FINAL REPORT

As Required by

THE ENDANGERED SPECIES PROGRAM

TEXAS

Grant No. TX E-138-R

F11AP00469

Endangered and Threatened Species Conservation

Using ecological niche modeling to predict the probability of occurrence of rare fish and mussel species in East Texas

Prepared by:

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12 November 2013

FINAL REPORT

STATE: Texas GRANT NUMBER: TX E-138-R-1

GRANT TITLE: Using ecological niche modeling to predict the probability of occurrence of rare fish and mussel species in East Texas

REPORTING PERIOD: 1 Sep 11 to 31 Aug 13

OBJECTIVE(S). To use ecological niche modeling of landscape characteristics (e.g., geomorphic, geological, topographic) and fish and mussel distributions to predict the probability of occurrence for rare species in East Texas rivers.

Segment Objectives:

Task 1. Oct 2011 – Aug 2012 – *Compile GIS data layers and data necessary for modeling.*
Task 2. Sept 2012 – May 2013 – *Ecological niche modeling:* a tool that can be used to predict the distribution of our target species in other river systems in East Texas, or in similar types of streams in the southeastern United States where those species occur.

Significant Deviations:

None.

Summary Of Progress:

Please see Attachment A. Electronic files for GIS and Maxent layers loaded on USB drive to be sent under separate cover.

Location: Delta, Fannin, Lamar, Red River, Bowie, Cass, Morris, Titus, Camp, Upshur, Franklin, Hopkins, Delta, Rains, Wood, Van Zandt, Smith, Henderson, Cherokee, Anderson, Houston, Trinity, Polk, Tyler, Angelina, Nacogdoches, Panola, Harrison, and Gregg Counties, Texas.

Cost: Costs were not available at time of this report, they will be available upon completion of the Final Report and conclusion of the project.

Prepared by: Craig Farquhar Date: 12 November 2013

Approved by: Date: 12 November 2013
C. Craig Farquhar

ATTACHMENT A

Final Report – Section 6

Title:

E-138-R - Using ecological niche modeling to predict the probability of occurrence of rare fish and mussel species in East Texas

Principal Investigators:

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Reporting Period:

1 October 2011 – 30 September 2013

Notes on Original Tasks

Task 1. Oct 2011 – Aug 2012 – *Compile GIS data layers and data necessary for modeling.* Layers required will include, but not be limited to, soils, geology, landuse/landcover, and DEM. We will create a GIS layer based on landscape-level geomorphic features (e.g., floodplain width, sinuosity). We will use the digital elevation model to calculate the topographic index (TOPMODEL) to predict areas of groundwater upwelling. We will use our georeferenced fish and mussel database (Ford et al. 2010) for predictive modeling using MAXENT. Additional, georeferenced historical data will also be incorporated into our database (e.g., Ford and Nicholson 2006).

Completed

Task 2. Sept 2012 – May 2013 – *Ecological niche modeling.* We will use the GIS layers compiled in Task 1 and all validated historical and current biology data to model the probability of presence or absence of each species in each spatial cell in the rivers. Ecological niche modeling will be conducted using the MAXENT software package. MAXENT produces a predictive model, which can be displayed geospatially, that represents the relative probability of a species occurring in a particular cell, given a set of environmental conditions associated with that cell and known species distributions (Pineda and Lobo 2009, Urbina-Cardona and Flores-Villela 2010). Ecological niche modeling has been used to model spread of invasive species (Thuiller et al. 2005), impacts of climate change (Thomas et al. 2004), and spatial patterns of diversity (Graham et al. 2006). Recent evaluations have shown to MAXENT to be a robust method for modeling geographic distributions of species, especially with conservation implications (Phillips and Dudik 2008).

Completed for mussel species. Not enough data were collected for the fish species to conduct modeling. The report, hereafter, consists of the journal article (to be submitted) resulting from this work.

Using Maxent to model rare freshwater mussel distributions using regional abiotic characteristics

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ABSTRACT: Unionid mussels are important components of aquatic ecosystems and the population declines of these organisms are a topic of concern across North America. Currently, there are six state-threatened Unionid species that occur in east Texas. However, little information is known about the ecology of these species and there are no models of their distributions or habitat affinities. We used ecological niche modeling to forecast the habitat preferences of these mussels at large spatial extent (all of east Texas), based on six abiotic environmental parameters. The ecological niche models of the individual mussel species were significantly different from one another, indicating that their distributions are distinct. Soil type and terrestrial vegetation cover were the most important determinants of predicted occurrences of the various mussel species. We also present here a new approach to groundtruthing, where sampling effort is concentrated into a single field season and then used iteratively to verify and improve the ecological niche models, equivalent to several years worth of traditional groundtruthing efforts.

