Prevalence of infectious diseases in cats and dogs rescued following Hurricane Katrina

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Objective—To determine the prevalence of infectious diseases of animal and zoonotic importance in cats and dogs rescued and transferred from the Gulf Coast region following Hurricane Katrina.

Design—Cross-sectional study.

Animals—414 dogs and 56 cats rescued and transferred from the Gulf Coast region within 4 months after the hurricane.

Procedures—EDTA-anticoagulated blood and serum samples were tested via PCR and serologic assays for infectious diseases.

Results—In dogs, prevalence was highest for anti–West Nile virus (WNV) antibodies (218/390 [55.9%]), *Dirofilaria immitis* antigen (195/400 [48.8%]), anti–*Toxoplasma gondii* antibodies (92/366 [25.1%]), and hemotropic mycoplasma DNA (40/345 [11.9%]). The DNA of *Bartonella* spp, *Ehrlichia* spp, or *Babesia* spp or anti–canine influenza virus antibodies were identified in < 2% of dogs. In cats, prevalence was highest for antibodies against *Bartonella* spp and DNA of *Bartonella* spp combined (49/55 [89.1%]), anti–*T gondii* antibodies (13/55 [23.6%]), hemotropic mycoplasma DNA (5/47 [10.6%]), anti–WNV antibodies (5/48 [10.4%]), *D immitis* antigen (4/50 [8.0%]), and anti–FIV antibodies (4/56 [7.1%]). A total of 308 (74.4%) dogs and 52 (92.9%) cats had evidence of previous or current vector-borne infections.

Conclusions and Clinical Relevance—Cats and dogs rescued from the disaster region had evidence of multiple infectious diseases. The dispersal of potentially infectious animals to other regions of North America where some infections were not typically found could have contributed to new geographic ranges for these organisms or to underdiagnosis in affected animals because of a low index of suspicion in regions with low disease prevalence. (*J Am Vet Med Assoc* 2011;238:311–317)

An unprecedented animal rescue operation followed the 2005 landfall of Hurricane Katrina in the Gulf Coast. An estimated 50,000 cats and dogs were left behind by fleeing owners, which was in addition to the unknown number of stray and feral animals in need of rescue.[1] Mass sheltering of animals affected by disasters presents special challenges for control of infectious diseases. Hurricane Katrina destroyed much of the existing animal shelter infrastructure in the Gulf Coast region, and temporary shelters were quickly overwhelmed by the number of homeless animals requiring aid. Some shelters housed > 1,000 cats and dogs at a time when there was limited electricity, potable water, or climate control.[2,3] Guidelines for managing such large numbers of homeless animals and controlling the spread of infectious diseases and for the disposition of unclaimed animals did not exist at the time of the disaster.

Abbreviations

CI	Confidence interval
OR	Odds ratio
SLEV	St Louis encephalitis virus
WNV	West Nile virus

Temporary mass animal shelters ultimately took in > 11,000 cats and dogs in the 2 months following the disaster.[2] Resources were focused on humanely and safely housing the animals with the intent of returning them to their owners whenever possible. Infection control focused on vaccinations and parasite control at the time of shelter entry, but thorough diagnostic evaluations for infectious diseases endemic to the region were not feasible. By the end of 2005, thousands of unclaimed animals were transferred to adoption agencies throughout North America.[2]

The dispersal of animals possibly carrying locally endemic infectious diseases to other regions where these infections are not typically found could contribute to new geographic ranges for these organisms. It could also lead to underdiagnosis in affected animals because of a low index of suspicion in their new loca-

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tions. The purpose of the study reported here was to determine the prevalence of infectious diseases of animal and zoonotic importance in cats and dogs rescued and transferred from the Gulf Coast region following Hurricane Katrina.

Materials and Methods

Animals—The study involved cats and dogs rescued and transferred from the Gulf Coast region during the 4 months after Hurricane Katrina. Criteria for inclusion included any dog or cat transferred from the hurricane disaster area from which blood or serum samples could be obtained and submitted to the University of Florida for analysis.

