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Predominance of Ehrlichia ewingii in Missouri dogs

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Predominance of Ehrlichia ewingii in Missouri dogs

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To investigate the species distribution of Ehrlichia present in Missouri dogs, we tested 78 dogs suspected of having acute ehrlichiosis and 10 healthy dogs. Blood from each dog was screened with a broad-range 16S rRNA gene PCR assay that detects known pathogenic species of Ehrlichia and Anaplasma. The species was determined by using species-specific PCR assays and nucleotide sequencing. Ehrlichia antibody testing was performed by using an indirect immunofluorescence assay with Ehrlichia chaffeensis as the antigenic substrate. The broad-range assay detected Ehrlichia or Anaplasma DNA in 20 (26%) of the symptomatic dogs and 2 (20%) of the asymptomatic dogs. E. ewingii accounted for 20 (91%) of the symptomatic dogs, E. chaffeensis accounted for 1 (5%) of the positives. Anaplasma phagocytophilum DNA was detected in one dog, and the sequence of regions of the 16S rRNA gene and the groEL operon amplified from the blood of this dog matched the published sequences of this organism. Antibodies reactive with E. chaffeensis were detected in 14 (67%) of the 21 PCR-positive dogs and in 12 (19%) of the 64 PCR-negative dogs. Combining the results of PCR and serology indicated that 33 (39%) of 85 evaluable dogs had evidence of past or current ehrlichiosis. We conclude that E. ewingii is the predominant etiologic agent of canine ehrlichiosis in the areas of Missouri included in this survey. E. canis, a widely recognized agent of canine ehrlichiosis, was not detected in any animal. The finding of E. ewingii in asymptomatic dogs suggests that dogs could be a reservoir for this Ehrlichia species.

Ehrlichiosis is an important emerging infection of dogs and humans. The first species recognized, Ehrlichia canis, causes monocytic ehrlichiosis in dogs. A closely related species, E. chaffeensis, was subsequently identified as the cause of an acute monocytic ehrlichiosis (I). E. chaffeensis has also been detected in dogs (12), coyotes (21), goats (13), and deer (3, 10). A further closely related species, E. ewingii, was initially recognized as the cause of granulocytic ehrlichiosis in dogs (15) and was recently found to cause some cases of granulocytic ehrlichiosis in humans (7). Most cases of human granulocytic ehrlichiosis are caused by a species referred to as the agent of human granulocytic ehrlichiosis (4). This bacterium has also been detected in dogs (19), deer (5), horses (20), and rodents (31). The name Anaplasma phagocytophilum has recently been proposed to include this bacterium, in addition to the species previously known as E. phagocytophilum and E. equi (14), and this proposed name is used in the present study.

Molecular studies of the prevalence of infection with Ehrlichia spp. in dogs have been based on semilogic methods that often used antigens derived from E. canis. Because of semilogic cross-reactions between E. canis and other Ehrlichia species, including E. chaffeensis and E. ewingii (25, 29), these studies do not provide identification of the species that elicits production of anti-Ehrlichia antibodies in the host animal. Four studies have used molecular techniques and/or cell culture methods to identify the Ehrlichia species infecting dogs. In these studies, conducted in North Carolina (6, 22), Virginia (11), and Oklahoma (25), 24 dogs were infected with E. chaffeensis, 21 were infected with E. canis, 19 were infected with E. ewingii, 10 were infected with E. phagocytophilum, and 1 was infected with A. phagocytophilum. A recent study described 15 dogs with E. ewingii infection proven by PCR (18).

