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RESEARCH ARTICLE

Using landscape epidemiological models to understand the distribution of chronic wasting disease in the Midwestern USA

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Abstract Animal movement across the landscape plays a critical role in the ecology of infectious wildlife diseases. Dispersing animals can spread pathogens between infected areas and naïve populations. While tracking free-ranging animals over the geographic scales relevant to landscape-level disease management is challenging, landscape features that influence gene flow among wildlife populations may also influence the contact rates and disease spread between populations. We used spatial diffusion and barriers to white-tailed deer gene flow, identified through landscape genetics, to model the distribution of chronic wasting disease (CWD) in the infected region of southern Wisconsin and northern Illinois, USA. Our generalized linear model showed that risk of CWD infection declined exponentially with distance from current outbreaks, and inclusion of gene flow barriers dramatically improved fit and predictive power of the model. Our results indicate that CWD is spreading across the Midwestern landscape from these two endemic foci, but spread is strongly influenced by highways and rivers that also reduce deer gene flow. We used our model to plot a risk map, providing important information for CWD management by identifying likely routes of disease spread and providing a tool for prioritizing disease monitoring and containment efforts. The current analysis may serve as a framework for modeling future disease risk drawing on genetic information to investigate barriers to spread and extending management and monitoring beyond currently affected regions.

Keywords Epidemiological modeling · Chronic wasting disease · Illinois · Risk mapping · Wildlife disease · Wisconsin · White-tailed deer

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Introduction

Understanding the distribution and spatial dynamics of an emerging infectious disease is crucial to predicting geographic spread, revealing the history of infection, and developing management strategies (Smith et al. 2005; Meentemeyer et al. 2012). Spatial clustering of

disease can reveal the point of introduction, particularly in early stages of emergence (Brownstein et al. 2002; Hess et al. 2002). After successful introduction, the risk of infection and prevalence typically decline with distance from hotspots as a function of the time since disease introduction and diffusion rate (Gesler 1986; Ostfeld et al. 2005; Joly et al. 2006). However, landscape heterogeneity and spatial arrangement, as well as movement patterns of hosts add complexity to the process of disease spread (Langlois et al. 2001; Kauffman and Jules 2006; Meentemeyer et al. 2012). Landscape and environmental factors influence the density, arrangement, and availability of susceptible hosts, thereby influencing the probability of pathogen invasion (Collinge et al. 2005; Hosseini et al. 2006; Perez-Reche et al. 2012), pathogen viability (Breban et al. 2009), and other host–pathogen dynamics (Hess et al. 2002).

Because disease prevalence directly relates to the probability of disease exposure and transmission, the pattern of prevalence on the landscape is an important indicator of disease risk (McCallum et al. 2001; Ostfeld et al. 2005). When disease distribution is related to landscape factors, these can provide a powerful predictor of spread to naïve areas (McGinnis and Kerans 2012; Meentemeyer et al. 2012). Establishing links between landscape features and disease patterns is fundamental to the field of landscape epidemiology (Pavlovsky 1966; Galuzo 1975), which emphasizes spatial modeling and risk mapping to understand disease dynamics (Ostfeld et al. 2005; Riley 2007). Recent advances in the availability of geographic data, spatial analysis, and concern about emerging diseases have facilitated applications of landscape epidemiology to wildlife diseases (Smith et al. 2005; Hosseini et al. 2006; Chuang et al. 2012). For example, habitat structure and avian community composition influence prevalence of West Nile Virus (Ezenwa et al. 2007), and can be used in mapping the geographic risk of infection (Chuang et al. 2012). Landscape structure has been linked to movement of rodent hosts and prevalence of Hanta virus (Langlois et al. 2001). Models combining landscape epidemiology and genetics have also identified landscape characteristics that impact host movement and broad-scale spread of rabies (Smith et al. 2002; Russell et al. 2004; Real et al. 2005).

Landscape characteristics shape patterns of disease spread by directing movement patterns and contact rates among hosts (Hess et al. 2002; Riley 2007). Theoretical models (Barlow 1995; Cross et al. 2005), and field studies demonstrate the importance of animal dispersal in facilitating spread of rabies in raccoons (*Procyon lotor*) (Jenkins and Winkler 1987; Moore 1999; Cullingham et al. 2008) and bovine tuberculosis (Hickling 2002; Gilbert et al. 2005; Ramsey and Efford 2010). Dispersing animals are also implicated in spreading chronic wasting disease (CWD) among cervid populations (Conner and Miller 2004; Miller and Conner 2005; Oyer et al. 2006). Despite the importance of contact between populations in epidemiological processes, determining the role of environmental characteristics and animal movement remain significant challenges within landscape epidemiology (Ostfeld et al. 2005). In many cases, disease research has benefited from the integration of landscape ecology and landscape genetics to reveal patterns of connectivity, barriers, and potential routes of disease spread between populations (Biek and Real 2010).

Here we used landscape genetics (Blanchong et al. 2008; Robinson et al. 2012) of white-tailed deer (*Odocoileus virginianus*) to understand the spread of CWD across the landscape of the Midwestern USA. CWD is a fatal neurodegenerative prion disease of North American cervids (Williams 2005) with significant implications for white-tailed deer management. In the Midwest, CWD was detected in 2001–2002 (Illinois Dept. Natural Resources 2003; Joly et al. 2003), and is now endemic in two distinct core areas, or disease foci, one in south-central Wisconsin (W_{CWD}) and one straddling the eastern Illinois–Wisconsin border (E_{CWD}) (Fig. 1). Previous research on CWD distribution has focused on the W_{CWD}, and has shown that prevalence was correlated with spatial, environmental and demographic factors (Joly et al. 2006; Blanchong et al. 2008; Osnas et al. 2009). These studies highlighted the potential importance of landscape heterogeneity in the distribution of CWD and the need to investigate disease spread beyond the W_{CWD}.

