

# A unifying approach for evaluating the condition of wetland plant communities and identifying related stressors

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**Abstract.** Assessment of vegetation is an important part of evaluating wetland condition, but it is complicated by the variety of plant communities that are naturally present in freshwater wetlands. We present an approach to evaluate wetland condition consisting of: (1) a stratified random sample representing the entire range of anthropogenic stress, (2) field data representing a range of water depths within the wetlands sampled, (3) nonmetric multidimensional scaling (MDS) to determine a biological condition gradient across the wetlands sampled, (4) hierarchical clustering to interpret the condition results relative to recognizable plant communities, (5) classification and regression tree (CART) analysis to relate biological condition to natural and anthropogenic environmental drivers, and (6) mapping the results to display their geographic distribution. We applied this approach to plant species data collected at 90 wetlands of the U.S. Great Lakes coast that support a variety of plant communities, reflecting the diverse physical environment and anthropogenic stressors present within the region. Hierarchical cluster analysis yielded eight plant communities at a minimum similarity of 25%. Wetlands that clustered botanically were often geographically clustered as well, even though location was not an input variable in the analysis. The eight vegetation clusters corresponded well with the MDS configuration of the data, in which the first axis was strongly related ( $R^2 = 0.787$ ,  $P < 0.001$ ) with floristic quality index (FQI) and the second axis was related to the Great Lake of occurrence. CART models using FQI and the first MDS axis as the response variables explained 75% and 82% of the variance in the data, resulting in 6–7 terminal groups spanning the condition gradient. Initial CART splits divided the region based on growing degree-days and cumulative anthropogenic stress; only after making these broad divisions were wetlands distinguished by more local characteristics. Agricultural and urban development variables were important correlates of wetland biological condition, generating optimal or surrogate splits at every split node of the MDS CART model. Our findings provide a means of using vegetation to evaluate a range of wetland condition across a broad and diverse geographic region.

**Key words:** *biological condition; classification and regression trees; emergent wetland; Great Lakes, USA; hydrogeomorphic; land use; marsh; vegetation classification; watershed.*

## INTRODUCTION

The U.S. government collects data on the status and trends of wetland area within the country, but no comparable data currently exist for wetland quality. Scientists and environmental managers acknowledge that not all wetlands are of equal condition; some wetlands are perceptibly better than others in terms of their ecological functions and diversity of biota. Recognizing the need to evaluate wetland quality in

the United States, the U.S. Environmental Protection Agency is planning for a national survey of wetland condition in 2011 (information *available online*).<sup>7</sup>

Assessment of vegetation is an important part of evaluating wetland condition, but is complicated by the variety of plant communities that are naturally present in freshwater wetlands. Adjoining wetlands may contain vastly different plant communities even in undisturbed landscapes due to different edaphic conditions such as soil type, water source, biogeochemistry, and depth and duration of inundation; anthropogenic disturbances superimpose additional stress on this already complex set of vegetation drivers. Developing vegetation indicators of condition capable of factoring out natural vegetation variability is a challenge to evaluating

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<sup>7</sup> (<http://www.epa.gov/owow/wetlands/survey/>)

wetland quality. Existing approaches include comparison with “reference” wetlands, or assigning a “coefficient of conservatism” to individual wetland plant species to rank their fidelity to remnant natural habitats, but both of these approaches involve some subjectivity. We propose an alternative approach that “lets the vegetation tell the story,” utilizing vegetation ordination to generate a biological condition gradient (*sensu* Davies and Jackson 2006) that allows comparison of wetlands with vastly different plant communities spanning broad geographic regions.

The combined information provided by an assemblage of plant species can often reveal more about wetland condition than that provided by individual species (Keddy 2000, Cronk and Fennessy 2001). Freshwater wetland vegetation responds to the depth, timing, and duration of inundation (Keddy and Reznicek 1986, Toner and Keddy 1997, Whitehouse and Bayley 2005, Hudon et al. 2006), soil pH (Nekola 2004), soil texture (Kirkman et al. 2000, De Steven and Toner 2004), and soil and water fertility (Gaudet and Keddy 1995, Templer et al. 1998, King et al. 2004). Anthropogenic disturbances that alter these attributes, either directly within wetlands or indirectly by off-site water level or watershed alteration, can thereby alter wetland plant community composition (Johnston 2003, Zedler 2003, Houlahan et al. 2006, Craft et al. 2007). Because plant communities encompass species with different adaptations, ecological tolerances, and life history strategies, the composition of plant communities can reflect the biological integrity of the wetland, often with great sensitivity (U.S. Environmental Protection Agency 2002).

The contemporary statistical methods of nonmetric multidimensional scaling (MDS) and classification and regression trees (CART) can aid detection of ecological communities and interpretation of their environmental linkages. MDS (also abbreviated as NMS or NMDS) is an ordination technique for constructing sample maps whose interpoint distances have the same rank order as the corresponding dissimilarities between samples. It is superior to other ordination methods for community data (Kenkel and Orloci 1986, Clarke and Warwick 2001) and has been successfully applied to wetland plant communities in many locations (Grace et al. 2000, De Steven and Toner 2004, Nekola 2004, Bowles et al. 2005, Whitehouse and Bayley 2005, Mack et al. 2008). CART is a nonparametric technique that is ideally suited for complex ecological data with hierarchical structure, and it can overcome the complications of categorical data and nonlinear relationships (Breiman et al. 1984, De'ath and Fabricius 2000). Physical parameters that are known to affect wetland plant communities, such as hydrogeomorphology and soil type, are usually categorized as discrete classes that require nonparametric statistical methods. CART can select from among a large number of variables, both numerical and categorical, those that are most important in determining the

outcome variable to be explained (Urban 2002). CART analyses have been used to predict seasonal-wetland abundance based on land type (Palik et al. 2003), relate coastal urbanization to *Phragmites australis* abundance and foliar nitrogen (King et al. 2007), model historical changes in herbaceous wetland plant communities on the St. Lawrence River (Hudon et al. 2005), and evaluate nonlinear responses of wetland biota to generalized stressor gradients (Brazner et al. 2007a, Loughheed et al. 2007).

Our study area for developing this approach is the U.S. Great Lakes coast, a region encompassing a variety of wetland types and anthropogenic influences within its 1200-km span. The Great Lakes basin intercepts a range of climatic conditions, with average annual precipitation from 70 to 150 cm, and average annual maximum temperature from 8° to 16°C within the United States (PRISM 2006a, b). Like many coasts, the Great Lakes shoreline has been a magnet for human development and has a long history of human use for transportation, industry, and inhabitation that affects its wetlands. The vegetation diversity of Great Lakes coastal wetlands has long been celebrated by naturalists (Voss 1978), and contemporary Natural Features Inventories have done much to describe it (Epstein et al. 2002, Albert 2003). However, the diversity and dynamics of vegetation in Great Lakes wetlands have deterred basinwide generalizations about relationships between vegetation and anthropogenic stress (Wilcox et al. 2002).

Previous studies of vegetation responses to anthropogenic stress in Great Lakes coastal wetlands have typically focused on individual species rather than plant communities (Chow-Fraser 2005, Herrick and Wolf 2005, Stanley et al. 2005, Wei and Chow-Fraser 2006, Trebitz and Taylor 2007). This is a logical starting point for studying plant–environment relationships, and our own understanding of Great Lakes coastal wetlands has benefitted from analyzing individual plant species as indicators of wetland physical environment (Johnston et al. 2007) and anthropogenic stress (Brazner et al. 2007a, Frieswyk et al. 2007, Johnston et al. 2008). Most quantitative studies of plant community–environment relationships have considered only portions of the Great Lakes, rather than the entire region (Gathman et al. 2005, Stanley et al. 2005). An important exception is an analysis of 62 marshes on the Canadian side of the Great Lakes by Loughheed and coworkers (2001), but that study focused on macrophyte beds with standing water above the soil surface, and did not consider herbaceous wet meadows, fens, or bogs.

Our goal is to develop plant community metrics to evaluate the condition of U.S. Great Lakes coastal wetlands, using vegetation data that we collected at 90 wetlands for the Great Lakes Environmental Indicators (GLEI) project (Johnston et al. 2007, Niemi et al. 2007). Specific objectives are to: (1) define Great Lakes wetland plant communities based on multivariate analyses and

(2) relate those plant assemblages to anthropogenic and physical environmental variables using CART analysis.

## METHODS

### *Site selection and vegetation sampling*

Ninety wetlands ("sites") spread across the U.S. Great Lakes coast (Fig. 1) were selected using an objective, stratified random statistical design representing the entire range of anthropogenic stress occurring along the U.S. Great Lakes coast (Danz et al. 2005). Sampling within study sites was conducted by visual observation of plant taxa in 1 × 1 m plots distributed along randomly placed transects. Transects were established with a geographic information system (GIS) prior to field campaigns, using a program called Sample (*available online*)<sup>8</sup> to randomize transect placement (Johnston et al. 2009). Each transect intersected a randomly selected point generated by the Sample program, and was oriented along the perceived water depth gradient. Transect length and target number of sample plots were determined in proportion to the size of the wetland to be sampled (20 plots/60 ha, minimum transect length = 40 m, minimum plots/site = 8). Plot locations were established in the field by dividing each transect into 20-m segments and randomly locating a plot in each segment using a random number table. In all, 1963 plots were sampled in the 90 wetlands studied. All vascular plant species and large nonvascular species such as *Chara vulgaris* L. and *Sphagnum* spp. were identified to the lowest taxonomic division possible by trained botanists who were tested annually to ensure consistency of visual observations (see Plate 1). Plants were identified using published taxonomic manuals (e.g., Chadde 1998), but the Interagency Taxonomic Information System was used as the ultimate taxonomic authority (taxonomic information *available online*).<sup>9</sup> Percent cover was estimated visually for each taxon according to modified Braun-Blanquet cover class ranges (ASTM 1997): <1%, 1% to <5%, 5% to <25%, 25% to <50%, 50% to <75%, 75% to 100%. Cover-class midpoints were used to calculate average values for each taxon at each site. Vegetation sampling was conducted from 2001 to 2003 and was restricted to the months of July and August to ensure that most of the vegetation could be identified and peak annual growth observed. Site characteristics and details of vegetation sampling methods are described by Johnston et al. (2007, 2008).