Study participation—In an attempt to identify animals for the study, efforts were made to contact all groups that may have transferred animals from official disaster response shelters and unofficial rescue missions. A list compiled from media coverage of animal rescues and from lists of involved animal welfare groups compiled by national humane organizations was used to identify 350 groups believed to have received animals transferred from the Gulf Coast Hurricane Katrina disaster area. Those groups were sent a letter or an e-mail. In addition, a nontargeted appeal for participation was made via the e-mail list service of the Association for Shelter Veterinarians and another e-mail list service representing 1,250 animal welfare groups located throughout the United States.

Data and sample collection—Animal welfare groups that received dogs and cats transferred from the hurricane disaster area between August 29 and December 31, 2005, were asked to submit EDTA-anticoagulated blood and serum samples from those animals for analysis. These samples were used to screen for a panel of infectious diseases of animal or zoonotic importance and for which vaccination and parasite preventives administered in rescue shelters would not interfere with diagnostic test results. For each animal included in the study, participating groups were also asked to submit information on the date of sample collection, rescue date, city and state of rescue, original and current identification of the animal, microchip number, sex, estimated age at the time of rescue, and apparent predominant breed. Dogs were categorized into 4 breed groups (ancient, guarding, herding, or hunting) developed on the basis of results of studies of the canine genome, as described elsewhere.[2] In those canine genome studies, genetic analysis of 85 dog breeds allowed identification of 4 breed groups (clusters). The first cluster consisted of ancient breeds of Asian and African origin, the second cluster consisted of guarding breeds, the third cluster consisted of herding breeds, and the fourth cluster consisted of hunting breeds. Dogs representing breeds not yet assigned to a cluster were assigned to the cluster with the most closely related breeds. For example, American bulldogs and other bulldog breed–type dogs were assigned to the guarding breed cluster for analysis. Because of the small number of samples submitted for cats, no attempt was made to analyze breed as a risk factor for cats.

Diagnostic testing—Dogs were tested for the antigen of *Dirofilaria immitis* (heartworm)[a] and for antibodies against *Borrelia burgdorferi*,[b] *Toxoplasma gondii*,[c] *Ehrlichia canis*,[b] canine influenza virus,[d] and WNV.[e] Dogs were tested for DNA of *Wolbachia pipiens* (the endosymbiont bacterium present in all heartworms),[c] *Bartonella* spp,[c] *Ehrlichia* spp,[c] *Anaplasma* spp,[c] hemotropic *Mycoplasma* spp,[c] and *Babesia* spp.[f] Cats were tested for antigens of *D immitis*[a] and FeLV[g] and for antibodies against *T gondii*,[c] *Bartonella* spp,[c] FIV,[g] and WNV.[e] Cats were tested for DNA of *W pipiens*,[c] *Bartonella* spp,[c] *Ehrlichia* spp,[c] hemotropic *Mycoplasma* spp,[c] and *Cytauxzoon felis*.[f] The PCR products were sequenced to confirm species identification; PCR products of the appropriate size but with insufficient DNA for sequencing were classified as indeterminate species of the appropriate genus. Because *D immitis* antigens can only be reliably detected in animals that have been infected for at least 6 months, only animals estimated to be at least 7 months old were tested for this agent.

All serum samples were tested for antibodies against WNV. Because of serologic cross-reactivity with another flavivirus (ie, SLEV), all samples with positive results for the WNV assay were subsequently screened for antibodies against SLEV. Titers that were at least 4-fold higher in one of the assays (WNV or SLEV) were considered diagnostic of infection for the virus with the higher titer. Titers with less than a 4-fold difference were considered diagnostic of flavivirus exposure but of indeterminant type.

Statistical analysis—All analyses were performed with statistical software.[h–j] Prevalence was defined as the number of animals with positive test results divided by the number of animals tested. The χ^2 test or Fisher exact test was used to determine whether the risk factors age (juveniles [< 7 months old] vs adults [≥ 7 months old]), sex, or breed group were significantly associated with infection. Associations between *D immitis* infection and other infectious diseases were evaluated in a similar manner by use of univariate logistic regression to calculate ORs and their 95% CIs. Risk factors and evidence of other infectious diseases determined to be significant in univariate analyses were analyzed by means of multivariate logistic regression. Potential confounders were retained if they changed the OR of other factors by at least 10%. For unequally distributed risk factors, analyses were stratified to account for potential confounding. Interactions between risk factors were tested and retained when *P* values were significant. Values of $P < 0.05$ were considered significant.