Our primary objective was to identify the landscape drivers shaping the distribution of CWD in the Midwestern USA. We describe CWD infection patterns for the W_{CWD} and the E_{CWD}, evaluate both local and landscape-scale factors affecting the spatial distribution of CWD, and develop a model of disease spread. We hypothesized that, in addition to the simple diffusion process, local habitat characteristics and barriers to deer dispersal would shape the distribution of disease. We constructed models of CWD

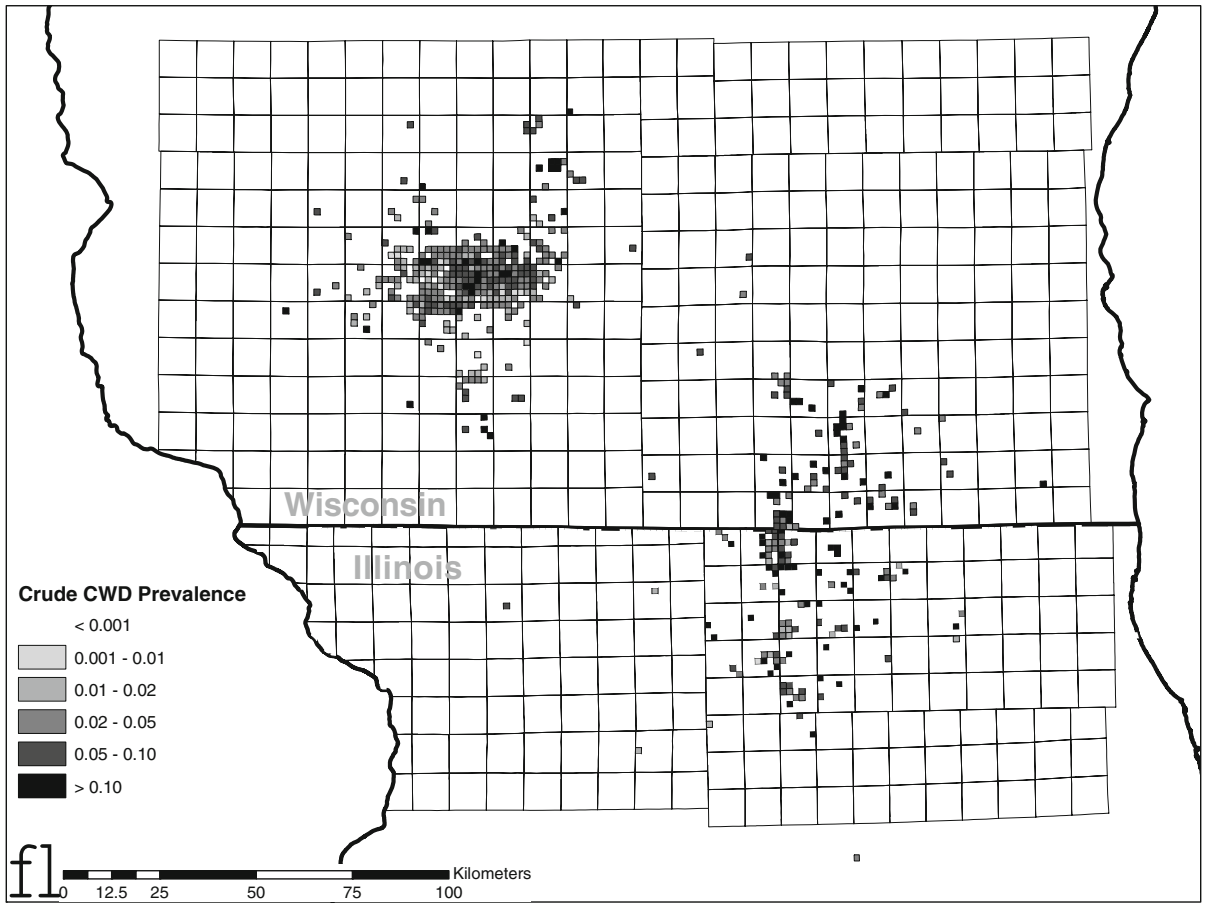

Fig. 1 A map of the CWD-affected area of Wisconsin and Illinois, USA, indicating CWD cases and sample townships for landscape epidemiological modeling. Small squares show the prevalence (number positive/number tested) of CWD in each section (2.6 km^2), these data were summarized at the township level (93.2 km^2) for analysis. The grid of 498 townships was used for spatial analysis of CWD prevalence and predictive risk models based on CWD surveillance data from 2001 to 2007

prevalence incorporating distance from disease foci, local habitat characteristics, and landscape barriers to deer dispersal from previous landscape genetics studies (Blanchong et al. 2008; Robinson et al. 2012). We interpret results related to potential CWD risk, spread of disease, and surveillance to aid disease monitoring and management.