### *Environmental data*

Forty-four environmental variables were summarized for each site, many of which were initially computed for our prior publications (Table 1). These included several integrated measures of watershed anthropogenic stress, derived by principal components (PC) analysis of

multiple stressors of a common anthropogenic origin (Danz et al. 2007, Johnston et al. 2009): agriculture (PC1\_AG), human population and development (PC1\_URB), atmospheric deposition (PC1\_ATDEP), point source pollution (PC1\_NPDES), and the cumulative stress index (CSI), which was a generalized stress gradient derived from the preceding four PCs and land cover. These integrated measures were derived from existing geospatial data sources, but they have been confirmed by field studies to be related to wetland water quality (Trebitz et al. 2007, Morrice et al. 2008). In addition, two integrated measures of watershed soil characteristics were used, related to soil texture (PC1\_SOIL) and soil water availability, cation exchange capacity, and organic matter content (PC2\_SOIL; Danz et al. 2005). The metrics were summarized within watersheds that were specifically created by Hollenhorst and coworkers (2007) for each wetland site (watershed\_C, *n* = 90) or for "segment-sheds," lands draining to a segment of shoreline containing the wetland site (watershed\_S, *n* = 83), as noted in Table 1. Additional watershed variables used included total nitrogen and total phosphorus export from U.S. Geological Survey hydrologic units (watershed\_H, *n* = 34) computed by SPARROW surface water quality modeling (Smith et al. 1997), human population within wetland site-specific watersheds calculated from U.S. Census data, and cropland water erosion within wetland site-specific watersheds calculated from National Resources Inventory data (USDA 2000).

Several types of land use (row crops, development, forest, and wetlands and inland water; Wolter et al. 2006) were summarized for buffer areas of different widths (100, 500, 1000, 5000 m) around each wetland, and for the entire watershed draining to each wetland. The row crop and development buffers had previously been developed to assess the spatial scale of influence of anthropogenic disturbance on wetlands (Brazner et al. 2007b).

Two wetland hydrogeomorphic classifications were used as categorical data (Table 1). The three GLEI hydrogeomorphic classes (protected wetlands, river-influenced wetlands, and open coast wetlands) were applied as in Johnston et al. (2007). We also applied 12 hydrogeomorphic classes defined by Albert and coworkers (2005) and mapped by the Great Lakes Coastal Wetlands Consortium (*available online*).<sup>10</sup> In addition, each wetland was classified by its majority soil type (sand, silt, clay, organic) based on field determinations at each vegetation sample plot (Johnston et al. 2007) and its Strahler (1957) stream order based on a modified River Reach File 3 database provided by the U.S. Environmental Protection Agency.

Two environmental variables described hydrologic alterations within the wetlands studied. The hydrologic

<sup>8</sup> <http://www.quantdec.com/sample>

<sup>9</sup> <http://itis.gov>

<sup>10</sup> <http://www.glc.org/wetlands/>

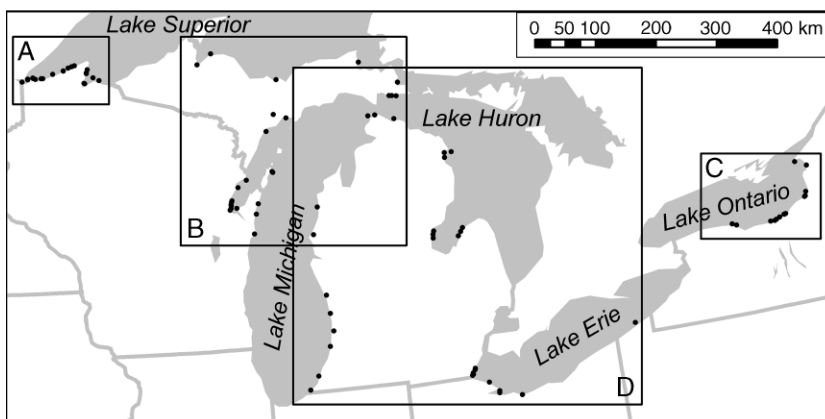


FIG. 1. Wetland study sites (solid circles) and locations of map extents along the U.S. Great Lakes coast, used in Figs. 3 and 9.

TABLE 1. Environmental variables used in CART (classification and regression tree) analysis of 90 wetland sites along the U.S. Great Lakes coast.

Parameter	Description	Units of measure	Continuous or categorical (no. categories)	Scale	Source
LAT	latitude	decimal deg	continuous		
LON	longitude	decimal deg	continuous		
LAKE	Great Lakes and Saginaw Bay	unitless	categorical (6)		
STATE	state	unitless	categorical (6)		
GDD	growing degree-days	deg C	continuous	wetland	McKenney et al. (2007)
HYG_GLEI	hydrogeomorphic type	unitless	categorical (3)	wetland	Johnston et al. (2007)
HYG_GLC	hydrogeomorphic type	unitless	categorical (12)	wetland	Albert et al. (2005)
WETL_SOIL	sand, silt, clay, organic	unitless	categorical (4)	wetland	Johnston et al. (2007)
WETL_AREA	wetland area	ha	continuous	wetland	Brazner et al. (2007b)
SHED_AREA	watershed area	ha	continuous	watershed	Brazner et al. (2007b)
STRAHLER	Strahler stream order	unitless	continuous	watershed	see <i>Methods</i>
DIKED	presence/absence of dikes	unitless	categorical (2)	wetland	Johnston et al. (2008)
CSI	cumulative stress index	unitless	continuous	watershed	Danz et al. (2007)
HMI	hydrologic modification index	m/ha	continuous	wetland	Johnston et al. (2008)
POPU	human population	count	continuous	watershed	see <i>Methods</i>
PC1_AG	agriculture PC	unitless	continuous	watershed	Danz et al. (2007)
PC1_URB	human population PC	unitless	continuous	watershed	Danz et al. (2007)
PC1_ATDEP	atmospheric deposition PC	unitless	continuous	watershed	Danz et al. (2007)
PC1_NPDES	point source PC	unitless	continuous	watershed	Danz et al. (2007)
PC1_SOIL	soil texture	unitless	continuous	watershed	Danz et al. (2005)
PC2_SOIL	soil water avail/CEC/organic matter	unitless	continuous	watershed	Danz et al. (2005)
EROS	cropland water erosion	kg·ha <sup>-1</sup> ·yr <sup>-1</sup>	continuous	watershed	USDA (2000)
TN_export	mean total nitrogen export	kg/d	continuous	watershed	Smith et al. (1997)
TP_export	mean total phosphorus export	kg/d	continuous	watershed	Smith et al. (1997)
RC_100	row crops	areal fraction	continuous	100-m buffer	Brazner et al. (2007b)
DEV_100	development	areal fraction	continuous	100-m buffer	Brazner et al. (2007b)
FOR_100	forest	areal fraction	continuous	100-m buffer	see <i>Methods</i>
WETW_100	wetlands and inland water	areal fraction	continuous	100-m buffer	see <i>Methods</i>
RC_500	row crops	areal fraction	continuous	500-m buffer	Brazner et al. (2007b)
DEV_500	development	areal fraction	continuous	500-m buffer	Brazner et al. (2007b)
FOR_500	forest	areal fraction	continuous	500-m buffer	see <i>Methods</i>
WETW_500	wetlands and inland water	areal fraction	continuous	500-m buffer	see <i>Methods</i>
RC_1000	row crops	areal fraction	continuous	1000-m buffer	Brazner et al. (2007b)
DEV_1000	development	areal fraction	continuous	1000-m buffer	Brazner et al. (2007b)
FOR_1000	forest	areal fraction	continuous	1000-m buffer	see <i>Methods</i>
WETW_1000	wetlands and inland water	areal fraction	continuous	1000-m buffer	see <i>Methods</i>
RC_5000	row crops	areal fraction	continuous	5000-m buffer	Brazner et al. (2007b)
DEV_5000	development	areal fraction	continuous	5000-m buffer	Brazner et al. (2007b)
FOR_5000	forest	areal fraction	continuous	5000-m buffer	see <i>Methods</i>
WETW_5000	wetlands and inland water	areal fraction	continuous	5000-m buffer	see <i>Methods</i>
RC_shed	row crops	areal fraction	continuous	watershed	Brazner et al. (2007b)
DEV_shed	development	areal fraction	continuous	watershed	Brazner et al. (2007b)
FOR_shed	forest	areal fraction	continuous	watershed	see <i>Methods</i>
WETW_shed	wetlands and inland water	areal fraction	continuous	watershed	see <i>Methods</i>

Note: Key to abbreviations: PC, principal components; CEC, cation exchange capacity.



modification index (HMI) was computed as the length per unit wetland area of within-wetland features that likely disrupt the natural flow and fluctuation of water within wetlands, such as road beds, dikes, and ditches (Bourdagh et al. 2006, Johnston et al. 2008). The presence or absence of dikes was also used as a separate categorical variable.

A climate surface of average growing season growing degree-days (GDD) for the period 1961–1990, interpolated to a 30 arc second grid, was obtained from the Canadian Forest Service (McKenney et al. 2007). Data were extracted for each wetland study site by intersecting their locations with the gridded climate data using ArcMap version 9.2 (ESRI 2006).

#### Statistical analysis

A data matrix was constructed of taxa cover (columns) by site (rows). Infrequently occurring species were removed prior to statistical analysis (Clarke and Warwick 2001); taxa were retained that occurred at  $\geq 10\%$  of sites, plus taxa that occurred at fewer sites but had relative percent cover  $> 15\%$  in any wetland. Of the 138 taxa used, 120 were identified to species and 18 were identified to genus. The taxon, “invasive *Typha*,” included both *Typha angustifolia* and *Typha*  $\times$  *glauca* but did not include the native species *Typha latifolia*. Square-root transformation was done to downweight high abundance species, and similarity was computed after Bray and Curtis (1957). Plant communities were classified by agglomerative hierarchical clustering with group-average linking based on Bray-Curtis similarities. The SIMPER procedure (Clarke and Gorley 2006) was used to determine taxa contributions to the average similarity within a cluster and the contributions to the average Bray-Curtis dissimilarity between pairs of clusters. Nonmetric multidimensional scaling (MDS) was used with the Bray-Curtis similarity data to ordinate sites, using 25 restarts and a minimum stress of 0.01. All plant community analyses were conducted with PRIMER version 6 (Clarke and Gorley 2006).

