought to most commonly feed on dogs (and people) in the USA: *I. scapularis* and *I. pacificus*. Metastriate ticks considered as pathogen vectors (e.g., of *Ehrlichia* spp. and *A. platys*) included, in alphabetical order, *A. americanum, A. maculatum, D. andersoni, D. variabilis* and *R. sanguineus*. The general distributions of these ticks are relatively well documented in the literature and via voucher specimens in the USA. However, the spatial resolutions of these data vary in different regions, and defining the minimum useful scale can be complicated by discontinuous geographic distributions of tick populations in a given area.

Abundance

Defining permanent values of tick abundance levels is problematic, because tick population levels within a given area are temporally and spatially variable and can change rapidly. Tick abundance depends on host abundance and availability, relative humidity, precipitation and temperature, and can reflect conditions from previous years when immature tick stages or prior generations were active.

Figure 1 Approach to rational identification of quantitative factors proposed to influence the exposure of dogs to vector-borne pathogens.
Background information, meeting objectives and guidelines were presented to participants before they were divided into three separate panels, according to vector taxa, for mosquitoes, prostriate ticks and metastriate ticks. Each panel was asked to identify, discuss and to rank candidate factors for evaluation with statistical prevalence models of pathogens transmitted to US dogs by each vector taxon. All of the participants were subsequently reconvened for further discussion and refinement of the results from each panel.

Activity

Activity is indicative of questing behavior, host-seeking behavior, host contact and the feeding preferences of different developmental stages. The presence of ticks in an area is not alone indicative of activity. For example, tick activity will depend on temperature, precipitation, relative humidity and photoperiod.

Host factors

Deer

The deer population is a major driver of abundance for certain ticks, such as *I. scapularis, I. pacificus* and *A. americanum*. Deer are also a reservoir of *E. chaffeensis* and could be involved in the maintenance of *E. ewingii*.

Table 1 Factors initially considered as potential contributors to canine prevalence of disease agents transmitted by *Ixodes scapularis* and *I. pacificus*

Vector factors

Distribution

Abundance

% Infected

Canine contact

Local phenology

Tolerance to temperature and humidity

Activity

    Focus on adults as primary vector to dogs

    Host seeking behavior

    Host contact

    Feeding preferences and opportunities

        Deer population drives tick abundance

        Small mammal population drives infection prevalence

        Lack of lizards

        Diversity/dilution effect

    Tick encounters

    Questing behavior versus relative humidity

    Peridomestic encounters – access to areas

    Urbanization/Rate of development

Infection status (decreased survival versus increased cold tolerance)

Host factors

Presence and abundance (deer, small mammals, lizards)

    Dilution effect/host diversity

Habitat availability and quality

    Mast crop as a surrogate for host reproduction/fitness

Migratory bird patterns

Reproductive capacity and timing of vertebrate host reproduction

Population control programs in place locally

Abiotic host survival factors

    Temperature, water availability, substrate/nesting material, snow cover

Feeding preferences

Herd immunity of reservoir host populations

Hunting pressure/success

    Number of deer killed per county – harvest rates

    Hunting license versus hunting harvest – how active hunting is for that area

    Hunting limits due to development

Abiotic factors

Snow cover – depth, duration

Miles of roads – neighborhood roads (non-interstate/parkway/highway), trails

Soil type – clay versus sand in Northeastern USA

Table 1 Factors initially considered as potential contributors to canine prevalence of disease agents transmitted by *Ixodes scapularis* and *I. pacificus* (Continued)

Hydrological features

I. scapularis

    Maximum temperature, warmest month

    Annual precipitation

I. pacificus

    Minimum temperature, coldest month

Daily temperature (high, low and average)

Relative humidity (average, high, low, duration)

Habitat factors

Land cover classification

    Urbanization in 3 categories – low, medium, high

    Rate of change

Forest cover

    Land cover classification (categorical), % canopy cover, NDVI, EVI (canopy structure)

    Crop phenology – maximum greening, minimum greening – when greening is happening

    Supervised vs unsupervised satellite imagery, derived data not currently off the shelf

    Forest type, forest fragmentation, forest edge length, forest composition, forest connectivity

    Forest fragments within X distance of road or urban area, close to population centers

Understory- could be modeled but is not measured

Detritus layers/leaf litter

    Targeted for future research but perhaps not currently available dataset

Soil maps/soil types

    World harmonized soil database

    Classification scheme

Proximity to rivers/drainage areas

Proximity to coast

Rain shadows

Rivers and streams

    Attract hosts

    Serve as corridors

    Provide humidity

Aspect/slope/topo index – derived from digital elevation models, available from hydro dataset

    More nymphal deer ticks on north- and east-facing slopes

    Effective distance – more ticks on uphill side of a payout

Ticks associated with east-facing woodland edges that slope down to water

Fire

    Eliminates leaf litter, changes food availability, changes microclimate

Table 1 Factors initially considered as potential contributors to canine prevalence of disease agents transmitted by *Ixodes scapularis* and *I. pacificus* (Continued)