Results

Study participants and animals—A total of 21 animal welfare groups in 13 states (California, Colorado, Delaware, Florida, Illinois, Michigan, Missouri, North Carolina, New York, Ohio, Pennsylvania, Texas, and Washington) that had received cats and dogs rescued and transferred from the Gulf Coast Hurricane Katrina disaster area between August 29 and December 31, 2005, provided blood or serum samples for analysis. Samples were received for 56 cats rescued from Louisiana (n = 42), Mississippi (1), Texas (2), and unknown states (11) and for 414 dogs rescued from Louisiana (274), Mississippi (20), Texas (2), and unknown states

(118). The majority of cats (50/56 [89.3%]) and dogs (400/414 [96.6%]) were adults (**Table 1**).

Infectious diseases of dogs—Prevalences of infectious agents in dogs were calculated (**Table 2**). Approximately half of the dogs were infected with *D immitis*. A total of 156 of the *D immitis*–infected dogs were tested for circulating DNA of *W pipiens*, the endosymbiont of *D immitis*; of these, 67 (43.0%) had positive results. Only 3 of 176 (1.7%) dogs with negative results for *D immitis* antigen had positive results for DNA of *W pipiens*.

A total of 92 of 366 (25.1%) dogs had IgM or IgG antibodies against *T gondii*. Only 2 dogs had antibodies against canine influenza virus, but seroreactivity for WNV was detected in most dogs and was the most common finding. When dogs with antibodies against WNV, SLEV, and indeterminate flaviviruses were combined, 272 of 390 (69.7%) dogs tested had evidence of exposure to flaviviruses.

The DNA of the vector-borne hemotropic organisms, including those of the ehrlichiosis-anaplasmosis group, *Bartonella* spp, and *Babesia* spp, was amplified from the blood samples of only a few dogs. Positive PCR assay results for the hemotropic mycoplasmas were more common, with 41 of 345 (11.9%) dogs tested having positive results for DNA of a hemoplasma organism in a blood sample. The DNA of both *Mycoplasma haematoparvum* and *Mycoplasma haemocanis* were amplified from the blood sample of 1 dog.

Among the 5 dogs with *Bartonella* spp DNA amplified from the blood samples, > 1 species were observed in 3 dogs (2 dogs had DNA of *Bartonella henselae*, *Bartonella clarridgeiae*, and *Bartonella vinsonii*, and 1 dog had DNA of *B clarridgeiae* and *B vinsonii*). Five of the 7 dogs with DNA from *Babesia gibsoni* were described as pit bull–type dogs, whereas pit bull–type dogs represented only 34 of the 342 (9.9%) dogs tested for *B gibsoni*. Pit bull–type dogs reportedly have an increased risk for infection with *B gibsoni*[4,5] and were significantly ($P < 0.001$) more likely to have DNA for *B gibsoni* (5/34 [14.7%]) than were non–pit bull–type breed groups (2/308 [0.6%]). Three of the dogs with DNA of *B gibsoni* also had DNA of *M haemocanis*, and 1 of the 3 also had DNA of *M haemotaparvum*. Even though each dog was not tested for all infections, 220 of 413 (53.3%) dogs had positive results (consistent with current infections) for tests to detect DNA or antigen of vector-borne infectious agents. The prevalence increased to 308 of 414 (74.4%) dogs when serologic evidence of exposure to vector-borne infections was included. There were no differences in sex or breed groups for the vector-borne infections evaluated. Sig-

Table 1—Demographic information for 414 dogs and 56 cats rescued and transferred from the Gulf Coast Hurricane Katrina disaster area in 2005.

