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Research Paper

Factors Affecting the Geographic Distribution of West Nile Virus in Georgia, USA: 2002–2004

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ABSTRACT

The distribution of West Nile virus (WNV) is dependent on the occurrence of both susceptible avian reservoir hosts and competent mosquito vectors. Both factors can be influenced by geographic variables such as land use/landcover, elevation, human population density, physiographic region, and temperature. The current study uses geographic information systems (GIS) and logistic regression analyses to model the distribution of WNV in the state of Georgia based on a wild bird indicator system, and to identify human and environmental predictor variables that are important in the determination of WNV distribution. A database for Georgia was constructed that included (1) location points of all the avian samples tested for WNV, (2) local land use classifications, including temperature, physiographic divisions, land use/landcover, and elevation, (3) human demographic data from the U.S. Census, and (4) statistics summarizing land cover, elevation, and climate within a 1-km-radius landscape around each sample point. Logistic regression analysis was carried out using the serostatus of avian collection sites as the dependent variable. Temperature, housing density, urban/suburban land use, and mountain physiographic region were important variables in predicting the distribution of WNV in the state of Georgia. While weak, the positive correlation between WNV-antibody positive sites and the urban/suburban environment was consistent throughout the study period. The risks associated with WNV endemicity appear to be increased in urban/suburban areas and decreased in the mountainous region of the state. This information may be used in addressing regional public health needs and mosquito control programs. Key Words: West Nile virus—Avian—Risk—Land use—Physiographic region—Geographic information systems. Vector-Borne Zoonotic Dis. 6, 73–82.

INTRODUCTION

West Nile virus (*Flaviridae*, *Flavivirus*; WNV) is a vector-borne pathogen of global importance. The geographic range of this virus has expanded since its discovery in Uganda in 1937 (Smithburn et al. 1940) and now includes Africa, Asia, Europe, North America, Central and South America, and the Caribbean (McIntosh et al. 1968, Hubalek and Halzouka 1999, Malkinson and Banet 2002, Steele et al. 2000, OIE 2004, Cruz et al. 2005, Mattar et al. 2005, Quirin et al. 2004). The distribution of WNV is dependent on the occurrence of susceptible avian reservoir hosts and competent mosquito vectors, mosquito host preference, and availability of hosts. These factors can be influenced by geographic variables such as land use/landcover, elevation, human population density, physiographic region, and temperature.

The potential influence of environmental and social factors on WNV transmission has been

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of great interest since the discovery of the virus. Taylor et al. (1956) noted differences in WNV seroprevalence between study zones along the Nile River Delta in human and hooded crow (*Corvus corone sardonius*) samples. While climatic and geologic features in these areas were not markedly different, there were significant differences in human population density and land use patterns. The increased mosquito breeding habitat and improved farmland created by irrigation in the Nile River Delta was also cited as one of the most important manmade modifications to the environment influencing the transmission of WNV (Hayes 1989).

In a more recent study, spatial analysis of WNV case distribution in the New York City area in 1999 revealed that vegetation abundance was significantly and positively associated with human WNV cases (Brownstein et al. 2002). This association was used to predict areas of greatest human risk for WNV infection; the model constructed in the study showed that the less populated suburban regions were at greatest risk. A study in the Chicago area found that risk factors associated with clusters of human cases and dead birds included vegetation, age, income, race, distance to reported WNV positive dead birds, age of housing, mosquito control activities, and geological factors (Ruiz et al. 2004). Mosquito abatement activities accounted for approximately 53% of the variation between clusters in that study. In Florida, spatial and temporal differences in periods of drought and rain were associated with variability in human WNV cases and infection of sentinel chickens (Shaman et al. 2005). The authors suggested that close proximity of birds and mosquito vectors during times of drought are responsible for increased virus transmission.