The floristic quality index (FQI) was also computed for each site as a widely tested metric of biological condition (Lopez and Fennessy 2002, Bourdagh et al. 2006, Mack et al. 2008). The FQI computation weights plant species based on their coefficient of conservatism (*C* value), a zero-to-10 ranking of a species’ fidelity to remnant natural plant communities:

$$FQI = \bar{C} \times \sqrt{N} \quad (1)$$

where  $\bar{C}$  is mean coefficient of conservatism, and *N* is the number of native species present (Swink and Wilhelm 1979). *C* values were obtained for Wisconsin, Michigan, and Ohio (Herman et al. 2001, Bernthal 2003, Andreas et al. 2004), and used to compute FQI values for wetlands in those states. Ohio *C* values were also applied to the one site in Pennsylvania (Presque Isle on Lake Erie) and 13 sites in New York State, which lacks a state-specific *C* value list. FQI was computed for each

sample plot and averaged by site so as to reduce sampling area bias, after Bourdagh et al. (2006).

Classification and regression trees (CART) were constructed, using FQI and the first MDS axis values as the response variables and the environmental variables (Table 1) as potential predictor variables. We used the recursive partitioning and regression trees package (RPART version 3.1-39; Therneau and Atkinson 1997) in the statistical software R, version 2.7.0 (R Development Core Team 2008), which is programmed according to the algorithms suggested by Breiman et al. (1984). RPART allows cross-validation runs on the data to determine the optimally sized tree, selected as the subtree that performs best on a validation set. We performed a 10-fold cross-validation, where each run consisted of 10 random divisions of the data into 90% learning and 10% test sets. For each split we computed the complexity parameter (cp), a measure of how much additional accuracy a split must add to the entire tree to warrant the additional complexity. Any split that did not decrease the overall lack of fit by a factor of cp was not attempted, meaning that the overall  $r^2$  must increase by cp at each step. We determined the optimal tree size from the table of cross-validation error values for various tree lengths as the number of splits corresponding to the minimum cross-validation error, and pruned the tree to the cp value for this optimum. Output from the summary function of RPART was examined to evaluate surrogate split variables. A surrogate split best reproduces the optimal split but on a different covariate. Greater detail on CART and its application to ecological data can be found in De’ath and Fabricius (2000) and Urban (2002).

## RESULTS

### Plant community clusters

The hierarchical cluster analysis yielded eight plant communities at a similarity level of 25%, each containing one to 22 sites (Fig. 2). Plant communities were defined by the species that contributed most to each cluster’s similarity (Tables 2 and 3). The plant communities also appeared to group geographically, even though location was not an input variable in the analysis (Fig. 3).

The Grand Mere wetland (site 49, Fig. 3D), the first community distinguished in the cluster analysis, was in a class by itself. This site on the southeastern shore of Lake Michigan was geomorphologically and hydrologically distinct from the other Great Lakes coastal sites, consisting of a shallow lake behind a 43-m high sand dune, with a narrow stream providing the only surface water connection to Lake Michigan. The predominant vegetation sampled consisted of submergent plants and water lilies surrounded by emergent plants (*Peltandra virginica*, *Pontederia cordata*, *Schoenoplectus acutus*) and a floating mat of buttonbush shrubs (*Cephalanthus occidentalis*; Table 3).

The next group separated by the cluster analysis consisted of two sites adjacent to North Maumee Bay

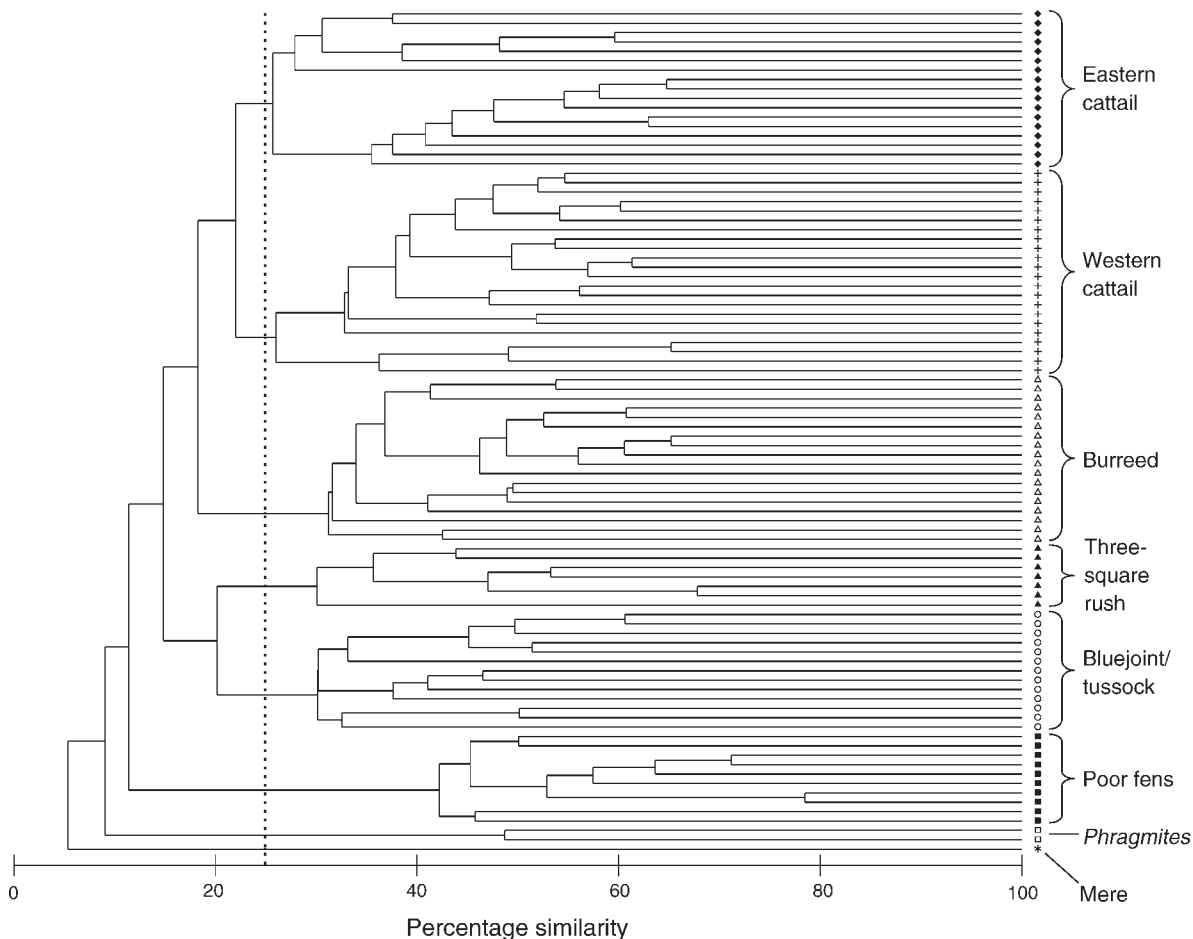


FIG. 2. Dendrogram showing results of hierarchical clustering. The dashed line at 25% similarity is used to define the eight broad plant community clusters.

on western Lake Erie that were dominated by the invasive common reed, *Phragmites australis* (sites 71 and 72, Fig. 3D). Although *Phragmites* occurred at about one-third of the sites sampled throughout the Great Lakes, these two wetlands were distinctive in their abundance of *Phragmites*, which constituted 53% and 64% of their average cover. Only two plant species (*Phragmites* and *Stuckenia pectinata*) contributed to the average similarity of this cluster, which was 48.7% (Table 3).

The third group distinguished was “northern poor fens,” wetlands vegetated by woolly-fruit sedge (*Carex lasiocarpa* var. *americana*) and ericaceous shrubs growing on *Sphagnum*-covered organic soils. Species contributing to the similarity of this group included *Sphagnum* moss, woolly-fruit sedge, common bogbean (*Meyenanthus trifoliata*), pitcher plant (*Sarracenia purpurea*), and several short-stature shrubs: bog rosemary (*Andromeda polifolia* var. *glaucophylla*), leatherleaf (*Chamaedaphne calyculata*), and sweetgale (*Myrica gale*; Table 2). Eight of the sites classified as northern poor fens were on Lake Superior; the other two sites were at

the northern end of Lake Michigan (Fig. 3A, B). The average similarity of northern poor fens was 48.6%, comparable to the high similarity of the *Phragmites* group despite the greater number of sites and species contributing to similarity.

Sites in the “bluejoint/tussock sedge” group, named for the two species that contributed most to the group’s similarity (*Calamagrostis canadensis* and *Carex stricta*; Table 2), were located primarily on northern Lakes Huron and Michigan (Fig. 3B, D). A geographic outlier included in this group was the Presque Isle site, a recurved sandspit projecting into Lake Erie in northeast Pennsylvania (site 77, Fig. 3D).

“Burreed/lake sedge” (*Sparganium eurycarpum* and *Carex lacustris*) marshes occurred almost exclusively on Lake Superior (Fig. 3A), with one geographic outlier on the Thunder Bay River wetland on northern Lake Huron (site 60, Fig. 3D). Other species that contributed to the similarity of the 18 sites in this large group included common arrowhead (*Sagittaria latifolia*), broadleaf cattail (*Typha latifolia*), marsh cinquefoil (*Comarum palustre*), and two other sedges (*Carex*

TABLE 2. Average percentage similarity across sites for taxa in plant communities of the northern Great Lakes basin.