In our laboratory at Washington University Medical Center in St. Louis, Mo., we have detected nearly 200 cases of human ehrlichiosis in recent years by using PCR; 89% of these cases were caused by E. chaffeensis and 11% were caused by E. ewingii. To learn more about possible relationships between human and canine ehrlichiosis, we studied the occurrence and species distribution of Ehrlichia in pet dogs in Missouri. The focus of the study was on ill dogs with clinical manifestations suggestive of ehrlichiosis, but we also studied a small number of asymptomatic dogs.
presence of m onocytes in a peripheral blood smear, and presence of ticks on the
dog. EDTA-anticoagulated whole blood and serum specimens were collected
from each dog for laboratory testing. For each dog with suspected ehrlichiosis
included in the study, veterinarians were also asked to submit whole-blood and
serum specimens from another dog under their care at the same time that was
not ill (e.g., dogs being seen for routine medical examinations or dogs being boarded
under the supervision of the veterinarian). Thirty-five veterinarians submitted
amoeba from 88 dogs from Missouri (2000 through January 2001); the same samples
were mailed to the Veterinary Laboratory at St. Louis Children’s Hospital. The vet-
ninarians also provided clinical and epidemiologic data for each dog by using a
standardized data collection form. The first day of observed illness was known for
23 dogs. For these 23, amoeba samples were obtained after a median interval of 4 days
(range, 0 to 31).

PCR testing. Leukocyte lysates were prepared from whole-blood specimens as
described previously (7). Broad-range Ehrlichia PCR was performed ed with prim-
ers (ECA and H E3) that bind to genomic fragments of the 16S rRNA gene that are
conserved among all pathogenic Ehrlichia and A. phagocytophilum. The Ehrlichia
species was determined by additional reactions with sets of primers specific for
E. chaffeensis (H E3 and H E3) (2), E. ewingii (OW 1 and H E3) (3), and E. canis
(21). Same samples positive with the broad-range primer were also tested with prim-
ers EHR 521 and EHR 747 that amplify A. phagocytophilum, as well as other
Anaplasma spp. (27). Same samples positive with EHR 521 and EHR 747 were also
tested with primers GSHF and GSE that am phily a portion of the 16S rRNA gene
of A. phagocytophilum, as well as the closely related white-tailed deer agent (23).
PCR-positive samples were analyzed on an automated DNA sequencer (model
377; Applied Biosystems, Foster City, Calif.), and AmpliTaq FS DNA polymerase.
Extension products were analyzed in an automated DNA sequencer (model
377; Applied Biosystems). The primers used for sequencing of the broad-range PCR
products were H E3 (2) and PER-1R (7).

Nucleotide sequence accession number. The GenBank accession number for
the 1,256-bp groESL sequence amplified from a Missouri dog isAY219849.

RESULTS

A total of 88 pet dogs were included in the study, including
78 (89%) that were ill and 10 (11%) that were asymptomatic.
The dogs included a wide variety of breeds, of which the most
common were Labradors and Golden Retrievers (22 of
22, including 10 males). Fifty-six percent were female, and the
ten mean age was 4.6 years (range, 1 to 13 years). Fever and
or musculoskeletal signs (i.e., lameness, reluctance to rise or walk,
with a stiff or stilted gait, or painfull or swollen joints) were
the most frequent clinical findings. Other reported findings
included current or recent hem orrhage, organomegaly, uveitis,
and neurologic signs.

Routine laboratory test results were available for only a
minority of the dogs and indicated that 19 dogs had thrombo-
cytopenia (platelet count, 200,000/ μl), 20 had anemia (10 had
leukopenia, and 4 had hypergammaglobulinemia). Monocytes
were observed on peripheral blood smears from two dogs
that were later found to be PCR positive for E. ewingii.

The results of PCR testing of the 88 dogs are shown in Table
1. Ehrlichia or Anaplasma DNA was detected in the blood of
22 (25%) of the 88 dogs, including 20 (23%) of the ill dogs
and 2 (20%) of the asymptomatic dogs. Species-specific PCR
testing revealed 19 infections with E. ewingii, 1 with E. chaffeensis,
and 1 with A. phagocytophilum. No additional dog was deter-
mined to be positive by the broad-range assay but negative by
the species-specific assays. The species identity of this dog’s
infection was determined to be E. ewingii by nucleotide se-
quence of a portion of the 16S rRNA gene. The failure of
the species-specific assay to yield the species identity was prob-
ably related to the fact that the species-specific assays are less
sensitive than the broad-range assay for the detection of Ehrlichia
DNA (unpublished data). E. canis was not detected in any dog.