Spatial analyses have also have been applied to the surveillance data associated with dead bird submissions. Using geographic information systems (GIS), dead bird data was shown to be an effective indicator of WNV amplification and could be used to predict potential areas of high human risk at least 13 days prior to the onset of human illness in those areas (Theophilides et al. 2003). Another study applied a spatial scan statistic to detect small-area clustering of dead birds (Mostashari et al. 2003). This information was used to predict areas of active virus transmission and served as a basis on which to target mosquito surveillance activities. In a retrospective study conducted on dead crow report data from Chicago in 2002, spatial analysis of the data showed that human cases were three times more likely to occur in areas of high early-season crow deaths (Watson et al. 2004).

Environmental conditions affecting both avian reservoir hosts and the mosquito vector populations may regulate WNV amplification. Identifying such factors will not only aid in understanding WNV epidemiology, but also will serve in predicting and possibly reducing the risk of WNV infection. In a recent study (Gibbs et al. 2006), wild birds were used as fine scale indicators of WNV transmission over the physiographic and land use variation present in Georgia. The current study builds on this work by examining these data using GIS and logistic regression analyses to predict the distribution of WNV in the state of Georgia based on a wild bird indicator system, and to identify human and environmental predictor variables that are important in the determination of WNV distribution.

METHODS

West Nile virus database construction

The serologic database used for the current study was derived from previous work in which avian serum samples (n = 10,865) from 70 species of birds captured throughout Georgia at approximately 200 sampling locations during the summers of 2002–2004 were tested by plaque reduction neutralization test (PRNT) for antibodies to WNV and St. Louis encephalitis virus (SLE) (Gibbs et al., 2006). Antibodies to WNV were detected in 850 (7.8%) of these samples.

A database for Georgia was constructed that included (1) location points of all the avian samples tested for WNV, (2) local land use classifications including temperature, physiographic divisions, land use/landcover, and el-

evation, (3) human demographic data, and (4) statistics summarizing land cover, elevation, and climate within a 1-km-radius landscape around each sample point. The GIS software packages used to develop the database, extract summary statistics, and create map displays were the Environmental Systems Research Institute (ESRI) ArcView 3.3 and ArcGIS 9 (ESRI, Redlands, CA). Data layers for each environmental factor were created as ArcView shapefiles in the Universal Transverse Mercator (UTM) grid coordinate system tied to the North American Datum (NAD) of 1983. The database comprised 3 years (May–October of 2002–2004) of avian samples collected within the state of Georgia and tested for antibodies to WNV by PRNT.

Coordinates of the sample points were recorded in the field with hand-held Garmin Global Positioning System (GPS; Garmin International Inc., Olathe, KS) units in the UTM coordinate system. The sampled data points were arbitrarily distributed based on sampling opportunities and located in the two UTM zones (16 and 17) that cover the state of Georgia. Buffers of 1 km around each sampled data point were created with the ArcGIS proximity function in Arc Toolbox. Land use and demographic data falling within this 1-km buffer zone was then included in the database.

If one or more birds at a collection site were positive for WNV antibodies, that site was classified as positive. Site status was used in the analysis rather than WNV antibody status of individual birds in an effort to avoid bias introduced by species differences in prevalence and geographic distribution (Gibbs et al. 2006).

Logistic regression

Explanatory variables. Explanatory variables used in logistic regression modeling included land use/land cover, physiographic region, elevation, minimum and maximum temperatures for January and February, and 2000 census data for the state of Georgia, which included human population per acre and per hectare, and housing density per acre and per hectare.

A landscape-level land use/landcover of Georgia dataset was created by the University of Georgia, Institute of Ecology, Natural Resources Spatial Analysis Laboratory and obtained from the Georgia GIS Clearinghouse (<www.gis.state.ga.us>). The Landsat Landcover (18 class) dataset, dated 1998, was produced from Landsat Thematic Mapper (TM) satellite imagery of 30-m spatial resolution. Based on the requirements of this project, we reduced the number of classes to five: urban-suburban, forest, agriculture, wetland, and other. This dataset was converted to an ArcView grid with a cell size of 30×30 m. A second dataset of local land use characteristics for each sampling site was created based on field observations recorded during avian sample collection; this provided a finer scale assessment of land use than was available using the Landsat Landcover dataset.

