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Diatom communities along pH and hydrological gradients in three montane mires, central China

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ABSTRACT

The distribution patterns of epiphytic diatom assemblages in three montane mires in central China were investigated to examine their relationships with selected environmental variables (pH and depth to water table, DWT). Two of the mires are considered to be in good ecological condition (Dajiuhu and Qizimeishan Mires) while Erxianyan Mire is extensively affected by acid deposition and human activities. A total of 206 taxa belonging to 56 genera were found in 44 *Sphagnum* samples. Multivariate analysis revealed that pH and DWT were significantly correlated with diatom distribution. In Erxianyan Mire, the characteristic taxa (*Eunotia minor* and *Eunotia intermedia*) had lower pH optima and may therefore be useful indicators of highly-acidic conditions. In Dajiuhu Mire, the dominant species had higher pH optima, and abundant xerotolerant taxa (*Hantzschia amphioxys*, *Pinnularia borealis*, *Luticola mutica* and *Diadesmis contenta*) were observed. In the partial canonical correspondence analyses with mire location as a covariable, the correlation between diatom data and pH was insignificant, likely because pH differences between mires were greater than those within mires. In contrast, diatom data were significantly correlated with DWT, suggesting that diatoms are good sensors of hydrological variability along the hollow to hummock gradient. Together, these data can expand current autecological information for these potential diatom indicator species, which is critical for refining our interpretations of bio-monitoring and palaeolimnological studies in montane mires.

1. Introduction

Mires are a type of wetland in which organic matter has accumulated as peat. The carbon stocks within peatlands are significant (e.g. ca. 547 Gt carbon is stored in the peat carbon pool of northern peatlands) and substantial enough to exert impacts on the global cycling of carbon (Moore, 2002; Yu et al., 2010). The unique acidic and oligotrophic habitats in mires are associated with distinctive fauna and flora, many of which assume high conservation importance (Charman, 2002). Mires are also widely exploited archives of past environmental change and are an important resource for palaeoclimate research (Charman, 2002; Xie et al., 2013). However, mires are one of the most threatened ecosystems due to their ecological sensitivity to human disturbances (e.g. peat harvesting, drainage, reclamation and aerial pollutant inputs) and climate change (e.g. changing temperature and precipitation patterns) (Moore, 2002; Jiroušek et al., 2013; Poulíčková et al., 2013; Battarbee et al., 2014). For example, 15% of global peatlands have been drained and used for agriculture, livestock and forestry, compromising their ecosystem resilience (Joosten, 2009). For this reason, the analysis of biological assemblages inhabiting mires is a useful tool to establish reference communities to aid environmental assessment (O'Driscoll et al., 2012; Poulíčková et al., 2013).

Microorganisms have been used successfully as indicators of the ecological status of mires worldwide (Johansen, 1999; Hájková et al., 2011; Jiroušek et al., 2013), with diatoms widely used as sensitive bioindicators of environmental condition (Van de Vijver et al., 2004; Poulíčková et al., 2004; Buczkó, 2006; Kulikovskiy et al., 2010; Cantonati et al., 2011; Chen et al., 2012; Jiroušek et al., 2013). However, little baseline ecological data exists from montane mire habitats in central China. Montane mires are generally restricted to topographic lows and closed basins (Charman, 2002), and thus their low habitat connectivity can lead to the development of endemic diatom genera (Vyverman et al., 2007) and conservation of diatom diversity (Klemenčič et al., 2010). For example, abundant rare and

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'Red List' diatom taxa have been identified in montane mire samples from the Alps (Cantonati et al., 2011; Falasco and Bona, 2011).

In mires, *Sphagnum* species are ecologically dominant plants which contribute to substrate acidification and add complexity to the micro-topography, forming hollow-hummock structures (Clymo and Hayward, 1982). In these extreme and variable habitats, both water pH and moisture have been previously found to be associated with diatom distribution (Poulíčková et al., 2004; Cantonati et al., 2011; Hájková et al., 2011; Chen et al., 2012; Jiroušek et al., 2013).

We studied diatom assemblages in three montane mires located in Hubei Province, central China (Ma, 2008; Qin et al., 2012; Xie et al., 2013). Atmospheric contaminants (e.g. 'acid rain') and human activities are potential threats to the conservation and biodiversity of these mires (Du et al., 2008; Ma, 2008; Xu and Yang, 2010; Qin et al., 2013). For example, the annual mean pH value of precipitation in Hubei Province was around 4.17 in 2008, with an increasing frequency of acid rains since 1999 (Xu and Yang, 2010). We sought to provide information about the ecological preferences of epiphytic diatoms, to enhance their capacity as bioindicators in mire habitats. The objectives of this study were therefore to (1) investigate moss-inhabiting diatom communities in three montane mires; (2) provide important information concerning the ecological preferences of the main diatom species along pH and hydrological gradients.