Two dogs positive for E. ewingii were also positive in the
screening assay for A. phagocytophilum (primers EHR 521 and
EHR 747) but negative with the confirmatory assays that am-
ply specific segments of the 16S rRNA gene of A. phagocytophilum, as well as the
white-tailed deer agent (23), and also with a nested assay that specifically am-
piles a 126-bp segment of the A. phagocytophilum groESL operon (28).

Serology. Canine serum specimens were tested for immu-
no globulin G (IgG) antibodies reactive with B. burgdorferi by using an indirect immu-
nofluorescent-antibody assay (IFA), as described previously (9).
Fluorescein isothiocyanate-labeled goat anti-dog IgG (specific) conjugate was
used at a dilution of 1:350. Serum samples were screened at a 1:162 dilution; speci-
mens reactive at this dilution were tested at 1:324 dilutions. A positive result
was defined as the greatest reciprocal dilution for which specific reactivity was observed. Dogs were
categorized as seronegative if their IFA titer was 64.

Two dogs positive for E. ewingii were also positive in the
screening assay for A. phagocytophilum (primers EHR 521 and
EHR 747) but negative with the confirmatory assays that am-
ply specific segments of the 16S rRNA gene of A. phagocytophilum, and the species identity
was probably positive only for E. ewingii. Thus, infection with a multiple Ehr-
lia species was not detected in any dogs in the present study.

Because hum an cases of ehrlichiosis caused by A. phagocy-
tophilum have been rare in Missouri (24), we carried out nu-
cleotide sequencing of portions of the 16S rRNA gene and the
groEL heat-shock operon am phily aed from the blood of the
dog that was positive for A. phagocytophilum. Sequencing of the
16S rRNA gene segment was performed by using the se-
quencing primers PER-1R, which provides the sequence of a
126-bp segment that spans the highly variable region. The sequence data were matched to the published sequence of A.
phagocytophilum (GenBank accession no. U02521) (8). The nucleotide sequence of the gene segment of the groEL operon am phily aed by PCR was very similar to or identical to sequences
previously determined for A. phagocytophilum.

There were no significant differences between PCR-positive
and PCR-negative dogs in gender, proportion fertile, mean
age, or the presence of fever or musculoskeletal signs.

TABLE 1. Results of Ehrlichia PCR testing of Missouri dogs

<table>
<thead>
<tr>
<th>Status</th>
<th>Total no. of dogs</th>
<th>No. (%) of dogs PCR positive for:</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCR-positive</td>
<td>22</td>
<td>E. ewingii 19 (82%) E. chaffeensis 1 (4%) A. phagocytophilum 2 (9%)</td>
</tr>
<tr>
<td>PCR-negative</td>
<td>66</td>
<td>E. ewingii 2 (3%) E. chaffeensis 1 (1%) A. phagocytophilum 1 (2%)</td>
</tr>
</tbody>
</table>

The PCR-positive cases occurred during May through July. Figure
2 shows the distribution of PCR-positive and PCR-negative
samples within the state of Missouri. Most specimens were
submitted from the southern portion of the state. Positive
dogs were located throughout this region, with a cluster of positives
in four counties (Jefferson, Washington, St. Francois, and St.
Genevieve) located south of St. Louis and a smaller cluster in the
southeastern portion of the state.