The physiographic divisions dataset was derived from the U.S. Geological Survey (USGS) "Physiographic Provinces" ESRI Export File (e00), dated 1992 and based on a 1:7,000,000-scale map. These data were obtained from the Georgia GIS Clearinghouse. Physiographic divisions are areas having similar topography, rock types, geology, and geomorphic history as defined by USGS. The original data in the Lambert Conic Conformal coordinate system were reprojected to the UTM coordinate system, NAD 83. We used four major physiographic divisions: mountains, piedmont, coastal plain, and coastal. These data were also converted to an ArcView grid with a cell size of 30×30 m.

The source for the elevation dataset was the USGS 1:24,000 scale National Elevation Dataset (NED), dated 1999. The resolution for this data set was 30×30 m. Data were obtained from the Georgia GIS Clearinghouse. The file format was ERDAS Imagine (.img) in a geographical projection (latitude and longitude). The data were converted to an ArcView grid file and reprojected to the UTM coordinate system, NAD83.

The source for temperature datasets of monthly mean maximum and minimum temperature for January and February was acquired from the National Climatic Data Center (NCDC;<www.ncdc.noaa.gov/oa/ncdc.html>. Data from the weather stations in nine Georgia

climatic divisions were combined with data from stations in 11 adjacent divisions of the neighboring states (totaling approximately 300 stations) in order to insure an accurate and complete spatial interpolation. A Kriging interpolation method was employed in ArcView to create a continuous surface of temperature data for the study area. The resulting triangulated irregular networks (TINs) of temperatures covering the state of Georgia were created for January and February of 2002, 2003, and 2004. The TINs were subsequently converted to GRID format for spatial analysis in ArcView. Grids for temperature were created with a cell size of 100 × 100 m. Four grids were created for each year—January mean minimum temperature, January mean maximum temperature, February mean minimum temperature, and February mean maximum temperature.

Housing density was computed using U.S. Census data from 2000. Block-level data for the state of Georgia was queried from the CensusCD 2000/Short Form Blocks dataset (GeoLytics, Inc., East Brunswick, NJ). Census blocks are the smallest spatial units at which census data is released, and their sizes vary depending on population density. They can be as small as a city block in urban areas, or as large as 400 acres in rural areas. The total count of housing units within each census block was normalized by the acreage of each block to generate housing density.

An overlay analysis function in ArcView, clip, was used to extract the grid data cells of environmental factors within each 1-km-radius buffer area surrounding the sample points. The ArcView Map Calculator function was then used to extract and summarize the average values of environmental factors within a 1-km buffer area surrounding each sample data point. Mean maximum and minimum temperature for January and February, physiographic divisions, land use/landcover, and elevation were thus summarized. Data for temperature and elevation were summarized as a weighted mean for each buffer area, while land use/landcover and physiographic divisions were calculated as the percent area covered by each class in the buffer area. Housing density was obtained from the census block within which each sample point fell. Categorical variables, including physiographic region and local land use, were each coded as a set of (0, 1) dummy variables corresponding to each physiographic region or land use class.

Statistical analysis

Logistic regression analysis was carried out using S-Plus 6.1 (Insightful Corporation, Seattle, WA) using the serostatus of avian collection sites as the dependent variable. A forward stepwise procedure with a $p < 0.05$ was used to determine which environmental variables maximized the fit of the statistical model based on our data. Accuracy (percent of testing sites correctly classified), sensitivity (percent of positive testing sites correctly classified), and specificity (percent of negative testing sites correctly classified) were computed for the model. Also, the area under the receiver operating characteristic curve (AUC ROC) and the max rescaled R^2 were calculated as indices of the fit of the model (Fielding and Bell 1997, Nagelkerke 1991).

RESULTS

Avian samples were collected at sites within 151 counties of the state of Georgia (Fig. 1). The sampling sites were distributed throughout all land use types and physiographic regions present in the state. Background data for the avian samples on which the site data were based are shown in Table 1.