Species	Northern poor fens (n = 10)	Bluejoint/tussock sedge (n = 13)	Burreed/lake sedge (n = 18)
<i>Andromeda polifolia</i> var. <i>glaucophylla</i>	7.3		
<i>Calamagrostis canadensis</i>		27.2	
<i>Calla palustris</i>			3.7
<i>Campanula aparinoides</i>		5.3	
<i>Carex lacustris</i>			10.2
<i>Carex lasiocarpa</i> var. <i>americana</i>	19.3	7.1	
<i>Carex stricta</i>		17.7	4.8
<i>Carex utriculata</i>			4.5
<i>Chamaedaphne calyculata</i>	7.0		
<i>Cladium mariscoides</i>	3.2		
<i>Comarum palustre</i>			5.5
<i>Juncus nodosus</i>		3.5	
<i>Menyanthes trifoliata</i>	4.7		
<i>Myrica gale</i>	15.1		
<i>Sagittaria latifolia</i>			7.5
<i>Sarracenia purpurea</i>	4.3		
<i>Schoenoplectus tabernaemontani</i>		6.3	
<i>Sparganium eurycarpum</i>			13.0
<i>Sphagnum</i> spp.	12.1		
<i>Typha latifolia</i>			6.2
<i>Utricularia macrorhiza</i>			3.0
Number of sites	10	13	18
Average similarity (%)	48.6	33.8	37.5

Note: Data are shown for taxa contributing 3.0% or more to average similarity.

*stricta*, *C. utriculata*). Most of these sites were associated with rivers.

“Three-square rush marshes” consisted of sites dominated by *Schoenoplectus pungens* var. *pungens*, the

species that contributed 31.5% to the similarity of this group (Table 3). Six of the seven sites in this group were in Lake Huron’s Saginaw Bay (sites 62–67, Fig. 3D); the seventh site was Goose Bay on the northeast shore of

TABLE 3. Average percentage similarity across sites for taxa in plant communities of the southern Great Lakes basin.

Species	Grand Mere (n = 1)	<i>Phragmites</i> (n = 2)	Three-square rush (n = 7)	Western cattail (n = 22)	Eastern cattail (n = 17)
<i>Calamagrostis canadensis</i>			3.1	9.4	
<i>Cephalanthus occidentalis</i>	11.8				
<i>Ceratophyllum demersum</i>					6.4
<i>Chara vulgaris</i>			15.3		
<i>Decodon verticillatus</i>					3.0
<i>Hydrocharis morsus-ranae</i>					5.3
<i>Impatiens capensis</i>				10.9	
<i>Juncus balticus</i> var. <i>littoralis</i>			6.4		
<i>Juncus nodosus</i>			4.8		
<i>Leersia oryzoides</i>				7.2	
<i>Lemna minor</i>					12.2
<i>Nuphar lutea</i> ssp. <i>pumila</i>	6.7				
<i>Nymphaea odorata</i>	20.3				
<i>Peltandra virginica</i>	12.3				
<i>Phalaris arundinacea</i>				6.1	3.1
<i>Phragmites australis</i>		85.5	3.8		
<i>Pontederia cordata</i>	9.9				
<i>Sagittaria latifolia</i>				4.8	
<i>Schoenoplectus acutus</i>	17.3				
<i>Schoenoplectus pungens</i>			31.5		
<i>Schoenoplectus tabernaemontani</i>				5.0	
<i>Stuckenia pectinata</i>	14.0	7.0			
Invasive <i>Typha</i>				17.1	31.0
<i>Typha latifolia</i>					3.1
<i>Urtica dioica</i>				3.3	
<i>Utricularia macrorhiza</i>	6.2				
Number of sites	1	2	7	22	17
Average similarity (%)		48.7	39.0	35.4	32.9

Notes: Data are shown for taxa contributing 3.0% or more to average similarity. Grand Mere data are relative cover by species contributing 3.0% or more to total cover.

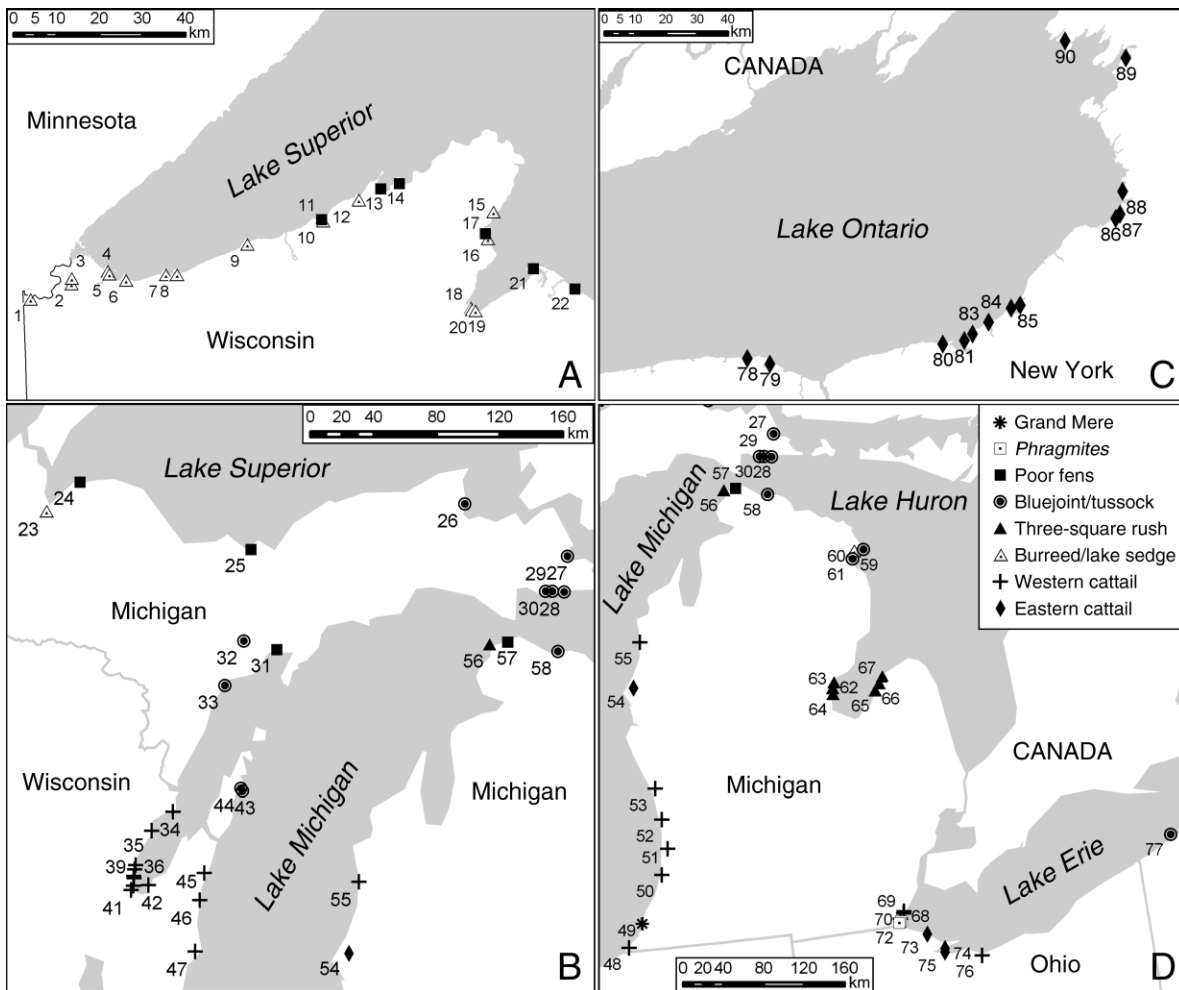


FIG. 3. Study sites by hierarchical cluster assignment: (A) western Lake Superior (sites 1–22); (B) eastern Lake Superior, northern Lake Michigan, and northern Lake Huron (sites 23–47, 54–58); (C) Lake Ontario (sites 78–90); (D) eastern Lake Michigan, Lake Huron, and Lake Erie (sites 27–30, 48–77).

Lake Michigan (site 56, Fig. 3B). All seven sites had similar geomorphology, consisting of open-coast wetlands where emergent plants grow out of shallow lakebed that is relatively exposed to wave action.

The two largest groups were dominated by invasive cattail taxa (*Typha angustifolia* and *Typha × glauca*). Named “eastern cattail marshes” and “western cattail marshes” due to their general geographic distribution, they differed in associated species (Table 3). The western cattail marshes included most of the wetlands on southern Lake Michigan, plus four sites on Lake Erie. The eastern cattail marshes included all 13 sites on Lake Ontario, three sites on western Lake Erie, and the Big Sable site on Lake Michigan (site 54, Fig. 3D). The Big Sable site contained six sedge species and remnant *Sphagnum* patches, yet it resembled the cattail-dominated wetlands of Lake Ontario more than its neighboring wetlands along the eastern shore of Lake Michigan due to extensive invasion by *Typha*.

A dissimilarity matrix showed the eight major plant communities to be quite distinct, with average dissimilarity values of 78% or more (Table 4). Not surprisingly, the two cattail groups were the most similar, and the Grand Mere wetland was least similar to other cluster groups.

The major plant communities varied significantly in quality as measured by FQI ( $F_{6,82} = 47.3, P < 0.001$ ). The poor fens had the highest average FQI, followed by the bluejoint/tussock sedge and burreed/lake sedge wetlands (Fig. 4). The remaining four plant communities, which included most of the wetlands sampled in the southern portion of the Great Lakes coast, had the lowest average FQI values but were statistically indistinguishable on the basis of FQI (Fig. 4).

Slicing the hierarchical cluster analysis dendrogram at a similarity level of 30% divided the two large cattail marsh groups into five smaller groups (Table 5). The western cattail marshes split geographically into “blue-



TABLE 4. Average dissimilarity (%) between major plant communities identified.