In lotic environments, biological patterns are influenced by abiotic conditions. Stream assemblages are structured through a hierarchical framework where landscape-level features constrain and control local factors such as hydrology, sedimentation, nutrient dynamics, and channel morphology (Frissel et al., 1986; Tonn et al., 1990; Smiley and Dibble, 2005). One of the most significant threats to riverine ecosystems is alteration of the natural flow regime (Dynesius and Nilsson, 1994; Nilsson and Berggren, 2000). Fragmentation of natural habitat and alterations of natural flow regime have been reported as the most significant threats to freshwater mussels and fishes of the southern United States (Williams et al., 1993; Warren et al., 2000; Vaughn and Taylor, 1999). Determining the impact river alterations may have on rare species can be accomplished with landscape-level knowledge of the availability and quality of habitat that currently exists within a watershed. In the state of Texas, there has been a recent rapid increase in human population size resulting in an increased demand for water. Depletion of groundwater resources places an increased demand on surface waters, which has been exacerbated by record drought the past few years (Wurbs, 1985). Northeast Texas is a prime site for reservoir development and commercial interest because of the abundance of water resources in the area. The Neches and Sabine River systems of east Texas contain the greatest quantity of water and so are the focus of this increased demand for water resources and the resulting planned reservoir projects.

Freshwater mussels belonging to the family Unionidae often occur in dense multispecies beds that perform functional ecosystem roles such as removing suspended organic matter, moving sediments, and providing habitat for other animals (Strayer et al., 1997; Vaughn and Hakencamp, 2001). Freshwater mussels are the most imperiled group of animals in North America. Over the last century, North American mussel populations have decreased with 35 species now considered extinct and approximately 50% imperiled (Shannon et al., 1993; Williams et al., 1993; Neves et al., 1997; Vaughn, 1997a). Historically, freshwater mussels were abundant in riverine systems in the southeastern United

States (Strayer et al., 1994; Parmalee and Bogan, 1998). There are approximately fifty species of unionid mussels in the state of Texas, of which many have a distinct species composition in east Texas (Neck,1982; Howells et al.,1996). In Texas, one species is federally listed as endangered, *Arkansia wheeleri* and fifteen species are state-threatened with six of these occurring in east Texas: *Obovaria jacksoniana*, *Pleurobema riddellii*, *Lampsilis satura*, *Potamilus amphichaenus*, *Fusconaia lananensis*, and *Fusconaia askewi.*

Local habitat parameters including water velocity, depth, and substrate type are commonly thought to influence mussel abundance and distribution (Vannote and Minshall, 1982; Strayer and Ralley 1991). These factors appear to have their influence at both the macro- and microhabitat level (Holland-Bartels, 1990; Strayer et al., 1994). Human alterations to lotic environments, including impoundments, are known to influence local habitat parameters and are thought to be one of the major factors leading to the imperilment of freshwater mussels (Yeager, 1993). Unionid mussels are largely sessile organisms and are very dependent on the local conditions at individual sites; however, these organisms are vulnerable to disturbances and may be excluded and extirpated from those same local sites by human disturbances. Understanding the influence of local conditions, geographic distribution, and various niche dimensions are important factors in the effective study and conservation of imperiled mussel species.

We sought to understand the ecological niches and geographic distributions of six state-threatened species of freshwater mussels endemic to east Texas. This information is important for the conservation and management of these specific species, as well as for a broader strategy aimed at the protection of global biodiversity (Margules and Pressey, 2000). We did this using spatially explicit methods that combine information from landscape characteristics and known localities of the species' occurrences. We specifically address four main questions: (1) What are the predicted distributions of state-threatened mussel species in east Texas? (2) Does Maxent create valid maps for this taxon? (3) What is the optimal threshold for creating a valid model of rare Unionid distribution? (4) Which abiotic environmental variables, that are available in spatially explicit format (i.e., soil, vegetation, groundwater recharge, landform, etc.), can be effectively used to infer habitat suitability for east Texas mussels?

MATERIALS AND METHODS

Predictive modeling of species geographic distributions is an important technique in analytical biology and has been applied to a variety of areas of conservation and ecology (Corsi et al., 1999; Welk et al., 2002; Yom-Tov and Kadmon, 1998). These models can be used to assess impacts of disturbances and to guide management decisions and restoration efforts (Gaston, 1996). We used the software package Maxent for our ecological niche modeling (Dudik et al., 2010; Phillips et al., 2006), which provides an understanding of habitat suitabilities of individual species on the landscape by modeling the species' multivariate environmental tolerances, also known as the realized niche (Hutchinson, 1957). Maxent is based on maximum entropy distribution modeling, which outperforms other computational methods (Elith et al., 2006; Ortega-Huerta and Peterson, 2008) and performs well even at small sample sizes (Hernandez et al., 2006; Kumar and Stohlgren, 2009; Wisz et al., 2008). The ability to provide significant results and accurate predictions with fewer occurrence data points is useful when considering rare or specialist species that occupy limited geographic distributions and occur in relatively low numbers (Gaston and Kunin, 1997). Maxent produces a geographic model of habitat suitability by searching for the best solution comparing the distribution of the occurrence points to the predetermined environmental variables (i.e., ArcGIS layers) (Phillips et al., 2006). It then produces a map with a logistic score for each grid cell (corresponding to the grain size of the environmental data), which can be interpreted as the degree of suitability of a particular location for the species, given the environmental attributes of that location (Phillips and Dudik, 2008). The resulting predictive models can be used as a conservation tool to predict patterns of species distributions across the landscape and aid in the development of recovery plans for imperiled fish and mussel species.