For the 2002 data, four variables were significantly related to WNV serostatus (Table 2). The probability of WNV being present in an area increased with field-observed urban-suburban land use and minimum January temperature. A unimodal response to the natural logarithm of housing density was observed, and the second-degree polynomial term was included in the final model. The probability of a site being WNV positive was highest at densities of approximately one housing unit per 10 acres, and was lower both in more rural areas (<1 housing unit per 10 acres) and in more heavily populated areas (>1 housing unit per 10 acres). The 2003 model included only the field observed urban-suburban land use vari-

able, which was positively associated with WNV presence. In the 2004 model, the probability of WNV positive sites was lower in the mountains than in other physiographic regions. As with the 2002 model, the second-degree polynomial term for the natural logarithm of housing density indicated that the probability of a site containing WNV seropositive birds was highest at intermediate housing densities of approximately one housing unit per 10 acres.

The accuracy, sensitivity, specificity, maximum rescaled R^2, and area under the receiver operating characteristic curve (AUC ROC) of the 2002 model were much greater than in the 2003 and 2004 models (Table 3).

The serologic status of collection sites that were sampled in more than one year are listed in Table 4. Approximately half of the sites which were initially negative changed status to positive upon re-sampling. Few sites initially found positive changed to a negative status.

DISCUSSION

The results of this study illustrate the widespread distribution of WNV in the state of Georgia in just three years after introduction. Antibodies against WNV were found for each sample year in both adult and hatch year birds, indicating that the virus was able to over-winter and become endemic in the state (Gibbs et al. 2006). This finding was supported by dead bird and mosquito surveillance data (SCWDS, unpublished data). As demonstrated by the poor accuracy of the logistic regression models in the last two years of the study, environmental and demographic variables became less