Species	Variable	Category	No.	%
Dogs	Sex	Male	207	50.0
		Female	181	43.7
		Unknown	26	6.3
	Age	< 7 months	14	3.4
		≥ 7 months	400	96.6
	Breed group	Ancient	55	13.3
		Guarding	129	31.2
		Herding	22	5.3
		Hunting	178	43.0
		Mixed-breed or unknown	30	7.2
Cats	Sex	Male	16	28.6
		Female	37	66.1
		Unknown	3	5.4
	Age	< 7 months	6	10.7
		≥ 7 months	50	89.3
	Breed	Siamese	1	1.8
		Mixed or unknown	55	98.2

Table 2—Results of testing for infectious agents in 414 dogs rescued and transferred from the Gulf Coast Hurricane Katrina disaster area in 2005.

Infectious agent	Assay	No. tested*	No. positive	Prevalence (%)
Dirofilaria immitis†	Antigen	400	195	48.8
Wolbachia pipiens	DNA	345	70	20.3
Borrelia burgdorferi	Antibody	97	1	1.0
Toxoplasma gondii‡	IgG antibody	366	88	24.0
T gondii‡	IgM antibody	366	9	2.5
Bartonella henselae	DNA	345	3	0.9
Bartonella clarridgeiae	DNA	345	4	1.2
Bartonella vinsonii subsp *berkhoffii*	DNA	345	3	0.9
Ehrlichia canis	Antibody	94	1	1.1
E canis	DNA	345	0	0
Anaplasma platys	DNA	345	1	0.3
Mycoplasma haematoparvum	DNA	345	18	5.2
Mycoplasma haemocanis	DNA	345	22	6.4
Indeterminate hemoplasmas	DNA	345	2	0.6
Babesia gibsoni	DNA	342	7	2.0
Babesia canis	DNA	342	0	0
Canine influenza virus	Antibody	394	2	0.5
WNV	Antibody	390	218	55.9
SLEV§	Antibody	271	7	2.6
Indeterminant flavivirus‖	Antibody	390	47	12.1

*Each dog was not tested for all agents. †Only adult (≥ 7-month-old) dogs were tested for *D immitis*. ‡A total of 92 of 366 (25.1%) dogs had positive results for *T gondii* IgG or IgM. §Dogs with WNV titers ≥ 10 were subsequently tested for SLEV. ‖The WNV titer was within a 4-fold value of the SLEV titer; thus, the specific virus could not be determined.

Table 3—Results of testing for infectious agents in 56 cats rescued and transferred from the Gulf Coast Hurricane Katrina disaster area in 2005.

Infectious agent	Assay	No. tested*	No. positive	Prevalence (%)
D immitis	Antigen	50	4	8.0
W pipiens	DNA	47	0	0
T gondii†	IgG antibody	55	9	16.4
T gondii†	IgM antibody	55	4	7.3
B henselae	DNA	47	11	23.4
B clarridgeiae	DNA	47	1	2.1
Bartonella spp	Antibody	55	48	87.3
Ehrlichia spp	DNA	47	0	0
Mycoplasma haemofelis	DNA	47	0	0
Mycoplasma haemominutum	DNA	47	5	10.6
Cytauxzoon felis	DNA	45	0	0
FeLV	Antigen	56	1	1.8
FIV	Antibody	56	4	7.1
WNV	Antibody	48	5	10.4
SLEV‡	Antibody	5	0	0

*Each cat was not tested for all agents. †A total of 13 of 55 (23.6%) cats had positive results for *T gondii* IgG or IgM. ‡Cats with WNV titers ≥ 10 were subsequently tested for SLEV.

nificantly ($P = 0.03$) more dogs in the guarding group had antibodies against any flavivirus than did dogs in the other breed groups.