We restricted our analysis to locations falling within East Texas, with the Trinity River as the western boundary and including the Cypress, Sulphur, Sabine, Neches, and Angelina rivers and their associated watersheds. Habitat suitability models were built separately for each species. Species with less than five occurrence points were considered too poorly sampled to be modeled accurately (Pearson et al., 2007). Occurrence data for mussels came from field surveys conducted in 2010 and 2011 (Dunithan 2012) and a database of historical records compiled by Robert Howells and N.B. Ford. Six GIS layers were incorporated in the model for each species: soils type, geology, vegetation type, landform, groundwater recharge, and land cover diversity. Soil types were obtained from the National Resource Conservation Service (NRCS) based on data from various members of the Soil Survey Staff (2006). The geology layer, bedrock that lies at or near the land surface, was obtained from USGS created by the North American Geologic Map Committee (2005). Vegetation types were obtained from USGS, based on data from McMahan et al. (1984). Landform datum such as slope, local relief, profile type, percentage of area occupied by sand, ice and standing water, and patterns of major peaks were obtained from USGS, based on data from Hammond (2011). The groundwater recharge layer, which provided the mean annual ground water recharge estimates (Wolock, 2003a), was obtained from USGS, based on data from Wolock (2003b). The land cover diversity layer was obtained from USGS and describes the variety of land covers surrounding a particular location (Ritters, 2012).

Most environmental data were obtained as raster files; vector data were converted to raster format in ArcMap. All rasters were sampled to achieve a common resolution of 100m x 100m, and all rasters were in the NAD 1983 UTM Zone 15N projection using a geographic (XY) coordinate system with meters as the unit. Environmental layers were clipped in order to constrain them to lotic habitats. We did this by adding a 100m buffer around water features (ponds, streams, rivers, canals, and dams), obtained from an environmental layer called “NHDFlowline” from USGS (USEPA and USGS, 2005), and clipping the environmental layers to match the lotic buffer.

In Maxent, we used AUC and “gain” to determine aspects of model fit. The area under the operator receiving curve, AUC (Fielding and Bell, 1997), measures the probability that a randomly chosen presence site will be ranked above a randomly chosen pseudoabsence site (Phillips and Dudik, 2008). Models with AUC > 0.75 are treated as good fits (Elith, 2002). Gain is the mean log probability of the occurrence samples, minus a constant that makes the uniform distribution have zero gain. Because gain is not bounded by zero or one, it is useful only for comparative purposes among nested models. For each species, we compared the gain of the full model (all variables included) to models based solely on one environmental variable. AUC and gain values were calculated first using “training data” and then using “test data.” “Training data” were a subset of the known occurrence points that were used to generate the models. “Test data” consisted of known occurrence points that were held back until after the models were developed. The test data were plugged into the models only after they were created, and therefore can be viewed as quasi-independent verification of the models. We used a cross-validation approach (Pearson et al., 2007) to subdivide our datasets into the training data points and test data points.

For niche models that had a good fit to the data (AUC > 0.75), we further tested whether models for each species were significantly different from one another. We did this using ENMTools, a software package that allows one to test whether the habitat suitability scores generated by niche modeling for two species exhibit statistically significant ecological differences (Warren et al., 2010). Specifically, for every possible pair of species’ niche models, we used the “niche identity test” module. It asks whether niche models generated from two or more species are more different than expected if they were drawn from the same underlying distribution. It does this by pooling empirical occurrence points and randomizing (permuting) their identities to produce two new samples with the same numbers of observations as the empirical data (Warren et al., 2010). We repeated this procedure 100 times, generating niche similarity values based on the permuted data from each run. This gave us our expected value (distribution under the null hypothesis of no difference in the niches of the two species), which we then compared to the observed level of niche differentiation.

ENMtools output provides three different statistics to measure niche similarity: Schoener's D (Schoener, 1968), the *I* statistic (Warren et al., 2008), and relative rank, RR (Warren and Seifert, 2011). All three metrics range from zero to one; zero indicating that species have completely different niche models and one meaning that the pair of species have identical niche models. The *I* and D statistic are calculated by taking the difference between the species suitability score at each grid cell, after the suitabilities have been standardized so that they sum to one over the geographic space being measured. The relative rank is an estimate of the probability that the relative ranking of any two patches of habitat is the same for the two models. Although the statistics emphasize different aspects of the data, we chose to use the *I* statistic because it has been shown that RR, *I*, and D metrics are highly correlated (Warren et al., 2008). We considered two species to have significantly different niches if the observed *I* statistic was below the five percent quantile from the null distribution (corresponding to a 5% chance that two niche models would be that different if they were estimated from two species that actually had the same niche).

Our sampling locations used to ground-truth the models were chosen based upon the original habitat suitability maps, which were divided into five different ranges of suitability based upon the suitability score. Grids in the maps were scored as either high, low, mid high, or mid low. A uniform distribution of sites was selected from the range of suitability scores for all six species. Sites were chosen via a stratified random sampling design to allow sites to be randomly chosen within the suitability scores found in the original maps which allowed sites to be within a certain suitability score set, but to be randomly chosen within that set. Sites were chosen to allow at least five sampling efforts for each of the score suitability categories for all six species and to provide adequate coverage of all the major rivers in east Texas. Sites were sampled in a 50m reach using tactile and visual searches until the area was completely sampled.

Evaluation of the optimal sampling effort required for best models was done by randomly assigning the sampling data into five sets with 0%, 20%, 40%, 60%, 80%, and 100% of the ground-truthed data included in each re-run of the models. Each time, the remaining data were considered to be the equivalent of sampling using these new maps because the suitability scores, AUC, and gain values were obtained from the new maps. Using the data in this way allowed each iteration used to create the suitability maps to be a "new" sampling effort without having to obtain fresh data from the field. By breaking the data up into percentages, we obtained five different sampling efforts from only one summer of field research. The maps could be compared to quantify the amount of data needed to generate useful maps for each species.