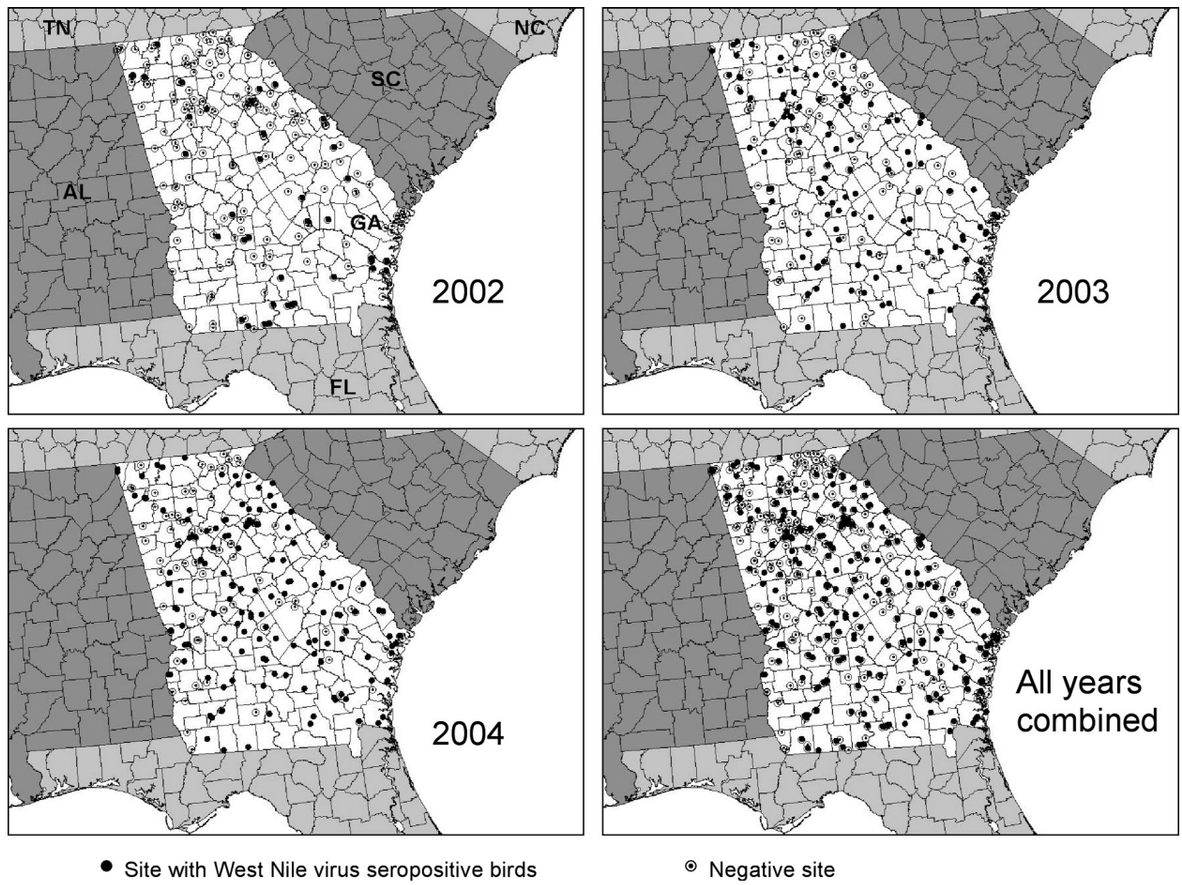

FIG. 1. Distribution of West Nile virus antibody positive and negative sites in the state of Georgia for 2002–2004.

Table 1. West Nile Virus Antibody Prevalence in Avian Samples by Site

	No. sites	*Avg. number of birds sampled per site (range)*	*No. sites positive (% pos.)*
2002			
Land use			
Ag	63	15 (1–71)	13 (20.6)
F	41	10 (1–56)	8 (19.5)
U/S	63	14 (1–165)	15 (23.8)
W	11	14 (1–37)	1 (9.0)
Phys region			
C	16	14 (1–37)	2 (12.5)
CP	74	18 (1–56)	24 (32.4)
M	32	9 (1–74)	3 (9.4)
P	56	17 (1–288)	8 (14.3)
2003			
Land use			
Ag	74	21 (2–72)	38 (51.4)
F	56	16 (1–65)	27 (48.2)
U/S	79	16 (1–137)	49 (62.0)
W	6	16 (4–28)	2 (33.3)
Phys region			
C	21	14 (3–32)	9 (42.9)
CP	83	20 (1–53)	49 (59.0)
M	43	13 (2–65)	19 (44.2)
P	68	18 (1–137)	39 (57.4)
2004			
Land use			
Ag	43	23 (2–47)	32 (74.4)
F	56	19 (2–83)	35 (62.5)
U/S	112	17 (1–139)	70 (62.5)
W	11	17 (5–41)	2 (18.2)
Phys region			
C	16	16 (4–30)	10 (62.5)
CP	91	18 (1–53)	64 (70.3)
M	29	16 (1–37)	13 (44.8)
P	86	21 (1–139)	51 (60.0)

Ag, agriculture; F, forest; U/S, urban/suburban; W, wetland; C, coastal; CP, coastal plain; M, mountain; P, piedmont; Phys region, physiographic region; No., number; Avg., average; pos., positive.

important in determining the distribution of the virus as time progressed. This is consistent with logistic regression findings based on data from individual avian samples in which the local land use variable was less important in the 2003 than 2002 model, and was not included at all in the 2004 model (Gibbs et al. 2006).

The thorough coverage of WNV across the Georgia landscape was most likely facilitated by the presence of several competent vectors. *Culex quinquefasciatus*, the primary vector in the state, as well as *Cx. nigripalpus*, *Cx. restauns*, and *Cx. salinarius*, each include Georgia in their distributions (Darsie and Ward 2005). The different behavioral characteristics of these mosquitoes, including host and habitat preference, allow for transmission in a diversity of environments. *Cx. quinquefasciatus* may be found in abundance in human modified habitats such as residential areas (Reisen 1992). Such modifications include creation of mosquito habitat in flower pots, used tires, flooded basements, sewage treatment areas, and water-catchment basins in housing developments. There are few areas within the state of Georgia that are not heavily impacted by human activities.