2. Materials and methods

2.1. Study sites and characterization

Our study sites included three montane mires, including Dajiuhu Mire (31°28′50″N, 110°00′09″E; ~1700 m a.s.l.), Qizimeishan Mire (29°57′51″N, 109°45′09″E; ~1800 m a.s.l.) and Erxianyan Mire (29°43′34″N, 108°48′08″E; ~1530 m a.s.l.), all of which are located in the mountainous region of Hubei Province, central China (Fig. 1 and Table 1), characterized by limestone and dolomite bedrock, and karstic landscapes (Du et al., 2008; Ma, 2008). This region is influenced by a subtropical monsoonal climate with an average annual precipitation of ~1500–1800 mm, and an average annual temperature of ~7–14 °C (Ma, 2008; Qin and Xie, 2011; Qin et al., 2013). In recent years, the incidence of acid rain has increased, with most acid deposition occurring during the autumn and winter months (Xu and Yang, 2010). Annual mean pH values of rainfall were below 4.5 in Enshi City (near Qizimeishan and Erxianyan Mires, Fig. 1) between 1998 and 2000 (Du et al., 2003). Vegetation within the three mires is dominated by *Sphagnum palustre*, and other plants include *Calamagrostis epigeios*, *Carex* sp., *Echinochloa crusgalli*, *Hosta ventricosa*, *Juncus setchuensis*, *Oenanthe dielsi* and *Polygonum senticosum*. Comprehensive descriptions of vegetation communities in the three mires are given in Du et al. (2008) and Ma (2008). Both Dajiuhu Mire and Qizimeishan Mire are considered to be in a good ecological status due to effective environmental management after the establishment of national nature reserves (Du et al., 2008; Ma, 2008). In contrast, the habitats in Erxianyan Mire have been severely degraded by mining, artificial drainage, deforestation, tea tree plantation and moss harvesting (Ma, 2008; Qin et al., 2013).

A total of 19 samples from Erxianyan Mire and 7 samples from Qizimeishan Mire were taken in July 2011, with 18 further samples from Dajiuhu Mire collected in October 2012. The sampling points span a broad range of microhabitats including hollows and hummocks. At each sampling point, depth to water table (DWT) was measured in a ~5 cm diameter hole (after 6–12 h) and water pH was measured in situ with a pH meter (Euteoh Instruments).

2.2. Diatom sampling, preparation and identification

Diatom samples were prepared following the methods of Battarbee et al. (2001) and Poulíčková et al. (2004). The upper 3–5 cm of bryophyte turf was collected at each sampling point. Bryophyte samples were then washed out in 100 ml of distilled water and thoroughly squeezed into beakers. The extract was heated to 80 °C with 30% H_2O_2 in order to remove organic components. Following digestion and centrifugation, all samples were mounted on microscope slides using Naphrax® and a minimum of 300 valves were identified per slide, using a Zeiss Axioscop 2 microscope at a magnification of 10 × 100. In five samples with sparse diatoms, a minimum of 200 valves were identified. Taxonomic identifications were based on Krammer and Lange-Bertalot (1986, 1988, 1991a,b), Kulikovskiy et al. (2010) and Pavlov and Levkov (2013). The taxonomy was corrected to current conventional names based on recent accepted nomenclature (Guiry and Guiry, 2014).

2.3. Data analysis and statistics

One-way analysis of variance (ANOVA) was used to test for differences in pH and DWT between the mires and the Kolmogorov Smirnov test was used to check for normality in the program SPSS version 11.5.

To study intra-group similarity and inter-group dissimilarity, multivariate analyses were performed on species abundance data following the methods of Clarke and Warwick (2001), using the PRIMER® software package. A similarity matrix was constructed to show similarity between each pair of samples using the Bray–Curtis index. Following this, the SIMPER procedure was used to assess the contribution of each species. A series of diversity indices (i.e. taxon richness, Shannon index, Simpson index and Buzas and Gibson's evenness) were calculated in the program PAST version 2.05 (Hammer et al., 2001).

In the ordination analyses, only those taxa with ≥5% abundance in at least one sample were included. Diatom data were analyzed with detrended correspondence analysis (DCA) to determine the first axis gradient length which was 2.95, and so a unimodal ordination technique (canonical correspondence analysis, CCA) was chosen (ter Braak and Šmilauer, 2002). CCA tests between diatom data, pH and DWT were performed to identify significant explanatory variables using automatic forward selection and Monte Carlo permutation tests ($n = 499$ unrestricted permutations). In order to examine the effects of pH and DWT independent of location, each mire was included as a covariable in a partial CCA. The ordinations were performed using the program CANOCO version 4.5 (ter braak and Šmilauer, 2002). To assist in defining their potential as bioindicators, a weighted averaging estimate of a taxon's optimum (u_k) and tolerance (t_k) was calculated based on the following formulae (Birks et al., 1990):

$$u_k = \sum_{i=1}^{n} y_{ik} x_i \Big/ \sum_{i=1}^{n} y_{ik} \quad (1)$$

$$t_k = \left[\sum_{i=1}^{n} y_{ik}(x_i - u_k)^2 \Big/ \sum_{i=1}^{n} y_{ik} \right]^{\frac{1}{2}} \quad (2)$$

where x_i is the value of the environmental factor x in sample i; y_{ik} is the abundance of taxon k in sample i ($i = 1, \ldots, 44$ sampling point). The calculations were performed using the program C2 version 1.6.7 (Juggins, 2007).