Plant community	Grand Mere	<i>Phragmites</i>	Northern poor fens	Bluejoint/tussock sedge	Three-square rush	Burreed/lake sedge	Western cattail
<i>Phragmites</i>	93.86						
Poor fen	98.43	97.88					
Bluejoint/tussock	95.12	93.29	83.94				
Three-square rush	96.32	85.02	94.72	79.81			
Burreed/lake sedge	95.02	95.17	82.17	81.90	91.17		
Western cattail	95.79	85.45	92.83	79.68	85.23	80.77	
Eastern cattail	89.40	89.89	90.76	89.20	90.66	82.93	77.96

joint/cattail marshes” on Lake Michigan and “arrowhead/*Phragmites*/cattail marshes” on Lake Erie; these two groups contained a similar proportion of invasive cattail but were distinguished from each other by associated species. The eastern cattail marshes split into three groups: “Magee Marsh” on Lake Erie (site 73), “duckweed/reed canarygrass/cattail marshes” on Lake Ontario (sites 80, 84, 86, 87) and Lake Erie (sites 74 and 75), and “cattail-dominated marshes” on Lake Michigan (site 54) and Lake Ontario (sites 78–79, 81–83, 85, 88–90).

Our study sites contained three northern rich fens (sites 58, 59, 61), a floristically unusual wetland community that grows on calcareous alkaline soils in northern Lakes Michigan and Huron. These wetlands contained the calciphiles *Argentina anserina*, *Chara vulgaris*, *Carex viridula*, *Clinopodium arkansanum*, *Dasiphora floribunda*, *Dichanthelium acuminatum* var. *lindheimeri*, *Hypericum kalmianum*, *Lobelia kalmii*, *Oligoneuron houghtonii*, *O. ohioensis*, *Parnassia glauca*, *Primula mistassinica*, and *Triglochin maritima*, but only the first two species were sufficiently common to be included among the 138 species used in this data analysis. These three sites would have split out from other members of the bluejoint/tussock sedge cluster had we sliced the hierarchical cluster analysis dendrogram at a similarity level of 30.2%, a threshold that also would have split the Goose Bay wetland from the six three-square marshes in Saginaw Bay, yielding a total of 13 clusters. However, we opted for a lower similarity level (25%) that identified fewer clusters.

*Nonmetric multidimensional scaling*

The most stable three-dimensional MDS configuration was achieved with a stress of 0.16. Clarke and Warwick (2001) advise that an MDS analysis with a stress value of this magnitude is usable but should be cross-checked against results from an alternative technique, and the MDS results agreed well with the results of the hierarchical cluster analysis (Fig. 5). The first axis (MDS1) separated the poor fens, bluejoint/tussock sedge, and burreed/lake sedge wetlands (negative coefficients) from the invasive-dominated *Phragmites* and cattail marshes (positive coefficients). The second axis (MDS2) separated the *Phragmites*, bluejoint/tussock sedge meadows, three-square marshes, and western

cattail marshes (positive coefficients) from the poor fens, burreed/lake sedge, and eastern cattail marshes (negative coefficients). The third axis (not shown) distinguished the Grand Mere site (MDS3 value = 1.68) from all other sites (MDS3 values ≤ 0.87).

We compared MDS1 values with existing indices representing wetland vegetative condition (the floristic quality index, FQI) and watershed anthropogenic stress (the cumulative stress index, CSI). The strong inverse linear regression ( $R^2 = 0.79$ ,  $P < 0.001$ ) between MDS1 and FQI indicated that MDS1 represented floristic condition (Fig. 6). The relationship between MDS1 and CSI was weaker ( $R^2 = 0.65$ ,  $P < 0.001$ ) because CSI values were bimodally clustered and strongly influenced by lake of occurrence (Fig. 7). Lake Superior had uniformly low CSI values (<1.8; low degree of anthropogenic stress) and Lakes Ontario and Erie had uniformly high CSI values (>2.5; high degree of anthropogenic stress), whereas CSI values for Lakes

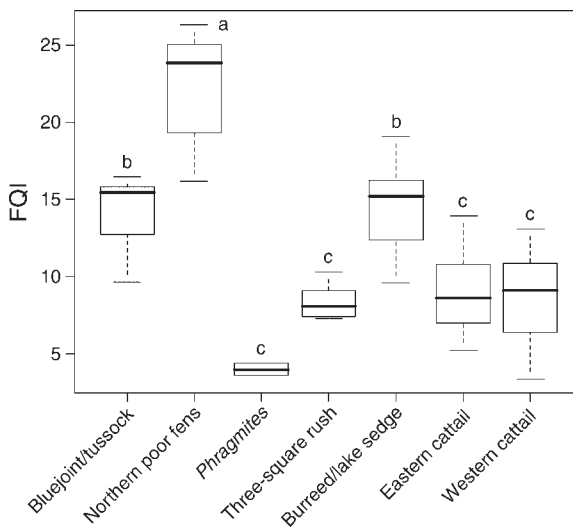


FIG. 4. Box plots summarizing FQI (floristic quality index) values by hierarchical cluster. FQI values are calculated as in Eq. 1. In each box plot, the heavy horizontal line crossing the box is the median, the bottom and top of the box are the lower and upper quartiles, and the whiskers are the minimum and maximum values. Clusters with the same letter code are not significantly different (Tukey multiple comparison of means,  $P < 0.05$ ).

TABLE 5. Taxa contributing 3.0% or more to average similarity of cattail communities identified, with average percentage similarity across sites.

Species	Western cattail marshes		Eastern cattail marshes		
	Bluejoint/ cattail, L. Michigan (n = 18)	Arrowhead/ <i>Phragmites</i> / cattail, L. Erie (n = 4)	Cattail- dominated (n = 10)	Duckweed/ reed canary grass/cattail (n = 6)	Magee Marsh, L. Erie (n = 1)
<i>Calamagrostis canadensis</i>	12.8				4.7
<i>Carex lacustris</i>					4.7
<i>Ceratophyllum demersum</i>			3.4	10.1	6.2
<i>Decodon verticillatus</i>			3.4		
<i>Eleocharis erythropoda</i>	3.0				
<i>Eleocharis palustris</i>					3.0
<i>Hydrocharis morsus-ranae</i>			7.3		
<i>Impatiens capensis</i>	11.5	3.2	4.4		
<i>Leersia oryzoides</i>	6.2	6.0			
<i>Lemna minor</i>			7.4	22.5	
<i>Lemna trisulca</i>					4.0
<i>Nelumbo lutea</i>		13.7			
<i>Nymphaea odorata</i>				3.1	3.6
<i>Phalaris arundinacea</i>	4.4	9.7		17.3	
<i>Phragmites australis</i>		15.4			
<i>Polygonum amphibium</i>					28.0
<i>Pontederia cordata</i>				9.0	
<i>Ricciocarpus natans</i>					5.1
<i>Sagittaria latifolia</i>		25.0			
<i>Schoenoplectus tabernaemontani</i>	4.1	5.0			
<i>Sparganium eurycarpum</i>				7.6	
<i>Stuckenia pectinata</i>					5.3
<i>Thelypteris palustris</i>			5.8		
Invasive <i>Typha</i>	14.9	15.1	41.9	11.1	
<i>Urtica dioica</i>	4.3				
<i>Utricularia macrorhiza</i>					15.4
Number of sites	18	4	10	6	1
Average similarity (%)	39.5	45.4	43.5	37.0	

Note: Magee Marsh data are relative cover by species contributing 3.0% or more to total cover.

Michigan and Huron spanned a broader range, reflecting their north-south contrast in land development. MDS1 was also highly correlated with several environmental variables: GDD ( $r = 0.80$ ), PC1\_AG ( $r = 0.75$ ), and latitude ( $r = -0.76$ ). MDS2 differed with lake of occurrence, being negative for most sites on Lakes Superior and Ontario, positive for most sites on Lakes Huron and Michigan, and wide-ranging ( $-0.71$  to  $0.89$ ) for sites on Lake Erie.

#### CART analysis

A classification and regression tree (CART) model that used the first MDS axis as the response variable had six terminal nodes (Fig. 8). The final CART solution used a combination of variables representing regional climate, watershed development, and wetland size. The first split utilized the cumulative stress index, splitting the data at CSI values above and below 1.72. Node 2 split the data by development ( $DEV\_5000 < 3.9\%$ ), resulting in two terminal groups, leaves A and B, which had average MDS1 scores of  $-0.92$  and  $-0.37$ , respectively (Fig. 8). Node 3 split off the warmest sites ( $GDD \geq 2422$ ), and the resulting leaf F had the highest average MDS1 scores (i.e., poorest quality wetlands), containing all of the Lake Erie wetlands plus the Galien River wetland at the southern extreme of Lake Michigan

(site 48, Fig. 3D). Node 6 split at PC1\_URB values less than  $-0.254$ , and the least urban sites from that split terminated in leaf C. The final split (node 13) differentiated wetlands by size: nine wetlands with an area of 58 ha or more were placed in leaf D, while the remaining 20 wetlands were placed in leaf E. A boxplot showed good separation of average MDS1 values among the six groups, with the only outlier being Magee Marsh in leaf F (Fig. 8). The complete model had an  $r^2 = 0.82$ .