Sites testing positive for WNV antibodies in 2002 may represent the areas to which WNV was first introduced in 2001. Serologic data from 2002 revealed two loose foci of positive sites, one in the coastal plain and one in the metro Atlanta area (Gibbs et al. 2006). A similar spatial distribution was also observed in dead bird surveillance data from 2001 (Gibbs et

TABLE 2. LOGISTIC REGRESSION MODELS FOR PREDICTING THE DISTRIBUTION OF WEST NILE VIRUS IN THE STATE OF GEORGIA BASED ON A WILD BIRD INDICATOR SYSTEM

Year	*Variable*	*Coefficient*	*Wald statistic*	p
2002	Minimum January temperature	0.02	3.31	0.0009
	log(housing/hectare + 0.01)	−1.62	−3.28	0.0010
	[log(housing/hectare + 0.01)]^2	−0.30	−3.11	0.0019
	Urban-suburban land use based on field observation	1.74	3.25	0.0012
2003	Urban-suburban land use based on field observation	0.61	2.11	0.0350
2004	Mountain physiographic region	−0.01	−2.72	0.0066
	log(housing/hectare + 0.01)	−0.21	−1.56	0.1190
	[log(housing/hectare + 0.01)]^2	−0.09	−2.29	0.0223

al. 2006). In the following transmission seasons, the range of the virus might have then extended through local bird movements rather than being reintroduced by migratory species. The effects of the land use and physiographic region on site serologic status during 2002 may have been enhanced due to a more localized distribution associated with initial introduction. The early distribution may also reflect the importance of microhabitat rather than broader habitat patterns within the 1-km-radius area surrounding the capture site in determining avian WNV exposure. It may also be that mosquito breeding habitat is locally important and could, in future, be added as a local variable.

Most collection sites were chosen for the presence of a factor which concentrated bird populations, thus increasing sample size. Many of these included sites with bird feeders. The practice of capturing birds around feeders and taking advantage of nuisance bird removal programs may have influenced distribution data.

TABLE 3. COMPARISON OF THREE MODELS CONSTRUCTED FOR PREDICTING DISTRIBUTION OF WEST NILE VIRUS IN THE STATE OF GEORGIA BASED ON A WILD BIRD INDICATOR SYSTEM

Analysis[a]	*2002*	*2003*	*2004*
Accuracy (%)	83.1	55.6	64.9
Sensitivity (%)	76.9	64.6	65.8
Specificity (%)	83.6	50.4	58.6
Maximum rescaled R^2	0.239	0.028	0.072
AUC ROC	0.751	0.57	0.622

[a]A sampling site was considered positive if ≥1 bird tested positive for West Nile Virus antibodies by plaque reduction neutralization test (PRNT).

AUC ROC, area under the receiver operating characteristic curve.

The overall fit of the 2004 model was better than the 2003 model, but neither predicted the presence of WNV as accurately as the 2002 model. Housing density was a strong predictor of WNV presence in 2002, with higher numbers of positive sites situated in areas with intermediate housing densities. While not as strongly correlated with WNV positive sites as it was in 2002, the housing density was also included in the model for 2004. Together with the inclusion of urban-suburban land use data (based on field observation) in 2003, this information supports the contention that human activities in the urban/suburban landscape provide reservoir host and vector habitats suitable for efficient WNV transmission.