Seroreactivity for WNV, a flavivirus, was highly correlated with the variable any flavivirus and therefore was not included in the multivariate regression model. Circulating DNA of *W pipiens* also was not included in this model because of its significant correlation with *D immitis* infection. Adult dogs infected with *D immitis* were more than twice as likely to have antibodies against *T gondii* (OR, 2.16; 95% CI, 1.32 to 3.54) than were dogs without *D immitis* infection. Adult dogs infected with *D immitis* were also more than twice as likely to have antibodies against WNV (OR, 2.53; 95% CI, 1.67 to 3.84) and > 3 times as likely to have antibodies for any flavivirus (OR, 3.59; 95% CI, 2.23 to 5.77). The expected association of *D immitis* with *W pipiens* was reflected in *D immitis*–infected dogs, which were > 40 times as likely to have detectable circulating DNA for the endosymbiont (OR, 43.41; 95% CI, 13.28 to 141.93). In multivariate analysis, *D immitis*–infected dogs remained nearly twice as likely to have antibodies against *T gondii* (OR, 1.91; 95% CI, 1.13 to 3.22) and > 3 times as likely to be concurrently infected with any flavivirus (OR, 3.55; 95% CI, 2.17 to 5.81).

Infectious diseases of cats—Prevalences of infectious agents in cats were calculated (**Table 3**). *Dirofilaria immitis* antigen was identified in 4 of 50 (8%) cats. None of these cats had circulating DNA of *W pipiens*.

Similar to the prevalence in dogs, 13 of 55 (23.6%) cats had IgM or IgG antibodies against *T gondii*. In addition, FeLV and FIV were detected in several cats, and seroreactivity for WNV was detected in approximately 1 in 10 cats, which was a much lower prevalence than was observed in dogs.

Prevalences of vector-borne hemotropic organisms in cats varied widely. Antibodies against *Bartonella* spp were detected in most cats, likely as a result of the high prevalence of fleas in the region. Whereas antibodies against *Bartonella* spp were detected in 48 of 55 (87.3%) cats tested, DNA of *Bartonella* spp was detected in only 11 of 47 (23.4%) cats tested. Of 11 cats with *Bartonella* spp DNA, 10 also had antibodies against *Bartonella* spp. Sequencing of PCR products revealed that all cats had *B henselae* and that 1 cat also had DNA of *B clarridgeiae*. When both antibodies and DNA were included, *Bartonella* spp were the most common agents identified in cats (49/55 [89.1%]). Approximately 1 in 10 cats had DNA of *Mycoplasma haemominutum*, which is considered minimally pathogenic, compared with the pathogenicity of *Mycoplasma haemofelis*; however, *M haemofelis* was not identified in any cats. No cats had evidence of infections with *Ehrlichia* spp–*Anaplasma* spp or *C felis*. Even though each cat was not tested for all infections, 19 of 53 (35.8%) cats had positive results (consistent with current infections) for tests to detect DNA or antigen of vector-borne infectious agents. Prevalence increased to 52 of 56 (92.9%) cats when serologic evidence of exposure to vector-borne infections was included. No associations were found between sex, age, or breed and any vector-borne infection.

Discussion

In the study reported here, most of the cats and dogs rescued and transferred from the Gulf Coast Hurricane Katrina disaster area had evidence of previous or current infection with 1 or more pathogens of animal or zoonotic importance.

Hurricane-force winds and flooding may initially decrease the risk of vector-borne infections via death or dispersal of vector and vertebrate reservoirs of infection, destruction of vector habitat, salinization, and reduction of vector food supplies. Conversely, postdisaster vector numbers and risk of disease transmission may increase as a result of standing water, disruption of vector control programs, increased outdoor activity of humans and other animals, and housing damage that permits intrusion of mosquitoes.[6,7] In the study reported here, most dogs, but not cats, had antibodies against WNV, a mosquito-borne arbovirus. Although the prevalence of WNV in dogs was extremely high, it is not possible to know whether dogs became infected before or after the hurricane because WNV is endemic in the Gulf Coast states. In other reports, seroprevalence of WNV in puppies in shelters in Houston

tested in 2005 peaked at 47% in August[8] and seroprevalence in feral cats in Florida tested in 2003 peaked at 65% in November.[k] In general, it appears that outbreaks of flaviviral disease in humans or other animals are not common after hurricanes, possibly because a large proportion of the population is already immune.[6,9,10]