The CART analysis done using FQI as the endpoint yielded a model with  $r^2 = 0.75$  that utilized only climatic (GDD), physiographic (hydrogeomorphology, watershed soil texture), and forest cover variables (Table 6). The first split, at a boundary of 1835 GDD, bisected sites 43 and 44 on Lake Michigan and separated Saginaw Bay sites (warmer than 1835 GDD) from northern Lake Huron sites; all Lake Superior sites were north of the 1835 GDD boundary, and all Lake Ontario and Lake Erie sites were south of it. The group of northern sites was subsequently split by geomorphology, which separated protected wetlands into terminal leaf A. The remaining northern sites were separated into those with forest cover greater or less than 11% within the 500-m buffer around the wetland. The group of 50 sites with  $GDD \geq 1835$  was further split by  $GDD \geq 2422$ , which

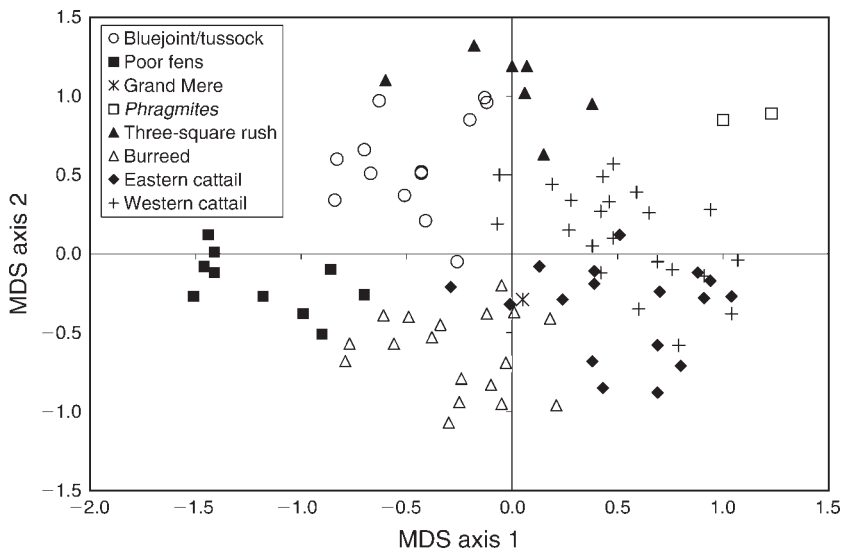


FIG. 5. Scatterplot of sites relative to the first and second MDS (multidimensional scaling) axes. Wetland sites are coded by hierarchical cluster.

yielded a terminal leaf G identical to terminal leaf F in the MDS1 model (western Lake Erie plus the Galien River on Lake Michigan), which had the lowest average FQI values. The  $GDD \geq 1835$  group with the highest average FQI had watershed forest cover  $\geq 38.3\%$ ; sites with less forest cover were distinguished into groups of coarser (PC1\_SOIL greater than or equal to  $-0.206$ ) vs. finer-textured watershed soils (PC1\_SOIL less than  $-0.206$ ).

We found similarities between the CART and hierarchical clustering classifications at low values of anthropogenic stress, even though we did not include information about individual plant species in the CART

analysis. Leaf A of the MDS1 CART model contained nine out of 10 northern poor fens, and leaf A of the FQI CART model contained eight out of 10 poor fens. At greater levels of anthropogenic stress, however, fewer floristic and geographic similarities emerged between the CART and hierarchical clustering classifications. The MDS1 CART leaves D–F contained primarily *Typha* wetlands, consistent with the positions of those community clusters relative to MDS axis 1 (Fig. 5). The wetlands of Saginaw Bay and Lake Ontario, which were respectively classified as three-square rush (Saginaw) and eastern cattail marshes (Lake Ontario) by the 25% similarity hierarchical clustering (Fig. 3C, D), were

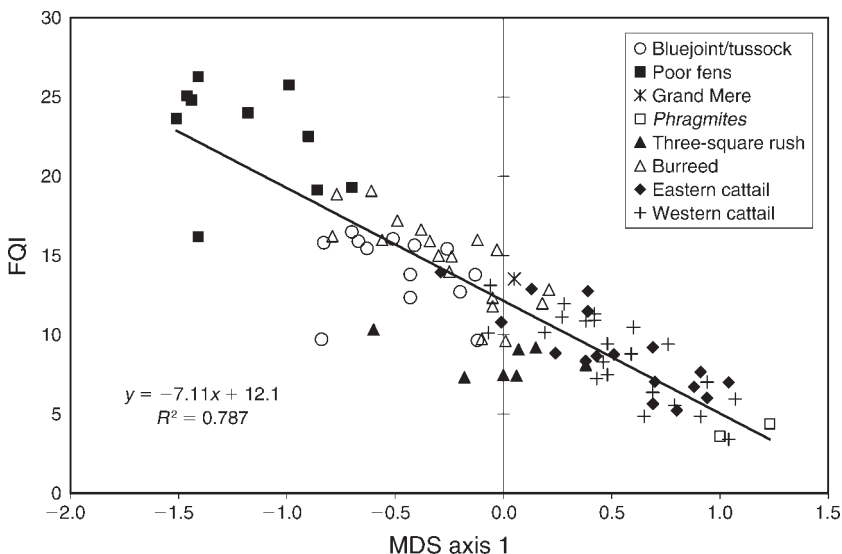


FIG. 6. Inverse regression between FQI and MDS1; points are classified by hierarchical cluster.

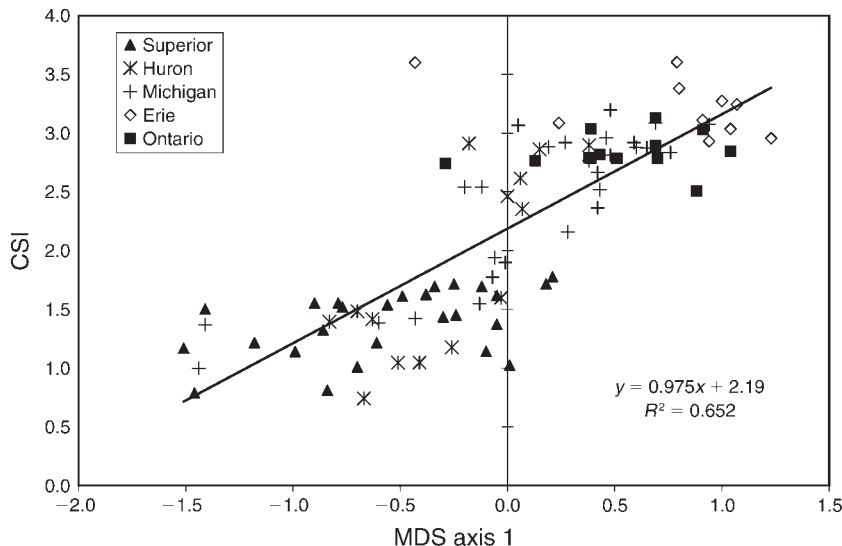


FIG. 7. Scatterplot between CSI (cumulative stress index) and MDS1; points are classified by lake.

assigned to leaves C, D, and E by the MDS1 CART analysis due to differing wetland sizes (node 13) and levels of urban development (node 6). In contrast, all of the western Lake Erie wetlands were included in leaf F of the MDS1 model (leaf G of the FQI model) due to their climate ( $\geq 2422$  GDD), despite being assigned to three different floristic groups by the hierarchical clustering analysis (Fig. 3D). Such differences in classification were expected, given that different input variables were used in the two classification procedures

plant species cover for the hierarchical clustering analysis and environmental variables for the CART).

Analysis of surrogate splits for the MDS1 model identified several environmental variables that produced nearly comparable results at the five split nodes (Table 7). The five surrogate splits at the first node had a high degree of concordance with the optimal split ( $\geq 92\%$ ), indicating that they were all relatively interchangeable: GDD, PC1\_URB, LAT, EROS, and RC\_5000. All of these splits coincided with a geographic/climatic/dis-

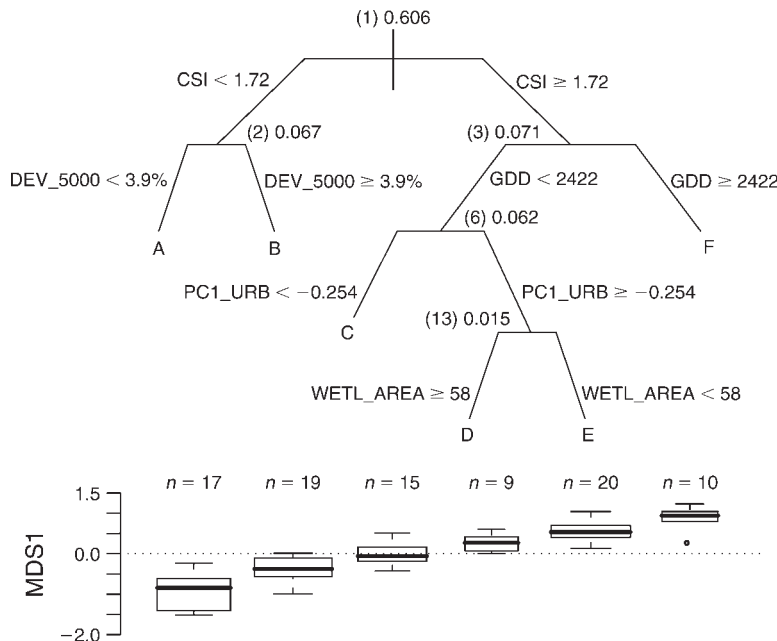


FIG. 8. Classification and regression tree between site MDS1 scores and environmental variables, with box plots showing MDS1 values for each terminal node group. Terminal nodes ("leaves") are labeled with letter codes A–F; split nodes are identified by the number in parentheses followed by the complexity parameter for that node. The outlier value in the box plot for terminal node F is Magee Marsh (site 73).

TABLE 6. CART (classification and regression tree) model using FQI as the endpoint value ( $r^2 = 0.75$ ).

Leaf	Characteristics	Mean FQI	<i>n</i>	Site numbers
A	GDD < 1835; HYG_GLEI = Pw	20.0	13	6, 11, 13, 14, 17, 20, 22–24, 31, 57, 58, 61
B	GDD < 1835; HYG_GLEI = Rw, Cw; FOR_500 ≥ 11%	15.8	18	1–5, 7–9, 12, 15, 16, 21, 25, 28–30, 33, 59
C	GDD < 1835; HYG_GLEI = Rw, Cw; FOR_500 < 11%	13.1	9	10, 18, 19, 26, 27, 32, 44, 56, 60
D	GDD ≥ 1835; GDD < 2422; FOR_shed ≥ 38.3%	11.4	12	34, 35, 49, 54, 55, 82–88
E	GDD ≥ 1835, GDD < 2422; FOR_shed < 38.3%; PC1_SOIL ≥ -0.206	9.6	16	36–40, 43, 45, 47, 50–53, 62, 64, 67, 77
F	GDD ≥ 1835, GDD < 2422; FOR_shed < 38.3%; PC1_SOIL < -0.206	7.2	12	41, 42, 46, 63, 65, 66, 78–81, 89, 90
G	GDD ≥ 1835, GDD ≥ 2422	5.5	10	48, 68–76

Note: See Table 1 for a definition of parameters.

turbance boundary separating northern and southern coastal wetlands at ~45° latitude, a boundary that affected both cultivated and natural vegetation (Fig. 9). Wetlands north of that latitude had a shorter growing season and were subject to less agricultural influence (particularly from row crop agriculture) and cumulative stress compared to wetlands below the boundary. At node 2, the closest surrogate split was a variable (DEV\_1000) that was a spatial subset of the optimal split (DEV\_5000). At node 3, a surrogate split occurred at 42° latitude, separating wetlands north of 42° from the Lake Erie wetlands, many of which were diked and had little forest within their 5000-m buffer (Table 7). At node 6, the strongest surrogate variable was watershed development (DEV\_shed), which had a concordance of 91% with the optimal split (PC1\_URB).