Comparisons of the models were conducted by graphing the test AUCs and test gains from each suitability map for each species and visualizing a trend. If the models improved with new data, then the test AUC and test gain should get larger with each data set. Determination of the suitability scores' overall ability to predict the abundance at a site was done via linear regression in Excel. Logistic regression was used to determine if sites with higher suitability scores were more likely to have a threatened mussel species than sites with lower scores. Percent contribution of each environmental variable for each subsequent run of the model was examined to determine if there were any changes in the importance of an environmental variable from the original models.

RESULTS

The training AUC values for mussels ranged from 0.9980-0.9995 and test AUC values ranged from 0.8537-0.9822 for the initial models, indicating that all of the models were good fits (Table 1). All of the models improved with the inclusion of additional data (increase in test AUC values) (Table 1).

The relative contributions of the different environmental variables to the niche models (as measured by test gain when the model only included that particular environmental variable) varied depending on the particular species. Soil type contributed the most information to niche models of all mussel species; however, with the addition of occurrence localities, the importance of land cover diversity increased and was the most useful predictor of habitat suitability for *F. lananensis* and *P. riddellii*.

In most cases, mussel species' niche models were significantly different from one another, as indicated by the permutation tests (Table 2), except for *O. jacksoniana* and *F. lananensis*, whose niche models were not significantly different from one another. *Fusconiana askewi* had the largest predicted distribution, including areas of the Trinity, Sabine, Neches, and Sulphur Rivers (Figure 1a). The highest habitat suitabilities were predicted in the Sabine and lower Neches River, where a majority of the sampling efforts were concentrated. *Pleurobema riddellii* and *F. lananensis* were both predicted to occur in the Neches and Angelina Rivers (Figure 1b and 1c). Despite similarities between the potential distributions of these two species, triangle pigtoe showed higher habitat suitability in the Angelina River. *Lampsilis satura* was predicted to occur in the Sabine, Neches, Trinity, and Angelina Rivers with the highest habitat suitabilities occurring in areas of the Sabine and the lower Neches Rivers (Figure 1d). The model for *P. amphichaenus* predicted a sparse distribution in the Neches and Sabine Rivers (Figure 1e). Southern hickorynut had the smallest predicted distribution, indicating occurrence only in the Neches

River (Figure 1f). The predicted distribution for Southern hickorynut corresponded with previous sampling efforts.

Using logistic regression, the suitability scores became significantly better at predicting the occurrence of a particular mussel species at a site with the addition of new data in all six species except for *O. jacksoniana* (p=0.25 at 0% of new data, p = 0.15 at 80% of new data). In this species the addition of data did not change how well the model predicted its occurrence at a site (Table 3). In all of the other species the addition of data significantly improved the model's ability to predict species occurrence; however, this improvement plateaued with the addition of new data. New data stopped improving the models for *P. amphichaenus* after an additional 56 sites were added to the model (p= 1.29 X 10^{-3} at 0% of new data, p= 0.18 at 40% of new data). Models for *F. lananensis* (p= 1.99 X 10^{-4} at 0% of new data, p= 0.17 at 80% of new data) and *P. riddellii* (p= 1.85 X 10^{-3} at 0% of new data, p= 0.12 at 80% of new data) continued to improve until an additional 111 sites had been added to the data. The model's predictive ability for *L. satura* continued to significantly improve with additional data (p= 0.07 at 0% of new data, p= 0.02 at 80% of new data) (Table 3).

The addition of new data significantly improved the model's ability to predict higher numbers of a mussel species at sites with higher suitability scores for all six mussel species (Table 4), however this improvement again eventually capped. The model's predictive ability for both *P. amphichaenus* (p= 3.45 X^{-3} at 0% of new data, p= 0.53 at 40% of new data) and *L. satura* (p= 0.27 at 0% of new data, p= 0.08 at 40% of new data) improved until an additional 56 sites had been added. For *F. askewi* the model's predictive ability continued to improve until an additional 84 sites had been added (p= 2.24X10^{-3} at 0% of new data, p= 0.46 at 60% of new data). For *F. lananensis* (p= 0.82 at 0% of new data, p= 0.05 at 80% of new data) and *P. riddellii* (p= 0.36 at 0% of new data, p= 0.06 at 80% of new data) and F. askewi (p= 0.02 at 0% of new data, p= 0.16 at 80% of new data) the model continued to improve until an additional

111 sites had been added. The model did not improve in its ability to predict higher numbers at higher scored sites for *O. jacksoniana* (p= 0.30 at 0% of new data, p= 0.02 at 80% of new data) until all of the sites had been used (Table 3).

DISCUSSION

Our study provides the first predicted niche distribution maps for rare mussels in east Texas. The models identify regions that have similar environmental conditions to where current populations are maintained and propose that surrounding soil, vegetation, and land use characteristics are important predictors of mussel habitat suitability. Our results correspond with a recent study that examined coarse-scale aquatic modeling to predict endangered mussel distributions in Ohio and found that substrate and land use conditions influence the distribution of freshwater mussel species (Weber and Schwartz, 2011). A recent study indicates that *F. lananensis* is not a valid species and that it is likely that only one *Fusconaia* species is currently present in east Texas (Burlakova et al. 2012); however, our analyses reveals distinct niche differentiation between the species currently belonging to the tribe *Pleurobemini*.