Methods

Study area and landscape data

Our research took place in the CWD management area of southern Wisconsin (27,500 km^2 in 15 counties) and northern Illinois, USA (15,000 km^2 in 6 counties) (Fig. 1). This landscape comprised 498 Public Land Survey System (PLSS) townships (9.6 × 9.6 km), which were the unit of study (grid cells). The area contained two distinct CWD outbreaks, and prevalence was similar in each (6.5 % in the E_{CWD} and 5.9 % in the W_{CWD}). This study landscape spans three ecoregions (ECOs), varying levels of urbanization, different land management regimes, and numerous potential corridors or barriers to animal movement. The ECOs (Fig. 2d) consist of the Western Coulee and Ridge (WCR) and Southwest Savanna (SWS) in the west and the Southeast Glacial Plains (EGP) in the east, with minor portions of the Great Lakes and Northern Sands (Omernik 1987). The WCR is characterized by rolling hills with extensive forest cover (about 40 % deciduous forest) and small agricultural fields (primarily corn and alfalfa). In the SWS, forest cover is limited to steeper slopes (above 10 %) with

the majority of land in agriculture or grassland. The EGP is a mix of agricultural and urban areas with forest fragments (about 10 %). All regions experience mild winters and deer were not seasonally migratory, as in more severe climates (Nelson 1995).

We based our epidemiological modeling on habitat characteristics and potential dispersal barriers previously shown to impact deer movement and CWD distribution (Long 2005; Joly et al. 2006; Blanchong et al. 2008; Robinson et al. 2012) (Fig. 2). We used three habitat variables to describe ecological features and habitats within townships. ECOs represented broad-scale ecological communities. Forest canopy cover (CAN), the percent of each township covered by deciduous forest canopy (National Land Cover Database; Fry et al. 2009), has been positively correlated with deer density and thus it may affect deer social structure and CWD transmission (Joly et al. 2006; Rolley 2007; Storm 2011), and has been shown to impact dispersal distance thus influencing contact rates between populations (Long 2005; Diefenbach et al. 2008). Soil clay content (CLAY) in each township was calculated as a weighted average of the percentage of clay in the top 10 cm of soil from each soil map unit (Natural Resources Conservation Service 2012). Clay soils have been identified as potential reservoirs for environmental transmission of CWD (Miller et al. 2004; Johnson et al. 2006; Schramm et al. 2006), and clay content has been correlated with CWD infection in mule deer (*O. hemionus*) (Walter et al. 2011). We also evaluated potential impediments to gene flow identified by landscape genetic studies (Blanchong et al. 2008; Robinson et al. 2012): interstate highways, US highways, and major rivers.

Landscape epidemiological model of CWD risk

Crude CWD prevalence in adult deer ($\geq$1.5 years) was summarized at the township level (number positive/number tested, between 2001 and 2007). Fawns were excluded due to their low probability of infection (Grear et al. 2006) and differential testing of fawns throughout the study region. Because CWD transmission dynamics in the Midwest depend on the prevalence of infected individuals in a population, prevalence provides the most informative measure of disease risk (Jennelle et al. submitted-a; Storm et al. 2013). We selected townships as the areal unit of study to ensure adequate sampling of CWD prevalence in each area. CWD status was determined by ELISA and confirmed by immunohistochemistry (by the WI Veterinary Diagnostic Laboratory or IL Dept. of Agriculture Animal Disease Laboratories, as described in Keane et al. 2008).

Fig. 2 Maps of the study area showing variables used in spatial genetic models for white-tailed deer in the Midwestern USA. Potential dispersal barriers include **a** INT = zones define by intervening interstate highways, 4–6 lane divided roads with high traffic, **b** HWY = zones define by intervening US highways, typically 2 lane with high traffic, **c** RIV = zones define by intervening rivers of class four or five water volume. Habitat features include **d** ECO = ecoregion classification, **e** CAN = % forest canopy, **f** CLAY = % clay content

We used the distance of each township from the center of the disease foci as a measure of CWD risk based on simple diffusion from the E_{CWD} (De) or W_{CWD} (Dw). We defined the center of each outbreak as the centroid of the township with the highest prevalence which corresponded with CWD hotspots identified based on spatial clustering of cases (Kulldorff and Nagarwalla 1995; Joly et al. 2006; Storm 2011). In a homogeneous landscape we expect a simple exponential decline in prevalence with distance from disease foci. However, because landscape heterogeneity can also impact disease spread, we tested the importance of environmental factors by evaluating models including landscape covariates.

We built a generalized linear model using the glm.nb routine in the MASS package within R (Venables and Ripley 2002) with the number of CWD cases per township as the response variable. We used a log link function with the number of CWD-tested deer as an offset to account for differential sampling (about 50 % of townships had <100 deer sampled while 5 % had over 1,000; average 234 samples/township) and to ensure our response variable was based on CWD prevalence. CWD prevalence was low and cases were rare across much of the study area and we observed spatial clustering of cases. Such spatial clustering is common in disease data (Shaw et al. 1998) and frequently leads to overdispersion (Alexander et al. 2000). We used a negative binomial model to account for overdispersed data; this provided greater flexibility to model the relationship between mean and variance, and allowing calculation of the Akaike Information Criterion (AIC) which would not