DISCUSSION

*A unifying approach*

Evaluating the existing condition of wetlands requires a new, systematic approach that unifies plant community analysis with methods to identify environmental drivers that alter biological condition. The process that we used to evaluate wetland condition and identify environmental drivers consisted of several key steps: (1) selecting sample wetlands using a stratified random approach that is designed to represent the entire range of anthropogenic stress (Danz et al. 2005), (2) collecting field data that represent the range of water depths within the wetlands sampled (Johnston et al. 2007), (3) evaluating the field data using MDS to determine a biological condition gradient across the wetlands sampled, (4) hierarchical clustering to interpret the condition results relative to recognizable plant communities, (5) analyzing with CART to relate biological condition to natural and anthropogenic environmental drivers, and (6) mapping the results to display their geographic distribution. We recommend this unifying approach for evaluating wetland biological condition and relating it to environmental drivers.

MDS analysis is the backbone of the approach. In contrast to the use of reference wetlands, in which a wetland deemed to represent a relatively unaltered condition is chosen for comparison with other wetlands

(Brinson and Rheinhardt 1996), the biological condition gradient defined by the MDS is the reference used to compare an individual wetland with all other wetlands sampled. This eliminates the subjectivity involved in choosing a reference wetland, which might not truly represent pre-disturbance floristic conditions. In addition, our approach is more suitable for studies over broad geographic regions than the reference approach.

Other authors have demonstrated the utility of MDS with vegetation data for evaluating wetland condition, but within much smaller geographic areas, such as the wetlands in the Muskegon River watershed (Lougheed

TABLE 7. Top five surrogate splits for split nodes shown in Fig. 8, and their agreement with the optimal split.

Node	Surrogate split	Agreement
Node 1 ( <i>n</i> = 90)	GDD < 1795	0.97
	PC1_AG < 0.04	0.96
	LAT ≥ 45.0°	0.94
	EROS < 0.79	0.93
	RC_5000 < 1%	0.92
Node 2 ( <i>n</i> = 36)	DEV_1000 < 6%	0.83
	HYG_GLC (BL, BSR, BSS, LOE, RCD)†	0.72
	DEV_500 < 10%	0.72
	WETL_SOIL (organic)	0.69
Node 3 ( <i>n</i> = 54)	PC2_SOIL < 0.89	0.69
	LAT ≥ 41.9°	1.00
	LAKE (Superior, Michigan, Huron, Ontario)	0.96
	FOR_5000 ≥ 5%	0.93
Node 6 ( <i>n</i> = 44)	DIKED (not)	0.91
	STATE (MI lower peninsula, NY, PA, WI)	0.89
	DEV_shed < 6%	0.91
	GDD < 1905	0.80
	PC1_AG < 0.31	0.80
Node 13 ( <i>n</i> = 29)	EROS < 1.66	0.80
	WETW_5000 ≥ 15%	0.80
	CSI < 2.48	0.83
	WETW_shed ≥ 8%	0.83
	PC1_SOIL ≥ 0.60	0.79
	WETW_500 ≥ 32%	0.79
WETW_1000 ≥ 16%	0.79	

Notes: The split threshold shows variables that would go to the left side of the split, with codes for variable categories in parentheses. See Table 1 for a definition of parameters.

† Key to abbreviations: BL, barrier-protected beach lagoon; BSR, barrier-protected ridge and swale complex; BSS, barrier-protected sand spit swales; LOE, lacustrine open embayment; RCD, riverine channel delta.



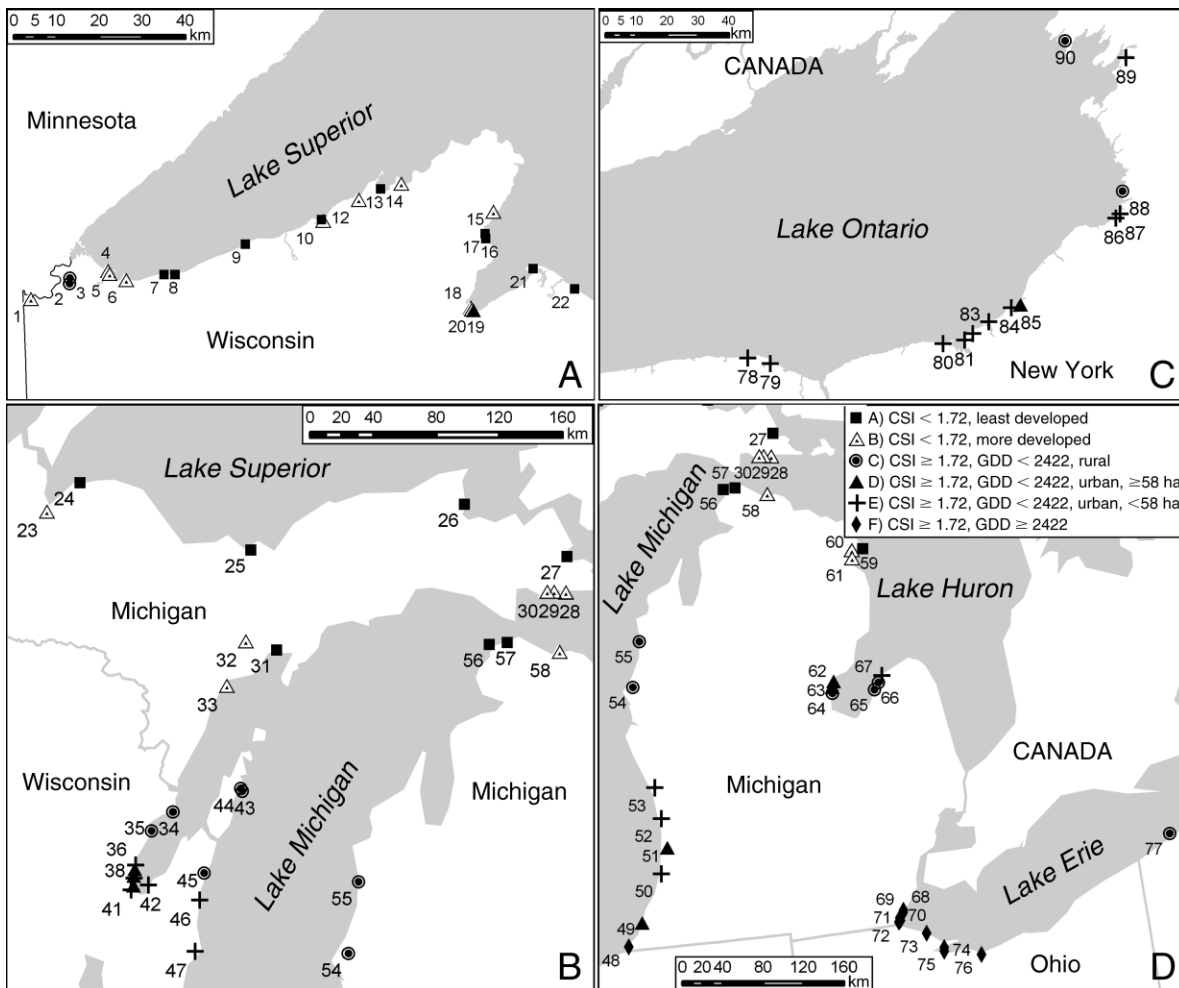


FIG. 9. Map of sites by MDS1 CART (classification and regression tree) category. Uppercase letters in the figure key correspond to leaves identified in Fig. 8. CSI is the cumulative stress index, and GDD is the growing degree-days.

et al. 2007), one of the Everglades' Water Conservation Areas (King et al. 2004), and the Ohio coast of Lake Erie (Mack et al. 2008). Lougheed et al. (2007) also recommended the use of MDS with diatom and zooplankton data for evaluating wetland condition. In order for the MDS analysis to yield condition information, however, the wetland sample set must represent the range of wetland condition; otherwise the MDS axes may represent other environmental gradients. For example, in several applications of MDS to relatively undisturbed wetlands, the first MDS axis represented gradients of elevation, soil chemistry, or moisture (Grace et al. 2000, Nekola 2004, Whitehouse and Bayley 2005). The GLEI project's approach of sample stratification by GIS-derived anthropogenic stressors prior to data collection worked well to ensure that the final sample set represented the range of environmental condition (Danz et al. 2005).

We used FQI as a basis for comparison with our MDS condition axis because of its widespread implementation

and our own favorable evaluation of FQI (Bourdaghs et al. 2006), but our work showed MDS to be superior to FQI under certain circumstances. For example, the three-square rush marshes had very similar FQI values, 7.3 to 10.3, representing only 13% of the range of FQI values found in our study (Fig. 6). The same sites were spread over MDS1 values (−0.60 to 0.38) that represented 36% of the range of MDS1 values observed, and the CART analysis assigned them to four different leaves, reflecting differences in their environmental drivers. Follow-up visits to five of the Saginaw Bay sites in 2005 showed that the three-square rush site assigned to CART leaf D (Caseville, site 67) became dominated by *Phragmites*, whereas sites assigned to the less stressed CART leaf C (sites 63–66) were less affected by *Phragmites* invasion (Tulbure 2008). This implies that our unifying approach may be useful as a forecasting tool, which could be tested in future research.



PLATE 1. Field assistant Cindy Williams prepares to observe plant cover at one of the plots in a Lake Erie coastal wetland. Photo credit: L. Vaccaro.