Approximately half of the dogs and a smaller proportion of cats in this study had heartworm infection. Heartworm antigen tests do not detect infection until 5 to 7 months after exposure, so these animals were infected prior to Hurricane Katrina. This prevalence is consistent with reports[11,12] of a prevalence between 45% and 50% in dogs of the Gulf Coast region and 67% in dogs rescued following Hurricane Floyd in North Carolina in 1999. All heartworms harbor the bacterial endosymbiont *W pipiens*,[13] but circulating bacterial DNA was detected in less than half of heartworm-infected dogs and none of the heartworm-infected cats. *Wolbachia* bacteria are found in highest numbers in circulating microfilariae, and it is likely that the use of heartworm preventive medication with microfilaricidal activity in rescue shelters reduced microfilaremia and subsequent detection of the endosymbiont in dogs. Cats rarely have circulating microfilaria when infected with heartworms, even when they do not receive heartworm preventive medication.[14] *Wolbachia pipiens* was identified in 3 dogs that lacked detectable heartworm antigen, which is consistent with occult or subadult heartworm infections in which *D immitis* shed insufficient circulating antigens to allow detection.

The high prevalence of heartworm infection created a risk for transmission to other dogs intensively housed in the rescue shelters after the hurricane and in receiving communities where heartworm preventive medication was not commonly used. Guidelines developed jointly by the Koret Shelter Medicine Program and the American Heartworm Society for efficient prevention and treatment of rescued dogs included routine chemoprophylaxis for all rescued dogs regardless of test results,[15] but the amount of compliance with this recommendation is unknown. Compliance would protect uninfected dogs and lessen the risk posed by infected dogs by reducing the number of circulating microfilariae. It is recognized that rapid treatment with microfilaricides is associated with adverse reactions in some dogs. A strategy to reduce the risk of reactions while providing a moderately rapid clearance of microfilaremia includes administration of 2 heartworm-preventive doses of ivermectin (6 µg/kg, PO, q 14 d), which is followed 2 weeks later by administration of a microfilaricidal dose of ivermectin (50 µg/kg, PO).[14]

The prevalence of seropositivity for *T gondii* was similar in dogs and cats. The increased risk for having antibodies against *T gondii* and flaviviruses in heartworm-infected dogs revealed that this population of dogs was at increased risk of developing multiple infections from mosquitoes as well as from the environment. Although all warm-blooded species may be infected with *T gondii*, only felids shed infective oocysts in the feces. Shedding is usually limited to the first few weeks after infection. Infection is most commonly acquired in all species by consumption of contaminated meat, prey, or sporulated oocysts in cat feces. Following a disaster, another source of infection may be scavenging of carcasses of infected wildlife and domestic animals that perished in the event. Wild and domestic felids have been implicated in oocyst contamination of drinking water reservoirs and coastal marine waters, which could lead to infections of humans and marine mammals, particularly if potable water supplies are disrupted.[16–18] Flooding, estuary disruption, and animal migration induced by disasters might increase contamination of water with oocysts.

Most of the cats and dogs in the study reported here had evidence of exposure to vector-borne infections. Although the prevalences observed in this study were typical for animals in the Gulf Coast region,[2,8,12,19–23] all of the animals tested in the study were transferred from the disaster region to other states. This raises concerns about the spread of infectious diseases and their arthropod vectors to regions where they do not currently exist. For these infections to spread and to become endemic, there must be a combination of circumstances, including the simultaneous presence of appropriate vectors, adequate numbers of intermediate hosts, and favorable climatic conditions.[24] The phenomenon of global climate change has been implicated in the spread of vector-borne and emerging diseases in humans and other animals.[25–28] Impacts on historical disease ranges may be facilitated by the dispersal of rescued animals and also by the transportation of pets that accompany owners who relocate to other regions. It was estimated that 2 million people were displaced from the region by the hurricane, and many of them likely took their pets with them.[29]

Furthermore, the rescue networks that were established following Hurricane Katrina have continued to transfer surplus animals, particularly dogs, from southern states to the Northeastern United States and Canada. This ongoing translocation of dogs between jurisdictions, often without veterinary input or health certification, poses a continued risk of disease translocation. Particular concern has been expressed regarding the role of rescued dogs in accelerating the spread of *D immitis* infection in northern regions.