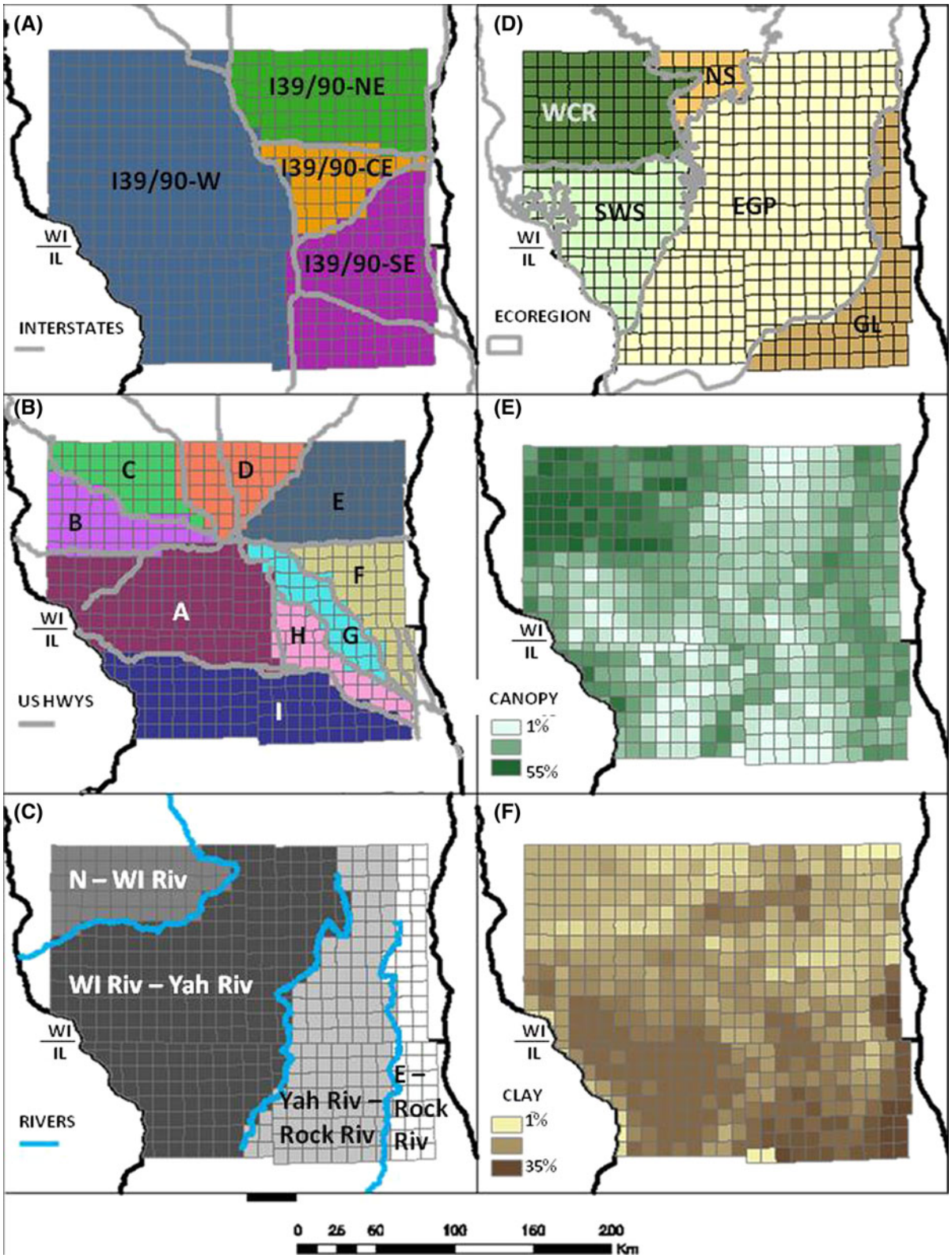
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Table 1 Alternative epidemiological models describing the distribution of CWD in Wisconsin and Illinois, USA

Alternative models	k	df*	ResDev	AICc	ΔAICc	AICc wt
De + Dw	2	495	209.240	811.066	119.608	0.000
Habitat only						
De + Dw + ECO	6	492	210.010	732.086	40.628	0.000
De + Dw + CAN	3	492	215.090	778.025	86.566	0.000
De + Dw + CLAY	3	487	222.440	812.040	120.581	0.000
De + Dw + ECO + CAN	***7***	***489***	***213.220***	***729.784***	***38.325***	***0.000***[a]
De + Dw + ECO + CLAY	7	484	220.650	734.056	42.597	0.000
De + Dw + CLAY + CAN	4	484	223.710	779.379	87.920	0.000
De + Dw + ECO + CAN + CLAY	8	481	222.200	731.792	40.334	0.000
Barrier only						
De + Dw + RIV	5	491	211.070	763.118	71.659	0.000
De + Dw + INT	5	494	212.520	764.951	73.492	0.000
De + Dw + HWY	10	487	209.420	753.337	61.879	0.000
De + Dw + RIV + INT	8	490	211.490	749.369	57.910	0.000
De + Dw + RIV + HWY	13	483	211.250	720.364	28.905	0.000
De + Dw + INT + HWY	13	486	212.290	721.883	30.425	0.000
De + Dw + RIV + INT + HWY	***16***	***482***	***211.180***	***713.197***	***21.738***	***0.000***[b]
Combined						
De + Dw + RIV + INT + HWY + ECO	20	477	221.140	694.573	3.114	0.137
De + Dw + RIV + INT + HWY + ECO + CAN	**21**	**476**	**221.210**	**691.459**	**0.000**	**0.649**
De + Dw + RIV + INT + HWY + ECO + CAN + CLAY	22	468	220.810	693.669	2.211	0.215