Despite its utility as an objective measure of wetland condition for our purpose of classifying vegetation and evaluating vegetation–environment linkages, MDS requires analysis of data from multiple wetlands in order to create the condition gradient, and must be recomputed as new wetlands are added. In contrast to an index like the FQI, MDS cannot be used to calculate a numeric score for an individual wetland that is immediately interpretable as a wetland ranking (e.g., on a scale of 1 to 10); MDS values must be interpreted relative to the scores of other wetlands. However, the ability of MDS to objectively compare biological condition across range of community types makes it a powerful tool for geographically extensive wetland evaluations.

#### *Classification of Great Lakes wetland plant communities*

A central theme of plant ecology concerns the propensity of vegetation to organize in assemblages along natural environmental gradients, but many vegetation classification systems are geared toward classifying the best remnant natural communities rather than the broad spectrum of vegetation present (e.g., Comer et al. 2003), and wetland conservation plans tend to focus on botanically charismatic communities that are worthy of preservation (e.g., Nature Conservancy 2000, Epstein et al. 2002). Although our study was not designed to identify unusual wetlands, it did so when wetlands had unusual assemblages of fairly common species (e.g., Grand Mere, Magee Marsh) and when wetlands were geographically separated from sibling

members of a community cluster (e.g., Goose Bay, Presque Isle). These wetlands are known to be areas of biodiversity significance (Nature Conservancy and Nature Conservancy of Canada 2006), and both Grand Mere and Presque Isle are National Natural Landmarks.

The eight plant communities that we identified were relatively consistent with prior studies. A classification of Great Lakes coastal wetlands by Albert and Minc (2004) described eight classes based on a combination of vegetation and geography that were similar but not identical to our eight clusters. Differences were expected because our hierarchical clustering was based solely on floristics, not geography, and because our sample sites encompassed a purposely wide range of wetland condition. On the Canadian side of the Great Lakes, Lougheed and coworkers (2001) used canonical correspondence analysis (CCA) to analyze macrophyte–environment relationships of 62 marshes with water depths of 5 to 260 cm. Similar to our results, they found that *Typha* marshes dominated low-latitude wetlands. Their CCA distinguished two groups of *Typha* marshes along a gradient of submergent vegetation richness and density, as well as high-latitude “*Scirpus* sp.” (i.e., *Schoenoplectus*) marshes.

Exotic/invasive species are a major threat to biodiversity in the Great Lakes region (Nature Conservancy 2000). The invasion of wetlands by nonnative *Typha* and other invasive species (*Hydrocharis morsus-ranae*, *Phalaris arundinacea*, *Phragmites australis*) in the warmer southern portions of the Great Lakes has blurred the boundaries among traditional plant communities. Prior

research by Great Lakes researchers has shown that invasive taxa are promoted by anthropogenic disturbance (Brazner et al. 2007a, b, Trebitz and Taylor 2007). We have also shown that species invasions can occur very rapidly, on the order of years to decades in some Great Lakes wetlands (Frieswyk and Zedler 2007, Tulbure et al. 2007).

Because our wetland sampling strategy was statistically designed to select wetlands representing the full range of anthropogenic disturbance along the U.S. Great Lakes coast, our sample contained a large proportion of relatively degraded wetlands. It was therefore not surprising that 43% of our sites (39 out of 90) were dominated by invasive cattail, a taxon that usually exhibits a monotype form of dominance (Frieswyk et al. 2007), which is an indicator of wetland degradation (Vaccaro 2005, Frieswyk and Zedler 2007, Johnston et al. 2007, Trebitz and Taylor 2007). Eastern and western cattail marshes spanned a huge geographic range (Fig. 3) and a wide range of floristic quality (Fig. 4). Finer hierarchical clustering levels sorted cattail wetlands into geographic subgroups (Table 5), but those subgroups did little to aid interpretation of wetland condition. Hierarchical clustering analysis alone was therefore inadequate for evaluating the condition of cattail marshes, but MDS1 scores provided a suitable metric of their biological condition (Fig. 6). The use of MDS allowed us to collapse complex floristic data into a single multivariate axis that identified biologically meaningful condition, derived independently of environmental parameters but clearly related to them.

*Relationship of wetland types to ecoregions,  
hydrogeomorphology, and disturbance*

Our CART analysis allowed us to identify the physical and anthropogenic environmental variables that most influenced wetland condition across the U.S. Great Lakes basin, but the choice of endpoints influenced the results. The model that used the MDS1 endpoint was slightly more explanatory ( $r^2 = 0.82$ ) than the model using FQI ( $r^2 = 0.75$ ), and the MDS1 model relied on several variables related to anthropogenic stress whereas the FQI model relied solely on climatic, physiographic, and forest cover variables. By choosing GDD as the variable on which to make the first split, the FQI model immediately segregated sites based solely on climate, with the northern 40 sites assigned to better-condition classes (FQI model leaves A–C). Although wetland condition is generally better in the northern Great Lakes than in the southern Great Lakes, such is not always the case. By selecting CSI for the first split, the MDS1 model allowed us to identify outlier wetlands of anomalously better (e.g., Presque Isle) or worse condition (e.g., Prentice Park) relative to their geographic location. The CSI was highly correlated with GDD ( $r = -0.72$ ) due to the greater agricultural and urban development in the warmer, southern portion of the Great Lakes, but was not in itself a climatic metric.

Thus, using MDS1 rather than FQI as the endpoint was preferable for discerning human impacts.

The GLEI project had anticipated a north–south division in wetland biota, and we divided the Great Lakes basin into the Laurentian Mixed Forest (northern) and Eastern Broadleaf Forest (southern; Keys et al. 1995) in our sampling design (Danz et al. 2005). However, both of our CART analyses showed that the ecoprovince boundary was too far south for coastal wetland vegetation. The ecoprovince boundary placed all of Wisconsin's Green Bay wetlands (sites 34–41) in the northern Laurentian Mixed Forest, but our CART models placed them with more southerly groups (MDS1 model leaves C–E, FQI model leaves D–F). Such a grouping is floristically consistent with our inclusion of these wetlands in the western cattail cluster. The use of predefined ecoprovince groupings to divide the data would have misrepresented 16 of the 90 wetlands (sites 34–47, 54–55).

Only after making broad regional divisions were wetlands distinguished by more local characteristics, such as watershed development (MDS1 model nodes 2 and 6), wetland size (MDS1 model node 13), and forest cover (FQI model). Forest cover can be interpreted as the lack of recent anthropogenic disturbance, because both agricultural and urban development tend to displace forest cover within the Great Lakes basin (Wolter et al. 2006), but the presence or absence of forest per se is probably not a direct driver of wetland condition.

The mapping of CART leaves in geographic space helped to identify wetlands with plant assemblages or MDS1 scores that were anomalous with their neighbors, such as the Grand Mere and Presque Isle sites, distinct from neighboring wetlands on both the hierarchical cluster and CART maps (Figs. 3 and 9). The CART map also identified the Prentice Park wetland near Ashland, Wisconsin (site 20) and the Caseville, Michigan wetland (site 67) as having higher MDS1 values (i.e., worse condition) than those of adjoining wetlands, even though the hierarchical clustering grouped them floristically with their neighbors. Both sites had relatively high urban development within their small (<1100 ha) watersheds, putting them at risk of degradation. The Prentice Park wetland had high cover of *Sagittaria latifolia*, *Sparganium eurycarpum*, and *Utricularia macrorhiza*, individual species shown to significantly increase with CSI on Lake Superior (Johnston et al. 2007), whereas the Caseville wetland had very high cover of the invasive *Phragmites australis* (average cover = 35.6% of plot area sampled). Thus, CART analysis and mapping of wetland classes can aid detection of anomalous condition, either positive or negative.

Much emphasis has recently been placed on the relationship between hydrogeomorphology and wetland vegetation (Brinson 1993, Keough et al. 1999, Albert et al. 2005), but none of the optimal splits in our MDS CART analysis used hydrogeomorphic variables. This is

consistent with our prior finding that geographic rather than geomorphic factors explained a greater proportion of variance in the vegetation of Great Lakes coastal wetlands (Brazner et al. 2007b). Geomorphology was locally important in defining the Grand Mere and three-square rush marsh hierarchical clusters, but our work implies that the influence of geomorphology on vegetation cannot be generalized to the entire Great Lakes basin.

Agricultural and urban development in watersheds draining to wetlands has been implicated as causing vegetation degradation (Lougheed et al. 2001, Houlihan et al. 2006, King et al. 2007, Trebitz and Taylor 2007). Development variables were important correlates of wetland condition in our CART model, generating optimal or surrogate splits at every split node. Land use metrics that characterized entire watersheds (CSI, PC1\_URB, EROS) or very large buffers (DEV\_5000, FOR\_5000, RC\_5000) related better to wetland condition than did more proximal land uses, consistent with the findings of Brazner et al. (2007b). Waterborne nutrient and/or sediment inputs to the wetlands are undoubtedly the real causes of degradation, rather than land use per se, but we had no field-measured water quality data to use as environmental variables. Land use metrics have been shown to be suitable surrogates for water quality (Craft et al. 2007, Trebitz et al. 2007, Morrice et al. 2008).

#### *Potential application*

Environmental managers pressured by time constraints often seek evaluation methods that are rapid and easy to implement, such as “Level 1” assessments that utilize easily obtainable GIS and remote sensing information to evaluate wetland condition. Our unified approach is neither rapid nor simple, requiring intensive fieldwork by scientists trained in botany, and support from database managers, GIS technicians, and statisticians. However, the ability of our approach to compare wetland condition across the variety of wetland types represented across the U.S. Great Lakes coastline has considerable strength.

In our previous research, we evaluated the potential of easily computed indicators such as species richness and percentages of invasive taxa, native taxa, and wetland obligate taxa (Brazner et al. 2007a, b), and we developed new indicators utilizing selected plant species (Frieswyk et al. 2007, Johnston et al. 2007, 2008). The approach that we propose here is not an indicator metric, but a way to evaluate wetland vegetation field data to compare the “apples and oranges” of diverse wetland types. Although our unified approach is computationally more advanced than some existing indicators, we believe that the superior results justify its application, and we recommend that this unified approach be applied to the data collected by the National Wetland Condition Assessment.

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