Our analyses indicate that these rare mussels are occupying different areas within the landscape, which suggests distinct functional roles in the aquatic ecosystem; however we know little about the functional role of this biodiversity. Research has shown that freshwater bivalve communities are important components of food webs; this taxon links and influences multiple trophic levels. Mussels filter food and sediment from the water column, and this filtration rate varies with bivalve species and size. It has also been shown that mussel communities have impacts on nutrient dynamics through excretion and biodeposition, which is also species dependent (Vaughn et al. 2008; Vaughn and Hakencamp, 2001).

Areas of Occurrence

State-threatened mussels were predicted to inhabit all major rivers in east Texas; however, our models predicted that all rare species modeled occur in the Neches River, one of the largest rivers in east Texas. The riparian corridor of the Neches watershed is considered to be a bottomland hardwood forest floor, with piney woods vegetation and oak-hickory pine forest in the uplands (Fish and Wildlife Service, 1979). The vegetation of this region helps reduce the influence of impervious overland flow that would cause increased velocities and is more typical of urbanized areas. Recent studies have also shown that the Neches River has sections that are adequately connected to its floodplain (Troia, 2010). The lack of human alteration to the Neches watershed allows the mussels to remain in the substrate during seasonal flooding and inundation of the floodplain. The Angelina River is a major tributary of the Neches River and shares characteristics with the Neches River because of its close proximity.

The Sabine River is characterized by flat slopes and wide timbered floodplains. The upper reaches flow through prairie lands and contain deep sandy loam substrates. The lower portions of the Sabine River flow through flat terrain with hardwoods and forests consisting of hardwoods and conifers. Because of anthropogenic impacts, the Sabine River has low channel-floodplain connectivity (Phillips, 2008a). The *F. askewi*, *L. satura* and *P. amphichaenus* were predicted to occur in the Sabine River and these species are known to occur in the Sabine River watershed (Howells et al., 1996).

The Trinity River is very different from other east Texas rivers with regards to soil and vegetation. The Trinity River basin is defined by gentle topography and mostly clay loam soils with cropland and rangeland as the dominant land cover. Research has shown that clay and loam soils impact surface water runoff and thus the addition of nitrogen in the Trinity River watershed (Chen et. al., 2000). Along with agricultural practices, urbanized areas are prominent throughout the Trinity River watershed including the cities of Fort Worth and Dallas. Anthropogenic impacts may influence the ability of rare mussels to survive in and inhabit the Trinity River watershed. However, the low habitat suitability scores we found in the Trinity River could be a result of the lack of sampling intensity in this portion of east Texas (Phillips, 2008b). Because the habitat in the Trinity River is drastically different from other east Texas rivers, correlations between mussel populations and environmental conditions in the Trinity River may not have been accurately portrayed. Three species were predicted to not occur or be extremely rare in the Trinity River (i.e., *F. askewi*, *F. lananensis*, and *L. satura,* all of which had habitat suitability scores lower than 0.04). Despite the fact that these species are known to inhabit a majority of east Texas rivers, few specimens have ever been reported in the Trinity River basin in previous studies. The sandbank pocketbook has not been reported in the Trinity River basin (Howells, 1996; Howells, 2011).

Environmental Associations

Soil type was the most important environmental parameter for all rare mussel species in our models. Landcover diversity and vegetation were also important variables for predicting mussel niche distributions. In streams and rivers, habitat parameters including land use and landcover characteristics, are known to influence local habitat and biological diversity (Allan and Flecker, 1993; and Strayer, 2008). Landcover is a vital component in determining species endangerment "hot spots" in the United States (Flather et al. 1998). Soil type, vegetation, and land-use characteristics influence the hydrology and movement of water into a watershed. Further, species richness can also be influenced by habitat parameters including landform, watershed slope, soil composition, vegetation and landuse characteristics (Morris and Corkum, 1996; Brainwood et al., 2006). River systems behave differently depending on the relative contribution of groundwater versus surface flow; therefore, alterations in overland flow and groundwater recharge result in variations in velocities which may select for individuals that are capable of surviving in modified flow regimes (Statzner et al. 1988).

Number of Individuals Vs Suitability Score

In all species, more individuals were found at sites with higher suitability scores, and this trend continued as more data were added to the models. However, there was a data plateau for each species, where new data no longer had an effect. The more data used to create the original models, the better those models were at predicting new locations, and the less of an effect any new data will have and the sooner the plateau appears. These plateaus are different for each of the six species and depend on the number of occurrence sites that were used to create the original maps, the number of new occurrence points added, and the total number of new individuals found of that species. Models for *P. amphichaenus* and *L. satura* both plateaued after an additional 56 sites had been added. These two species had fairly low sets of starting occurrence points, and had relatively few new occurrence points added. Had these species been found at more sampling sites, the suitability scores would have likely continued to increase in their predictive ability. The models for *F. askewi* plateaued after 84 sites had been added, and the models for *F. lananensis* and *P. riddellii* plateaued after an additional 111 sites had been added. These three species all had the largest number of new occurrence points, and likely their suitability scores would have continued to improve if more occurrence data had been available. The models for *O. jacksoniana* did not begin improving until all of the additional ground-truthed sampling sites had been added. *O. jacksoniana* also had the smallest starting data set and the smallest amount of new data added, implying that a large amount of data would be needed to improve predictions for this species.