We select among alternative models including geographic distance, habitat features, and potential dispersal barrier based on ΔAICc and AICc weights (best overall model in bold, best models within subsets for habitat or barriers in bold italics). Number of parameters (k), degrees of freedom (df), and residual deviance (ResDev) are also reported. De and Dw denote distance in km from eastern and western disease foci respectively. Habitat variables include ECO = ecoregions, CAN = % forest canopy, CLAY = % soil clay content. Putative dispersal barriers include RIV = major rivers, INT = interstates, HWY = US highways. See Fig. 2 for additional information on habitat and dispersal barriers

* $n = 498$ townships, degrees of freedom may differ in the case of missing data for some variables

[a] AICc wt = 0.555 within Habitat Models

[b] AICc wt = 0.961 within Barrier Models

be possible with a quasi-Poisson model (Ver Hoef and Boveng 2007; Linden and Mantyniemi 2011).

Our model was:

$$\begin{aligned} &\#\text{CWD positives} \sim \text{NB}(\mu, \kappa) \\ &\text{Log}(\#\text{CWD positives}_i) = \beta_0 + \beta_i \text{X}_i \\ &\quad + \text{offset}\,(\log(\#\text{deer tested}_i)) + e \end{aligned} \tag{1}$$

where μ is the expected number of CWD cases, κ is the negative binomial shape parameter, β_0 represents CWD infection at the foci, and X_i is the covariate matrix for township i with β_i coefficients. The error parameter e is assumed to be independent with a negative binomial distribution. Because we used a log-linked model, $\exp(\beta_i)$ represents the relative CWD risk for each variable (relative risk, RR). We assessed model fit based on residual deviance and plots of model residuals. We selected the best model based on fit, parameter significance, ΔAICc and AICc weights (Burnham and Anderson 2002). Because disease distribution is inherently spatial, we also evaluated spatial autocorrelation in the model residuals (using the lm.morantest routine in the spdep package in R; Bivand et al. 2011).

We mapped predicted CWD prevalence in each township based on a model fit to 2001–2007 data. To validate model predictions, we compared model-predicted CWD cases to observed testing data from 2008 to 2011. For each township we calculated the difference between the model prediction and observed

Table 2 Estimated epidemiological model parameters describing the distribution of CWD in Wisconsin and Illinois, USA

Variable	Parameter	β_i Estimate	SE	Significant comparisons
Intercept	Intercept	0.090	1.679	
Distance	De	−0.056	0.008	***
	Dw	−0.035	0.007	***
Canopy (CAN)	CAN	0.033	0.013	**
Rivers	N-WI Riv	−2.328	1.539	
(RIV)	Yah Riv-Fox Riv	0.116	1.278	
	WI Riv-Yah Riv	−1.690	1.438	E-Rock Riv*
Interstates	I39/90-NE	−1.197	1.094	I39/90-W**
(INT)	I39/90-CE	1.617	0.709	I39/90-NE***
	I39/90-SE	1.727	0.651	
Ecoregions	GL	0.962	0.828	
(ECO)	NS	2.341	0.926	
	SWS	1.961	0.686	
	WCR	3.137	0.979	EGP**
Highways	B (18 W-14 W)	0.904	1.180	
(HWY)	C (14 W-12 W)	0.131	1.128	
	D (12 W-151E)	1.994	0.995	C (14 W-12 W)*
	E (151E-18E)	−0.544	1.038	D (12 W-151E)**
	F (18E-12E)	−1.785	0.871	
	G (12E-14E)	−0.623	0.695	F (18E-12E)*
	H (14E-20E)	−0.692	0.656	
	I (S of 20)	0.069	0.638	

We show the estimated parameter coefficients (β_i) with standard error for a negative binomial glm explaining the prevalence of CWD cases: De + Dw + RIV + INT + HWY + ECO + CAN. Significant Comparisons column shows only significant parameter effects, based on parameter coefficients for numerical variables or on z score comparison of adjacent zones for categorical variables: * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$. Refer to Fig. 2 for location of zone classifications for categorical variables

prevalence for 2008–2011, plotted observed versus expected prevalence, and used a one-sample *t* test to determine whether predicted values differed significantly from the observed prevalence based on standard error for each township.

Results

Landscape epidemiological model of CWD risk

Models incorporating barriers, habitat features, and distance outperformed alternative models (Table 1). The best model, De + Dw + RIV + INT + HWY + ECO + CAN, was well-supported by AICc (AICc weight 0.649, Table 1), and predictions were strongly correlated with the observed prevalence from 2001 to 2007 (r = 0.865). Null deviance for the model was 789.5 for 497 degrees of freedom (df). Residual deviance of 221 with 476 df indicated good model fit to the data with pseudo $R^2 = 72$ %. CWD risk declined with distance from W_{CWD} or E_{CWD}, and landscape features significantly impacted disease distribution (Table 2). The second best model included CLAY and was close in AICc, but the CLAY parameter was not significant ($\beta = 0.004$; 95 % CI −0.064012 to 0.072012, ΔAICc = 2.211, Table 1).