While weak, the positive correlation between WNV antibody positive sites and the urban/suburban environment was consistent throughout the study period. The human impact on disease ecology has been studied intensively as humans continue to expand and modify their environment. In an assessment of emerging pathogens of wildlife in North America between 1998 and 2000, the majority of outbreaks were linked to human activities (Dobson and Foufopoulos 2001). As demonstrated by a number of arboviruses, disease emergence is most often related to human activities that increase disease vector habitats or change the density of nonhuman vertebrates involved in virus amplification (birds in the case of WNV) (Shope 1997, Mackenzie et al. 2004, Anonymous 1994). Urbanization and deforestation have been linked to emergence of arboviruses such as Rift Valley fever, SLE, and dengue (Wilson 1994). De-

TABLE 4. WEST NILE VIRUS SEROLOGIC STATUS OF COLLECTION SITES WHICH WERE SAMPLED DURING MORE THAN ONE TRANSMISSION SEASON

		Site status				
Years	*No. sites re-sampled*	*Negative to negative*	*Positive to positive*	*Negative to positive*	*Positive to negative*	*Variable*
2002–2003	64	21	13	22	8	—
2003–2004	81	14	43	11	8	—
2002–2004	35	10	7	17	1	—
2002–2003–2004	27	3	6	12	1	5[a]

[a]Variable: negative to positive to negative, or positive to negative to positive.
No., number.

spite an abundance of review literature on the topic, minimal data are available to confirm the impact of human activities on disease epidemiology (Kuiken et al. 2003). The current study provides some of these data, as well as insight into the potential of a human altered environment, specifically the urban/suburban environment, to support vector borne disease. Human activities not only support mosquito populations, but also provide food, nesting, and roosting habitat for both native and introduced birds.

The importance of minimum January temperature in the 2002 model probably reflects the dependence of WNV transmission on mosquito vectors. In future studies, examination of year-round data might help to further explain maintenance of WNV in an area from year to year. A variable for surface water was not included in this analysis as the primary mosquito species involved in WNV transmission in Georgia tend not to use large bodies of water (rivers and lakes) for breeding. The ephemeral water sources which generally serve as breeding sites for these species would not be accurately represented by the 1998 landcover dataset used in this study. The inclusion of mountain physiographic region in the 2004 model also emphasizes the importance of elevation, temperature, and physiographic region in WNV epidemiology. These three variables are interrelated in Georgia, and in combination appear to limit the transmission of WNV. Reasons for this limitation probably relate to lower temperatures in mountainous regions, consequent decreases in mosquito abundance, and differences in avian species composition.

The changing serologic status of re-sampled sites in this study agrees with antibody prevalence data obtained from individual birds in this dataset (Gibbs et al. 2006); antibody prevalence for all species increased from 5.2% to 7.3% to 10.1% in 2002, 2003, and 2004, respectively. The consistent rise in seroprevalence between years reflects the increasing geographic distribution of WNV taking place during the study. Approximately 30% of the sites initially negative converted to positive sites, however, only 8.7% went from positive to negative. This is surprising considering the low prevalence and small sample size at some sites.

As demonstrated by this work, WNV is distributed throughout the state of Georgia. West Nile virus poses a health risk to humans, livestock, and wildlife in all physiographic regions and land use types; the challenge we experienced in developing a model with high sensitivity and specificity for the data set reflects this broad distribution. The data were grouped according to sampling site rather than by individual serum sample in an effort to decrease bias potentially introduced by differences in susceptibility and antibody formation in avian species. Sites where the results were based on only one species (such as the Canada goose collections) were removed from the spatial analysis to help address sampling bias.

Modeling based on site status (as used in this study) will also work in future studies; however, a targeted approach towards sites with good avian indicators (such as the northern cardinal) would be a better approach. Seroprevalence data from individual samples could then be included in the model, making it more ac-

curate in defining the influence environmental and demographic factors have on WNV distribution. The importance of these factors will most likely change as the environment becomes increasingly impacted by human population expansion.

The trends observed both in this study and work conducted on WNV antibody prevalence in avian species (Gibbs et al. 2006) suggest that the virus will continue to circulate in the environment at endemic levels. The risks associated with endemicity appear to be increased in urban/suburban areas and decreased in the mountainous region of the state. This information may be used in addressing regional public health needs and mosquito control programs; priority should be placed on campaigns aimed at decreasing man-made mosquito habitats in urban/suburban areas.

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