Serum from 85 dogs, including 78 ill and 7 asymptomatic
anima ls, w ere tested by IFA for antibodies reactive with E. chaffeensis. Table 3 showsthe resultscompared tor e s u ltsof PCR testing. Ofthe 85 dogs, 26 (31% ) had IgG antibodies reactivewith E. c haffeensisatatiter of 64, including 14 (67% ) of21 thatwere PCR positiv ea n d1 2 ( 1 9 %)o f6 4thatwere PCR negative (P 0.001[chisquare]).IFA w asperformedon samplesfrom 19dogsthatwerePCR positive forE. ewingii by PCR. Oft hese,13 (68% ) had titers of 64 (range, 32 to 2,048; geom etric m ean titer, 142). The single dog thatwas positive for E. chaffeensis by PCR had a reciprocaltiter of 64, and the single dog that was positive for A. phagocytophilum by PCR was negative for antibodies reactive with E. chaffeensis. O f these, 13 (68% ) had titers of 64 (range, 32 to 2,048; geometric mean titer, 142). The single dog that was positive for E. chaffeensis by PCR had a reciprocal titer of 64, and the single dog that was positive for A. phagocytophilum by PCR was negative for antibodies reactive with E. chaffeensis. Of the 76 ill dogs tested, 26 (22% ) were IFA positive compared to 10 (13% ) of the asymptomatic dogs (P 0.7[Fisher exact test]). In all, 33 (39%) of the 85 dogs tested by PCR and IFA had evidence of either past or current Ehrlichia exposure based on either a positive PCR or positive serology.

Although most likely explanation for the finding of positive serology with a negative PCR in 12 dogs is that they had past infection, another possible explanation is the effect of antibiotic therapy given for the acute illness. Antibiotic prescribing information was available for 60 dogs at the time of sample collection. Nineteen had received antibiotics for at least 1 day before testing (range, 1 day to 7 months prior to sample collection); seven of these animals had received an antibiotic with significant anti-Ehrlichia activity (doxycycline or chloramphenicol). One of the seven was PCR positive and IFA negative after 6 days of chloramphenicol treatment, one was PCR negative but IFA positive after receiving 4 weeks of doxycycline, and the remaining five were PCR negative and IFA negative.

One possible explanation for the finding of seronegativity in seven PCR-positive dogs (six ill and one asymptomatic) could have been that blood samples were obtained early in the illness before a serologic response had occurred. Information on the day of onset of illness was available for three of the six ill dogs with this finding; in these dogs, the samples were obtained on days 3, 3, and 30 after onset of symptoms.

**DISCUSSION**

This study of the Ehrlichia species present in dogs in Missouri revealed several notable results. The first was the finding that more than 90% of dogs with molecular evidence of current Ehrlichia infection were infected with E. ewingii. Although E. ewingii had previously been demonstrated as a cause of ehrlichiosis in Missouri dogs (30), no study had yet documented its presence by molecular methods. The distribution of Ehrlichia species in Missouri dogs differs dramatically from that in humans with ehrlichiosis acquired in the state. In our laboratory, which receives human specimens from a geographic region similar to the region from which dog samples were provided for the present study, E. chaffeensis has accounted for 89% of the cases, with E. ewingii accounting for the remaining 11% . One possible explanation for this discrepancy may be differences in host pathogenicity; namely, E. chaffeensis may be more pathogenic for humans, and E. ewingii may be more pathogenic for dogs. Additional molecular studies of the prevalence of Ehrlichia in asymptomatic dogs would help clarify these results.

The absence of E. canis in the present study is also noteworthy. One other molecular study of canine ehrlichiosis, performed in Virginia, found only E. chaffeensis and E. ewingii, without any cases of E. canis infection (11). We do not think the absence of E. canis in the present study is the result of the failure of the PCR assay used to detect E. canis, since the PCR primers in the broad-range assay used for initial screening can...
FIG. 3. Geographical distribution of dogs included in the present study by county of residence. The results of Ehrlichia PCR assays are shown as designated in the key.
amplify the DNA of *E. canis*. Previous studies of the causes of canine ehrlichiosis that were based on serology may have failed to make definitive species identification because of serologic cross-reactions among members of the *Ehrlichia*, including *E. chaffeensis* and *E. ewingii*. Specifically, it is possible that some cases of *E. ewingii* infection were mistakenly attributed to *E. canis* infection. An alternative explanation for the discrepancy of infections with *E. ewingii* is that participating veterinarians selected dogs for inclusion in the present study who had symptoms such as arthritis that are associated with *E. ewingii* infection.