The impact of massive disasters on animals and their owners has been described in several reports.[11,30–34] Owners who are unprepared to evacuate with their pets may refuse to leave their homes, putting their pets, themselves, and rescuers in peril. In response to the large numbers of abandoned cats and dogs killed by Hurricane Katrina and the refusal of stranded residents to abandon their pets, the federal Pets Evacuation and Transportation Standards (ie, PETS) Act was passed in 2006. That act requires disaster planners to include provisions to evacuate and shelter both residents and their pets. Veterinarians and animal control managers are expected to provide consultation during planning for pet-friendly shelters and to participate in disaster responses when animals are involved.[35–39]

The finding that approximately half of the adult dogs were infected with heartworms suggests that many shelter animals arrived without receiving adequate preventive health care in the past. In such an environment, the risks of outbreaks of infectious diseases are high.

As shelter populations swelled in the weeks after Hurricane Katrina, guidelines for the care of shelter

animals and control of infectious diseases were developed by the American Heartworm Society,[15] the Koret Shelter Medicine Program,[15,40] the AVMA,[41,42] and the CDC.[41,42] Guidelines called for triage examination of all animals at time of entry to a shelter with separation of populations on the basis of date of arrival, species, age, disease status (particularly those with diarrhea or respiratory tract disease), and temperament. Vaccines (feline panleukopenia, feline herpesvirus-1, and calicivirus for cats and distemper virus, canine adenovirus-2, *Leptospira interrogans*, parvovirus, parainfluenza virus, and *Bordetella bronchiseptica* for dogs) were recommended for all animals > 4 weeks old at time of entry to a shelter. Although vaccination often requires administration of booster vaccines and several weeks for the development of an optimal response, protection against the most deadly viral infections (panleukopenia virus, parvovirus, and distemper virus) begins to develop within hours after vaccination when modified-live virus or canarypox-vectored vaccines are used.[43,44] Rabies vaccinations were recommended for all cats and dogs 12 weeks old and older. It was recommended that all cats and dogs be empirically treated with fenbendazole for gastrointestinal parasitism and with products effective against fleas, ticks, and heartworms as appropriate. Personal protective equipment (gloves, gowns, masks, and goggles) and frequent hand washing were also recommended to protect staff. Staff who have contact with animals should be vaccinated against rabies.[42,45]

For the study reported here, there were multiple infectious diseases in cats and dogs rescued and transferred from the Gulf Coast Hurricane Katrina disaster region in 2005. Although this represented a condition present in many animals prior to the hurricane, the dispersal of infected animals to other regions of North America where the infections were not typically found could have contributed to the development of new geographic ranges for these organisms or to underdiagnosis in affected animals because of a low index of suspicion in regions with low disease prevalence.

a. DiroCHEK heartworm antigen test kit, Synbiotics Corp, San Diego, Calif.
b. SNAP 3Dx test, IDEXX Laboratories, Westbrook, Me.
c. Center for Companion Animal Studies, College of Veterinary Medicine, Colorado State University, Fort Collins, Colo.
d. Department of Small Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, Fla.
e. New York State Animal Health Diagnostic Center, College of Veterinary Medicine, Cornell University, Ithaca, NY.
f. Vector Borne Disease Diagnostic Laboratory, College of Veterinary Medicine, North Carolina State University, Raleigh, NC.
g. SNAP Combo FeLV antigen/FIV antibody test, IDEXX Laboratories, Westbrook, Me.
h. Excel 2003 SP2, Microsoft Corp, Redmond, Wash.
i. Epi Info 2002, revision 1, CDC, Atlanta, Ga.
j. SPSS, release 11.5.0, SPSS Inc, Chicago, Ill.
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Correction: Effect of ammonium chloride supplementation on urine pH and urinary fractional excretion of electrolytes in goats

In the article "Effect of ammonium chloride supplementation on urine pH and urinary fractional excretion of electrolytes in goats" (*J Am Vet Med Assoc* 2010;237:1299–1304), the reference for the statement in the right-hand column on page 1300, "Goats were anesthetized and positioned in dorsal recumbency, and a Foley[d] catheter was surgically placed into the bladder as described,[7]" is incorrect. The correct reference is reference 9.