Depending on timing, burn can increase number of infected ticks, so fewer ticks but higher infection rate
Park boundaries – proximity to parks
Social factors
Human population centers
Dog ownership, dog lifestyle
Hunting styles that use dogs
Breed of dog
Dog ownership increase – by region
More homes in tick habitat – demographic factors
Deer/vehicle collisions – deer crossing signs
Acaricide use/quality of care for dogs
Average household income
Presence of clinics, proximity to clinics, number of vet clinics in an area, size of clinics
Cultural – forest foraging (mushroom hunting in Missouri)
Internet use
Social media
Smartphone use
Education level
Population density
Housing type (average lot size, median home price, age of house unit, census tract size)

Small mammals

Rodents are an important component of the ecologies of several tick species and some tick-borne infectious agents. Immature stages of several tick species acquire blood meals from small vertebrate hosts. Several tick-borne infectious agents, such as *B. burgdorferi*, *A. phagocytophilum* and *R. rickettsii* are adapted to rodent reservoir hosts.

Lizards

Small vertebrates such as lizards, which are permissive hosts for immature tick stages but are not definitively documented reservoirs of the pathogens under consideration, could dampen transmission of disease agents that are adapted to rodent reservoirs. Conversely, removal of lizards reportedly reduced nymphal tick numbers from an environment but did not affect the percentage of *B. burgdorferi*-positive ticks, suggesting that increased numbers of lizard hosts might actually increase the risk of pathogen transmission by serving to increase the overall number of ticks in a given area [6].

Migratory bird patterns

Migratory birds can introduce some tick species to new areas [7]. However, ticks that feed on dogs and that are dispersed by birds in the USA may be incapable of maintaining an active population cycle in the absence of larger vertebrate hosts (*e.g.,* white-tailed deer).

Abiotic factors

Different tick species and their natural hosts can be adapted to various environments that are influenced by abiotic factors such as precipitation, temperature, relative humidity and soil composition.

Habitat factors

Factors that influence the life cycles of ticks and their vertebrate hosts include vegetation, urbanization, land use in non-urban settings and detritus layers.

Social factors

Human behavior and population characteristics influence the exposure of dogs to ticks. These include access to preventive care, recreation, socioeconomic status, income, pathogen reservoir control, vector-amplification host control and news media coverage.

Unquantified variables

A number of variables were discussed for which comprehensive, nationwide data did not seem currently available. These variables included vector infection rates, detailed reservoir infection rates, vector abundances, vector efficiency indices, vector survival, vectorial capacities, temperature-dependent development rates of vectors (natural temperature regimes), total number of dogs (by county or zip code) and tick control product sales in each geographic region. Local data may be available for some of these variables in certain areas, but national datasets were not available at the time of this meeting.

Mathematical modeling

Each expert panel was asked to prioritize 10 factors most expected to drive a reliable mathematical predictive model. These lists, summarized in Tables 3 and 4, shared several common abiotic and habitat factors. Several other factors were specific to seroprevalence of the pathogens transmitted by *Ixodes* spp., *R. sanguineus* or the other metastriate ticks that were considered. For example, while deer populations and vegetation were considered important factors that affect the majority of these tick populations, social factors were given the highest priority for predicting the seroprevalence of agents transmitted by the brown dog tick, *R. sanguineus* (Table 4).

Table 2 Factors discussed as potential contributors to seroprevalence of metastriate tick-borne pathogens among dogs in the USA

Vector factors
Biology
Competence (different transmission scenarios)
Host preference
Persistence and interhost transfer of male ticks
Host seeking behavior (hunt, ambush)
Population dynamics
Distribution (established, intermittent or absent)
Relative abundance (species and stages)
Seasonality
Different stages
Stage overlap

Host factors
Principal host(s) of different tick stages
Susceptibility to pathogen
Distribution
Density-Dynamic
Ecologic diversity (dilution effect)
Shannon-Weaver Index
Tick-permissive, non-reservoir hosts
Behavior
Host grooming
Gregariousness
Host species
Home Range
Migration, dispersal
Anthropogenic translocation
Hosts permissive for pathogen
Persistence in reservoir
Prevalence of infection
Density
Other transmission routes
Life cycle/age distribution
Immune response
Amplification vs. reservoir
Domestic
Indoor/outdoor
Rural/urban
Relocation
Sylvatic vs. Suburban
Opportunistic or natural infection

Abiotic factors
Humidity
Maximum, minimum and average

Table 2 Factors discussed as potential contributors to seroprevalence of metastriate tick-borne pathogens among dogs in the USA *(Continued)*

Temperature
Maximum, minimum and average
Degree-day
Soil temperature
Photoperiod
Seasonal precipitation
El Niño effect
Snow and other ground cover
Catastrophic disturbance
Fire
Hurricane
Wind
Altitude

Habitat factors
Macrohabitat
Vegetation (density, type and fragmentation)
Elevation
Location of water sources
Rainfall
Microhabitat
Soil type
LIDAR data
Land use

Social factors
Land use
Indoor versus outdoor dogs
Dog use (*e.g.*, hunting)
Canine husbandry
Use of tick preventives
Nuisance permits
Housekeeping
Animal welfare violations
Socioeconomics
Average household income
Human population
Large-scale economic factors
Recreation
Hunting
Parks (rural and urban)
Pets per household