Presence/Absence of a Species at a Site Vs Suitability Score

The suitability score was also a good predictor for whether or not a species would be present or absent at a site, and higher scored sites were more likely to have a threatened mussel species than lower scored sites. The predictive ability of the suitability scores tended to increase with more data, though again a plateau was eventually reached. This plateau was caused by the model needing more and more data to improve what it had improved each time new data were added.

The model did not improve for *O. jacksoniana*. This was most likely caused by the very small amount of sites at which this species was found. This species is one of the least common in East Texas, and this is reflected in the few that were found, and the lack of improvement in the model's predictive ability for them. The plateau was reach for *P. amphichaenus* after an additional 56 sites were added. This species was found at relatively few sites because the majority of the sampling was done outside of the Sabine River where this species is primarily found. The model continued to improve for *P. riddellii, F. askewi, and F. lananensis* all of which continued to improve until an additional 111 sites had been added. These three species all had very high numbers of new occurrence points and these new points continued to improve their models. The model for *L. satura* did not stop improving with new data. This species had relatively few original occurrence points to use in the initial model, and a large number of new sampling locations were found. This caused each new set of occurrence points to have a larger impact on model improvement than for the other species.

CONCLUSIONS

In summary, we were able to successfully create niche models that predict the presences of several imperiled mussel species in known areas, and that forecast other suitable areas that may potentially contain the mussels as well or that may be suitable for reintroduction programs. Although several environmental layers went into producing the potential geographic distribution maps, many factors influencing the dimensions of the realized niche were not taken into account, such as biotic interactions (e.g., predators, parasites and possible fish hosts). Incorporating biotic components could improve the predictive accuracy of our models (Guisan and Zimmerman, 2000; Broennimann et al., 2007; Giovanelli et al., 2008). Fish are important components of unionid distributions because unionids experience an obligate ectoparasitic larval stage called glochidia that attach to a fish or salamander host after release from the adult female mussel. Some species of Unionidae are able to parasitize a taxonomically wide variety of fish species (Trdan and Hoeh, 1982) while others can use only a few closely related species (Zale and Neves, 1982; Yeager and Saylor, 1995). Integrating spatial information regarding the presence of known fish hosts data through identification of potential glochidia-host relationships into our ecological niche models may provide a better understanding of the geographic distribution of east Texas unionids and improve AUC test scores.

The information provided from the potential distribution maps may aid in field surveys and allocation of conservation resources by providing valuable biogeographical information that will help in planning land use management around existing populations, discovering new populations, identifying top-priority survey sites, or setting priorities to restore natural habitat (Kumar and Stohlgran, 2009; Raxworthy et al., 2003; Bourg et al., 2005).

We showed that MAXENT maps could be improved for the mussels of East Texas with additional data. A predictive map should be improved each time new data is collected for a species, and not considered a final product. Our data can also give a starting point for the amount of data necessary to model the ecological niche for this these taxa. If a map is made without enough data then inaccurate predictions for a species could be made, and these could have long term repercussions for the management of a species, natural resources, and many other management decisions.

ACKNOWLEDGEMENTS

Numerous students at UT Tyler assisted with field surveys. Funding was partially provided by U.S. Fish and Wildlife Service, Section 6 (TX E-140-R, F11AP00469; TPWD #417153) through Texas Parks and

Wildlife Department (niche modeling) and by the Texas Department of Transportation (ground truthing). We would like to thank Dr. Craig Farquhar (TPWD) for assistance with grant administration.

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Table 1. Summary information for the individual mussel species' niche models. The training AUC, test AUC, and test gains for the models are presented, as well as test gains for models fit with only the specified individual variables.

Species	**Percent of Data**	**# of Samples**	**Test Gain**	**Test AUC**	**Geology**	**Groundwater Recharge**	**Landform**	**LandcoverDiversity**	**Soils**	**Vegetation**
F. askewi	0	80	1.6775	0.922	10.0439	0.3039	4.7381	43.755	27.6469	13.5122
F. askewi	20	91	1.6806	0.9302	11.4285	1.5789	4.2362	43.0555	25.5176	14.1832
F. askewi	40	104	1.8746	0.9415	14.0611	2.4237	4.3339	40.7184	24.1696	14.2934
F. askewi	60	117	2.0556	0.9479	14.3835	2.2851	4.2808	38.6076	21.8849	18.5582
F. askewi	80	128	2.1425	0.9513	14.0697	2.0333	4.104	37.6473	22.1204	20.0252
F. askewi	100	145	2.1363	0.9443	14.952	6.1024	4.5083	34.3875	20.9868	19.063
F. lananensis	0	27	1.72	0.8537	1.7219	0.3182	7.5338	56.9069	18.2244	15.2948
F. lananensis	20	29	2.7508	0.9837	7.8884	0	1.0443	42.6042	47.2705	1.1926
F. lananensis	40	32	2.6912	0.9777	9.828	1.0037	1.6985	47.8852	38.7298	0.8547
F. lananensis	60	36	2.648	0.981	9.0762	0.5934	1.4725	44.5527	42.6807	1.6244