The detection of a dog infected with *A. phagocytophilum* or a closely related species was surprising. We have not detected *A. phagocytophilum* in our extensive experience with human an ehrlichiosis in Missouri. It is possible that the organism does exist at low levels in Missouri and simply escapes detection as a human pathogen. It is also possible that the agent detected was a species related to but not identical to *A. phagocytophilum*, although we think it is unlikely because of the very close similarity of the groESL sequence determined in the present study to any different *A. phagocytophilum* sequences determined in the laboratory of one of the authors (J.W.S.). Because complete travel histories were not available, we cannot exclude the possibility that this dog was infected out of the state.

Serologic testing for antibodies reactive with *E. chaffeensis* revealed that 33% of dogs had serologic evidence of past or present infection with *Ehrlichia*. Combining the results of molecular and serologic testing, 35% of all dogs tested had evidence of past or present infection with *Ehrlichia*, indicating frequent exposure of Missouri dogs residing in the survey region. Among dogs residing in the state of Missouri and in this group of bacteria, D-secreasers between the results of serologic and molecular tests observed for some animals were not unexpected. The 12 dogs that were seronegative but PCR positive probably had past *Ehrlichia* infection. The fact that these cases were evenly distributed throughout the year supports this explanation. It is also possible that some of these dogs had recent infection but were PCR negative because of antibiotic treatment. However, only seven dogs in the study were known to have received antibiotics with activity against *Ehrlichia*, and only one was PCR positive and IFA negative, which indicates that antibiotic therapy was not the explanation for this finding. Finally, the sensitivity of PCR as a method for detecting acute canine ehrlichiosis has not been determined, and it is possible that PCR was falsely negative in some of these cases.

Several explanations are possible for the seven dogs that were PCR positive but seronegative. Some of these dogs may have been sampled very early in the course of their infection before an antibody response had occurred. Unfortunately, the interval between the day of onset of symptoms and the day when the blood sample was obtained was not available for all dogs. A further possible explanation may have been failure to make an antibody response to acute *Ehrlichia* infection in some of these dogs. Convalescent-phase samples were not available to test this hypothesis. It is also possible that in some dogs, the *E. chaffeensis* antigen used in the IFA may have failed to detect antibodies produced in response to infection with *E. ewingii*. This possibility is supported by the observation of inconsistent seroreactivity with *E. canis* antigen in serum from dogs found to be positive for *E. ewingii* DNA by PCR (16, 18).

There were no differences among the dogs with or without confirmed *ehrlichiosis* by sex, age, breed, or fertility status. The larger overall representation of retrievers in the study may be explained by the popularity of these breeds as pets, but data on breed prevalence for the state were not available. Expected early summer peaks in both total suspected tick-borne illnesses and in actual PCR-positive cases of ehrlichiosis were noted. Prior studies have noted higher incidence, mortality rate, and chronicity among German shepherd dogs in South Africa with *E. canis* infection (32). However, no particular breed stood out in our study as having increased incidence.

We highlight here the potential relationships between human and canine ehrlichiosis. The finding that two of ten asymptomatic dogs were PCR positive for *E. ewingii* suggests that dogs might serve as a reservoir for *E. ewingii*. Gooch et al. (18) also recently showed evidence of asymptomatic dogs that were PCR positive for *E. ewingii*. The two asymptomatic dogs that were PCR positive in the present study were sampled in March and April, months which are earlier in the year than those in which most cases of human ehrlichiosis occur in Missouri. This finding raises the possibility that chronic canine *Ehrlichia* infection could be a source for subsequent infections with *Ehrlichia* in humans residing in the same area. It is probably more likely that dogs and humans share similar exposures to infecting ticks, suggesting that cases of canine ehrlichiosis may serve as sentinels for human an cases, as described for other tick-borne infections, including Rocky Mountain spotted fever (26). Most cases of suspected canine ehrlichiosis do not currently undergo testing to reveal the etiologic agent. If confirmatory testing becomes more widely adopted, results could assist human public health officials in identifying environments where the risk of acquiring human ehrlichiosis is high.

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