The predicted CWD prevalence map (Fig. 3) illustrated that disease risk did not diffuse evenly from foci. While proximity to either E_{CWD} or W_{CWD} were important risk factors, the regression coefficients differed significantly ($p = 0.008$), indicating more aggregation of risk around the W_{CWD} (RR = 0.966; 95 % CI 0.952–0.979) than the E_{CWD} (RR = 0.946; 95 % CI 0.931–0.960). Landscape features had strong impacts on the distribution of CWD compared to

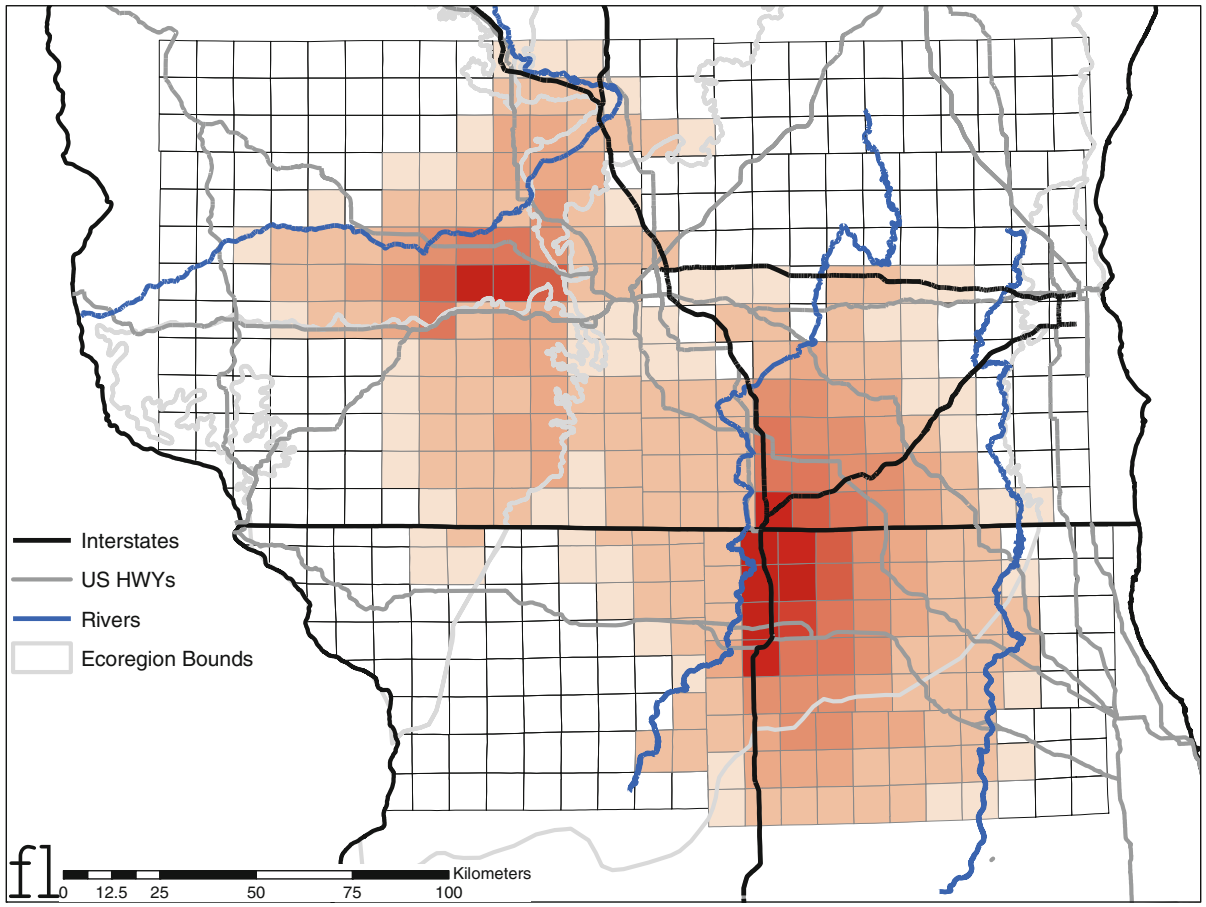

Fig. 3 Map of the predicted CWD risk across the disease management area of Wisconsin and Illinois, USA. Model based estimates of CWD risk are shown for each township within a grid covering the disease management zone of WI and IL. (Forest canopy cover was also a significant predictor in the model; however, forest shading is not shown to simplify the image.)

distance alone (Table 2; Fig. 3). For example, crossing the I39/90 interstate corridor (Fig. 2a) was equivalent to moving 45–50 km from a disease focus, and moving from the WCR to another ECO (Fig. 2d) was equivalent to moving 90 km from the W_{CWD} (based on ratios of coefficients). There was a small increase in CWD prevalence with each increase in percentage of forest CAN (RR = 1.033; 95 % CI 1.007–1.061).

Potential dispersal barriers also shaped the distribution of CWD on the landscape. In addition to the strong effect of interstate barriers (RR up to 5.624; 95 % CI 1.570–20.142, for regions east versus west of the I39/90: Fig. 2a), the Rock River was a marginally significant barrier ($p = 0.062$ comparing the E-Rock to WI Riv-Yah Riv zone, RR = 0.185; 95 % CI 0.011–3.091: Fig. 2c), perhaps acting as an additive impediment to the I39/90 corridor. US highways (Fig. 2b) were also important, particularly US 151(RR = 12.653; 95 % CI 1.801–88.899, separating zones A from B, and D from E) and US 12/18 (RR = 3.459; 95 % CI 0.627–9.076, separating zones C from D, and F from G) which appeared to influence the spread of disease from the W_{CWD}. While highway crossings typically decreased CWD prevalence more than distance, there was one anomaly near W_{CWD}; CWD prevalence was unexpectedly higher north of highway 12 W in zone C on Fig. 2b (RR = 7.343; 95 % CI 1.045–51.589). This finding suggests a secondary disease cluster became established in this area. This was the only case where prevalence was not well-described by distance and landscape features, demonstrating the rarity of disease clusters that indicate uncharacteristic dispersal or artificial movement events. The origin and characteristics of this cluster merits further research.