			6	2						
F. lananensis	80	38	2.4181	0.9723	8.6889	1.4245	1.7289	46.9688	40.4103	0.7787
F. lananensis	100	45	3.2329	0.9859	10.2607	3.0132	1.3032	45.8535	38.3209	1.2484
L. satura	0	42	1.7755	0.9389	12.4255	2.4853	0.1754	52.8962	12.6212	19.3964
L. satura	20	52	1.541	0.9531	14.3792	1.8127	0.2763	47.9358	14.7375	20.8585
L. satura	40	56	1.5641	0.9515	14.3569	2.9395	0.6061	46.4914	13.3334	22.2727
L. satura	60	63	1.7982	0.9539	14.8986	2.919	1.0171	45.7166	12.1679	23.2807
L. satura	80	72	1.9533	0.9592	14.5691	3.1435	1.991	38.8133	11.9706	29.5123
L. satura	100	78	2.0315	0.9604	12.1694	2.7912	1.3506	40.0066	15.9313	27.7509
O.jacksoniana	0	12	2.6168	0.9704	17.8152	0	2.3953	46.1683	19.2369	14.3843
O.jacksoniana	20	13	2.3282	0.9602	18.093	0	3.0261	45.5474	23.7355	9.598
O. jacksoniana	40	13	2.4076	0.9604	18.4113	0	2.5486	46.8279	23.4039	8.8084

O. jacksoniana	60	13	2.2885	0.9676	18.7386	0	2.5051	45.9405	21.8155	11.0003
O. jacksoniana	80	15	2.3615	0.9731	16.0103	0	3.5328	42.2862	23.6799	14.4908
O. jacksoniana	100	17	2.0721	0.967	11.2693	0	2.053	47.822	29.5236	9.3321
P. riddelli	0	34	2.2566	0.964	12.7698	1.7052	0.3019	56.4082	21.6379	7.177
P. riddelli	20	39	2.1842	0.9665	12.4631	2.1648	0.337	51.9457	25.5704	7.5191
P. riddelli	40	43	2.3643	0.9724	13.4944	2.0564	0.4442	49.1367	27.0668	7.8014
P. riddelli	60	50	2.6077	0.9725	13.3399	2.7871	0.3621	46.5758	26.4344	10.5007
P. riddelli	80	58	2.9584	0.9787	12.5306	2.2262	1.4624	39.6107	28.6952	15.4748
P. riddelli	100	66	3.0594	0.9775	10.6035	2.1028	1.415	38.129	32.4071	15.3425
P. amphichaenus	0	23	1.72	0.8537	1.7219	0.3182	7.5338	56.9069	18.2244	15.2948
P. amphichaenus	20	28	1.386	0.8507	1.9353	3.4025	6.6138	53.0307	19.8218	15.1959
P. amphichaenus	40	36	2.103	0.910	5.3775	4.5496	4.3983	47.2256	29.0054	9.4437

			2	3						
P. amphichaenus	60	39	2.1817	0.9157	3.5906	6.1153	7.7848	38.352	30.6069	13.5504
P. amphichaenus	80	42	2.3513	0.9334	4.0806	5.2734	8.9592	36.7142	28.6571	16.3155
P. amphichaenus	100	46	2.5236	0.9346	4.1157	5.8337	7.9235	37.053	26.4183	18.6558

Table 2. I values and 5% critical values. Significant results (non-identical niches) occur when the observed value is below the 5% critical value.

Species comparison	Observed value	5% critical value
L. satura Vs. *P. riddellii*	0.86	0.91
L. satura Vs. *F. askewi*	0.73	0.78
L. satura Vs. *F. lananensis*	0.68	0.91
O. jacksoniana Vs. *P. riddellii*	0.81	0.84
O. jacksoniana Vs. *L. satura*	0.78	0.82
O. jacksoniana Vs. *P.amphichaenus*	0.69	0.79
P. amphichaenus Vs. *F. riddellii*	0.61	0.86
P. amphichaenus Vs. *L. satura*	0.7	0.84
F. askewi Vs. *P. riddellii*	0.82	0.91
F. askewi Vs. P. amphichaenus	0.65	0.81
F. lananensis Vs. *P. riddellii*	0.78	0.87
O. jacksoniana Vs. *F. askewi*	0.77	0.79
O. jacksoniana Vs. *F. lananensis*	0.85	0.76
P. amphichaenus Vs. *F. lananensis*	0.49	0.86
F. askewi Vs. *F. lananensis*	0.75	0.84
O. jacksoniana Vs. *P. riddellii*	0.82	0.85

Table 3. The linear regression and logistic regression P values for each percentage band at which new occurrence points were added to the original data.