Table 3 Ranked factors identified for canine seroprevalence models of infections transmitted by *Ixodes* spp. in the USA

1.	Forest cover/NDVI or EVI[a]
2.	Relative humidity
3.	Annual precipitation (including snow cover)[a]
4.	Human population density[a]
5.	Deer/vehicle collisions[a]
6.	Topography/altitude/aspect
6.	Temperature – max warmest, min coldest[a]
7.	Proximity of forest to impervious surfaces or roads/built environment
8.	Human case distribution
8.	Distribution/abundance of *I. scapularis* and *I. pacificus*[a]
9.	Household income[a]
10.	Forest fragmentation index[a]

[a]Similar variables also ranked by the metastriate-borne pathogen panel.

The prevalence data at the foundation of this predictive model is largely based on serodiagnostic tests. Although seropositivity is reflective of past exposure, it does not demonstrate recent or active infections. Repeatedly seropositive samples from the same dogs at different times are also to be occasionally expected, because some dogs may have tested seropositive in previous tests and because some tests are conducted to monitor host responses to treatment. Travel histories and certainties of the individual test results are currently unavailable for the dogs reported in this dataset.

An analogous project for mathematical modeling of the prevalence of canine heartworm was simultaneously undertaken by CAPC [8,9], and each prioritized factor identified by the expert panel had significant predictive power with ≥95% confidence. Overall, the model explained 60%-70% of variability in the CAPC county-by-county dataset from 2011–2013. Similarly, preliminary analysis of canine seroprevalence of *Anaplasma* spp. indicated that temperature, precipitation, relative humidity, population density, median household income, forestation coverage, elevation and deer/vehicle strike rates were significant with ≥95% confidence, and that the total proportion of variability explained in the 2011–2013 data is around 60-70% [10]. Thus, the prevalence of heartworm and seroprevalence of *Anaplasma* among dogs appear amenable to quantification that could facilitate monitoring for outbreaks, remediation of vector abundance or for forecasting future seroprevalence levels.

Attempts to fit the seroprevalence of *B. burgdorferi* and of *Ehrlichia* spp. among dogs are also underway, with mixed results. The spatial seroprevalence of *B. burgdorferi* among dogs has been similar to and appears to be as quantifiable as that of *Anaplasma* spp. Conversely,

Table 4 Ranked factors for preliminary models of metastriate tick-borne pathogen prevalence among dogs in the USA

Majority of the metastriata:	
1.	Vector distribution (established, intermittent or absent)[a]
2.	Maximum, minimum and average temperature[b]
3.	Amount of precipitation[a]
4.	LiDAR (up to 6 layers)
5.	GAP/categorical analysis of vegetation[a]
6.	Reservoir host densities[a]
7.	Human population (census)[a,b]
8.	Median household income[a,b]
9.	Fragmentation of vegetation[b]
10.	Degree-days
11.	Seasonal precipitation (snow cover)[a]
***R. sanguineus*:**	
1.	Median household income [a,b]
2.	Registered dog breeders (kennels, puppy mills, *etc.*)
3.	Human population (census)[a,b]
4.	Tick preventive sales
5.	Animal welfare violations
6.	Latitude

[a]Variables also ranked by the prostriate-borne pathogen panel.
[b]Variables shared among all ixodid ticks considered for this report.

the canine seroprevalence of *Ehrlichia* spp. appears to be highly variable, with some neighboring areas reporting antipodal seroprevalence rates that could be reflective of vector ecology or social factors. Future work will address these issues.

Conclusions

This meeting brought together a range of junior and senior scientists engaged in various aspects of research in the biology of ticks and tick-borne infections. The specific objectives were to identify and to prioritize quantifiable factors expected to contribute to canine exposure to organisms transmitted by the two major subfamilies of ixodid ticks. The two panels ranked 12 and 17 factors associated with prostriate and metastriate ixodid ticks, respectively. Eight of these factors were independently prioritized by both panels; four of 12 factors were unique to prostriate-vectored agents, two of 11 factors were unique to metastriate-vectored agents transmitted by ticks other than *R. sanguineus*, and four of six factors were unique to agents vectored by *R. sanguineus*. The next phase of this project will move from rational identification of perceived factors to statistical assessment of factors for predictive power. Forecasting issues will also be explored.

Competing interests

The authors have no competing interests relative to the work presented in this report.

Authors' contributions

SEL, DDB, CL, CC, RL and RWS conceived of and organized the meeting that generated the information provided in this report. BLB, DDB, CC, MRC, SAE, DF, JEF, HG, GJH, RRL, SEL, CL, RL, TM, GRN, WLN, JS, RWS, AV-S and DW participated in the meeting and contributed to the identification of candidate factors. RWS tabulated the candidate factors from the meeting minutes, and SEL, DDB and RWS generated the initial draft of the manuscript. RWS was responsible for distribution of the manuscript to the co-authors, for revision in response to comments, and for formatting the final manuscript version for submission. All authors read and approved the final version of the manuscript.

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