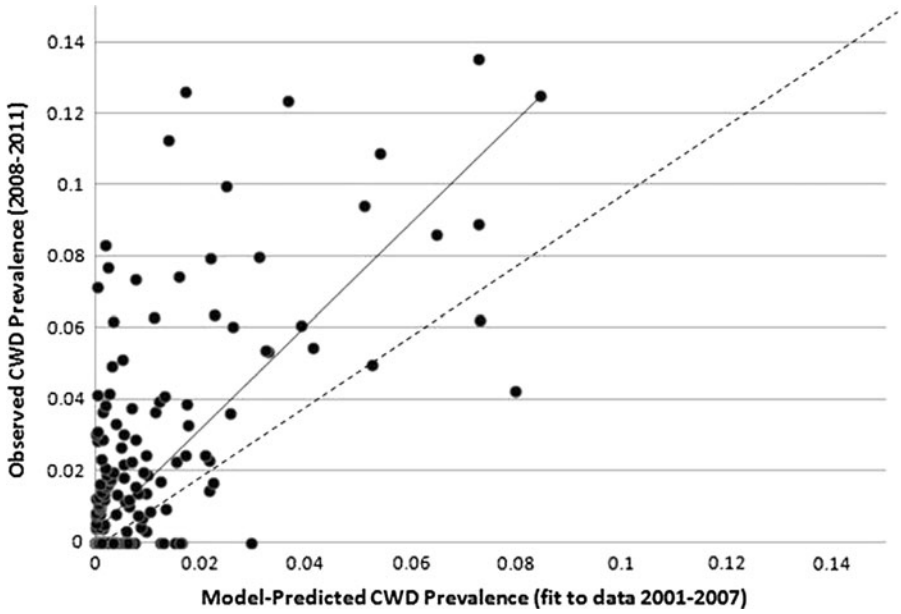

Fig. 4 The landscape epidemiological model fit to data from 2001 to 2007 provided strong correlation to observed CWD prevalence in surveillance samples from 2008 to 2011. Single-sample *t* tests showed significant differences in predicted and observed values for 17 % of townships where CWD occurred. The *dashed line* indicates a perfect relationship between predicted and observed values, the solid line shows the observed correlation of 0.595

Our model provided an informative prediction of 2008–2011 CWD patterns with a correlation of $r = 0.595$ between predicted and observed prevalence despite small sample sizes with high variability for the limited time frame (Fig. 4). Of 105 townships containing CWD cases, predicted prevalence was significantly higher than observed in 2 % and significantly lower than observed in 15 % of townships (p value <0.05 based on single sample t test) (Fig. 4). Most significant differences were detected in or adjacent to the focal townships in the W_{CWD} and E_{CWD} where disease prevalence has increased recently (Heisey et al. 2010; Jennelle et al. submitted-a).

Discussion

Landscape epidemiology of CWD in the Midwest

Across the CWD-affected area, disease prevalence was associated with distance from foci as well as township-scale habitat characteristics and broad-scale landscape features. These factors likely relate to epidemiological processes of disease diffusion, amplification of disease in local populations, and spread of disease to new areas. The spatial clustering of CWD has been noted in previous studies (Joly et al. 2006; Osnas et al. 2009), but evaluations of CWD distribution in the Midwest were limited to the W_{CWD} and noted the likely importance of long distance deer dispersal in spreading disease (Joly et al. 2006; Osnas et al. 2009). Our data strongly indicate that CWD has been spreading across the landscape from the W_{CWD} and E_{CWD} foci. Slow, but spreading movement of CWD has been noted in other mathematical models (Jennelle et al. submitted-a). While previous studies noted spatial autocorrelation indicating effects of unmeasured environmental heterogeneity or aggregation on disease patterns (Joly et al. 2006; Osnas et al. 2009), our landscape epidemiological modeling extends earlier studies, including both the W_{CWD} and E_{CWD} outbreaks, revealing the importance of each outbreak and the intervening landscape features in shaping the spread of disease risk to outlying areas.

Rather than incorporating spatial autocorrelation (as in Osnas et al. 2009), we explicitly consider both local habitat characteristics within each township and potential movement barriers between areas. The absence of residual spatial correlation in our model indicates we have accounted for ecological variables that are associated with patterns of spatial clustering. In particular, incorporating landscape barriers to gene flow helped understand the risk of CWD beyond current outbreaks. We found that the importance of deer habitat in CWD prevalence (as pointed out in Joly et al. 2006) extended to the landscape scale, but considered independently, barriers to host movement had a larger impact than land cover, suggesting the

relative importance of habitat features in local transmission and landscape features in spatial spread of disease.