F. askewi						
Test	0%	20%	40%	60%	80%	100%
	p	p	p	p	p	p
Linear Regression	2.24E-3	9.19E-3	0.05	0.46	0.55	2.43E-4
Logistic Regression	0.02	4.12E-3	2.04E-3	0.04	0.16	6.48E-11
F. lananensis						
Test	0%	20%	40%	60%	80%	100%
	p	p	p	p	p	p
Linear Regression	0.82	0.75	3.52E-4	2.06E-3	0.05	8.02E-4
Logistic Regression	1.99E-4	2.68E-4	3.10E-4	1.55E-3	0.17	2.74E-8
L. satura						
Test	0%	20%	40%	60%	80%	100%
	p	p	p	p	p	p
Linear Regression	0.27	0.02	0.08	0.93	0.46	1.48E-9
Logistic Regression	0.07	0.02	0.11	0.42	0.02	2.51E-10
O. jacksoniana						
Test	0%	20%	40%	60%	80%	100%
	p	p	p	p	p	p
Linear Regression	0.30	0.27	0.30	0.45	0.02	5.14E-9
Logistic Regression	0.25	0.20	0.24	0.36	0.15	3.10E-3
P. riddellii						
Test	0%	20%	40%	60%	80%	100%
	p	p	p	p	p	p

Linear Regression	0.36	6.59E-5	6.44E-4	0.01	0.06	2.78E-14
Logistic Regression	1.85E-3	5.20E-3	7.41E-3	8.64E-3	0.12	5.94E-8
P. amphichaenus						
Test	0%	20%	40%	60%	80%	100%
	p	p	p	p	p	p
Linear Regression	3.45E-3	0.03	0.53	0.53	0.39	6.82E-12
Logistic Regression	1.29E-3	3.58E-3	0.18	0.15	0.17	7.93E-9

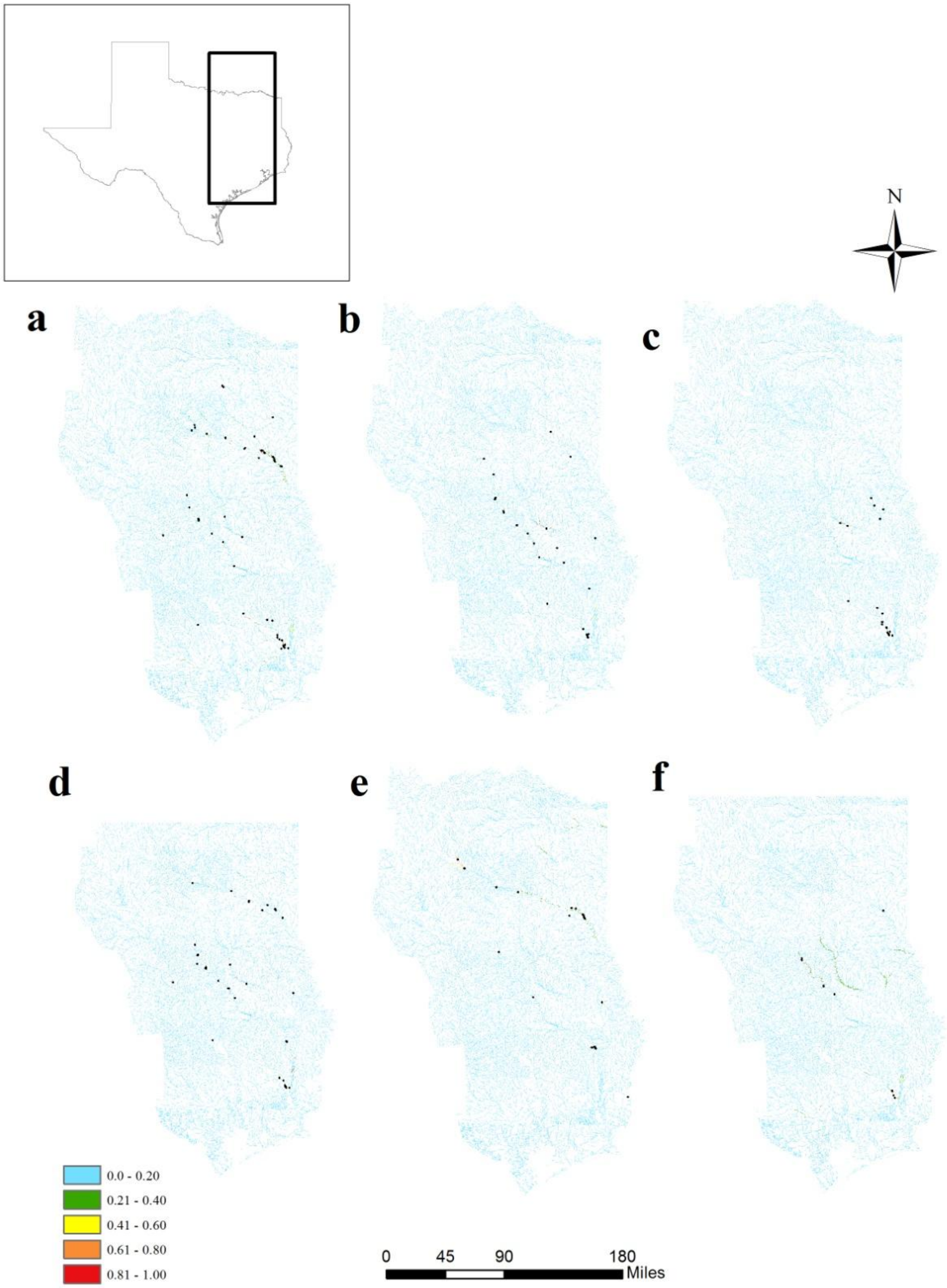

Figure 1. Predicted potential suitable habitat for (a) *Fusconaia askewi*, (b) *Pleuroblema riddellii*, (c) *Fusconaia lananensis*, (d) *Lampsilis satura*, (e) *Potamilus amphichaenus*, and (f) *Obovaria jacksoniana* in East Texas. The black points indicate known presence points that were used to train and validate the models.