Our model indicated that both natural and anthropogenic impediments to population connectivity (INT, HWY, RIV: Fig. 3) were influential in shaping CWD spread. Landscape genetics studies provided a biological link between gene flow impediments and reduced contact rates that impede disease spread. Blanchong et al. (2008), using a subset of our study area, also found that highways US 18W, US 14W, and the Wisconsin River were barriers to local gene flow and CWD spread around the W_{CWD}. Further, mitochondrial DNA haplotype patterns have shown similar patterns relative to landscape barriers (Rogers et al. 2011). Roadways and rivers have been widely acknowledged as barriers to dispersal and gene flow for several ungulate species (Nussey et al. 2005; Coulon et al. 2006; Perez-Espona et al. 2008; Long et al. 2010), and these landscape features have become an important focus of animal movement studies (Forman and Alexander 1998; Jackson 2000), as well as in landscape genetics (Balkenhol and Waits 2009). In other studies, landscape genetics may enhance epidemiological models by identifying landscape features that influence population contact rates (Jones et al. 2008; Biek and Real 2010).

As an epidemic persists, local factors affecting agent transmission and persistence (habitat, population density, contact rates, and environmental transmission) can play a key role in determining local prevalence (Conner and Miller 2004; Farnsworth et al. 2006). Both ECO and CAN were important factors in our model, demonstrating the importance of local habitat features. The WCR ecoregion around the W_{CWD} was heavily forested with small agricultural fields, providing excellent deer habitat and high deer density (Wisconsin Dept. Natural Resources 2007). In contrast, areas surrounding the E_{CWD} were fragmented by extensive agriculture and urbanization, leaving sparse patches of deer habitat, leading to lower deer densities, and higher movement rates. Landscape genetics has shown that group social structure is less aggregated in the fragmented EGP habitat (Rogers et al. 2011; Robinson et al. 2012), which could impact contact rates and disease transmission for social groups (Grear et al. 2010). Our analysis also indicates that CWD infection is likely more dispersed (less aggregated) around the E_{CWD} than in the W_{CWD}.

Despite the importance of soil minerals in prion infectivity (as demonstrated in experimental studies; Miller et al. 2004; Johnson et al. 2006; Schramm et al. 2006), CLAY was not an important predictor of CWD prevalence in the Midwest. An analysis of CWD transmission to young deer at a fine spatial scale (2.6 km^2) in Wisconsin reached similar conclusions (Storm et al. 2013). These results differ from analyses in Colorado (Walter et al. 2011) which concluded that CLAY was an important risk factor for CWD infection. Possible explanations include a low variability in the range of soil clay values in our study area, differences in soil characteristics and related habitat associations, and differences in disease prevalence or animal behavior between the two areas. Further research is needed to understand the potential role of soils and, more broadly, the importance of environmental reservoirs of CWD in the dynamics of disease in the Midwest.

Utility of landscape epidemiology to map CWD risk

Understanding how the landscape influences wildlife disease is critical to determining disease spread, risk to naïve populations, future infection rates, and developing effective disease management and surveillance strategies (Ostfeld et al. 2005). Risk maps based on disease occurrence are an important tool in landscape epidemiology, and have proven useful to the management of several diseases including hantavirus (Glass et al. 2000; Langlois et al. 2001), malaria (Rogers and Randolph 2000) and whirling disease (McGinnis and Kerans 2012). Risk maps based on current disease prevalence assume that future risk of infection is related to current infection rates (Ostfeld et al. 2005). Our risk estimates based on CWD prevalence are consistent with recent findings of frequency-dependent transmission in Wisconsin (Jennelle et al. submitted-a, Storm et al. 2013). While our landscape epidemiological model provided excellent fit to observed prevalence data (2001–2007), model validation underestimated prevalence of CWD for 2008–2011 (Fig. 4) likely because of increases in CWD prevalence (Heisey et al. 2010; Jennelle et al. submitted-a) making it difficult to predict future disease patterns. Future epidemiological modeling efforts should consider temporal as well as spatial changes in disease risk as increasing prevalence alters disease dynamics (Jennelle et al. submitted-a; Storm et al. 2013).

Implications for CWD management

To date, the two Midwestern CWD outbreaks have been managed separately (Wisconsin Dept. Natural Resources 2002; Illinois Dept. Natural Resources 2003; Wisconsin Dept. Natural Resources 2010). Yet, our results indicate that both CWD outbreaks contribute to spread of disease, suggesting coordination between both east and west regions will be necessary to achieve a goal of disease containment. When considering the risk of disease spread to naïve areas of Illinois or Wisconsin, management agencies might consider both impediments to host movement and distance from outbreaks. For instance, an area further from the foci might be at a higher risk of disease than a neighbor separated by multiple barriers (e.g., I39/90 corridor and Rock River in the E_{CWD}; Fig. 3). At the statewide (or regional) scale, additional landscape genetics research may help identify other barriers between distant naïve deer populations (Lang and Blanchong 2012).

The predicted risk map (Fig. 3) may help focus surveillance and management efforts at the edges of the current CWD-infected area. By weighting surveillance where risk of spread is highest, sampling efforts can most efficiently detect new cases or increasing disease prevalence (Conner et al. 2007; Jennelle et al. submitted-b). Further, preventing spread of disease is likely more effective than efforts to eradicate disease and clean-up potentially contaminated environments (Miller et al. 2004; Mathiason et al. 2009). Finally, management agencies might be more successful in building community support for proactive management to keep CWD out of new areas than with management in established infected areas (Vaske et al. 2004).

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