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Indicators of Diptera diversity in wet grassland habitats are influenced by environmental variability, scale of observation, and habitat type

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ABSTRACT

In low intensity agri-ecosystems such as wet grassland habitats, the inclusion of invertebrates in conservation assessments and monitoring is usually limited to charismatic groups such as bees or butterflies. However, wet grasslands support a wide range of inveterate groups, some of which may exhibit limited movement not generally represented by more mobile groups such as those typically examined. The use of surrogate species which exemplify broader invertebrate diversity has been suggested as a possible means of including these overlooked invertebrates (such as Diptera) in conservation planning within these habitats. Based on collections made by Malaise trap, we utilized two families of Diptera (Sciomyzidae and Syrphidae) as indicators of a wider range of dipteran diversity (nine Diptera families identified to parataxonomic unit level [PUs]) in wet grassland habitats. We examined the role of environmental variability, spatial scale, and habitat type on patterns of cross-taxon congruence for all three assemblages. Both environmental correlation and community congruence were significantly stronger among assemblages when examined at low spatial scales, highlighting the need to examine dipteran groups at scales untypical of current agri-environmental assessments; namely field and farm level. Furthermore, when wet grasslands were differentiated into two habitat categories (sedge and rush dominated grasslands), the significance of the community congruence increased markedly. This correlation was particularly strong between Sciomyzidae and PUs which demonstrated similar differentiation based on habitat type, implying that assemblages which exhibit comparable ecological partitioning are more likely to be useful surrogates of one another. Correlations between richness, abundance and Shannon's diversity were highly variable among groups, suggesting compositional analysis as the most appropriate examination of dipteran diversity for surrogacy studies. The results indicate that cross-assemblage congruence of Diptera is influenced by similarity of response to environmental variability, scale of observation, and examination of assemblages differentiated into appropriate habitat categories. The results illustrate the need to investigate invertebrate biodiversity surrogates at scales appropriate to the indicator groups and examine congruence among assemblages within specific habitat categories. Such an approach has the potential to maximise gamma diversity in areas where wet grasslands are under threat of intensification or abandonment.

1. Introduction

European wet grassland habitats are typically low-intensity agricultural systems with semi-natural habitats which support a rich mosaic of plant and animal communities (Bignal and McCracken, 1996, 2000; Billeter et al., 2008). While much of the conservation of this lowland wet grassland is driven by botanical or ornithological interests, wet grasslands also sustain a high diversity of invertebrates (Drake, 1998; Hayes et al., 2015; Joyce and Wade, 1998; Maher et al., 2014). While some invertebrate groups have previously been utilized as indicators within wet grasslands, e.g. spiders (Oxbrough et al., 2007) and Carabidae (Luff et al., 1992; Williams et al., 2014), the difficulties associated with collecting comprehensive invertebrate data from habitats has contributed towards the continued limited inclusion of invertebrate groups in broad scale conservation planning and for monitoring conservation objectives (Cardoso et al., 2011). This is particularly relevant in a European agricultural context, where intensification and abandonment of traditional farming practices in areas such as wet grasslands is threatening biodiversity (Henle et al., 2008). The use of invertebrates in the designation and management of agricultural areas considered as being of a high nature value is usually limited (if included at all) to a few well known, easily identifiable, and often iconic groups such as

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butterflies or bees (Andersen et al., 2004). Other invertebrate groups such as Diptera are largely overlooked despite contributing significantly to the overall biodiversity of such habitats (Keiper et al., 2002).

While the need to include a wider suite of invertebrates in conservation strategies for wet grasslands makes ecological sense, the sheer abundance and diversity of groups such as Diptera are perceived as barriers to their inclusion in routine habitat assessments. Alternative approaches such as the use of selected invertebrate groups as biodiversity surrogates for a broader range of taxa has been suggested as a possible means of including invertebrates in conservation and monitoring programs (Anderson et al., 2011; Duelli et al., 1999; Duelli and Obrist, 2003; Hayes et al., 2015). Such biodiversity indicators generally include a well-studied taxon or group of taxa which are ubiquitous within the habitat of interest and can be easily collected and identified (Lindenmayer et al., 2000; McGeoch et al., 2002). A predetermined measure of the diversity of the selected indicator is then used to reflect the diversity of similar, or sometimes different, taxa. One such approach has been the examination of species richness congruence between indicator groups and the taxa they are deemed to represent (Duelli and Obrist, 2003; Moreno and Sánchez-rojas, 2007; Prendergast, 1997). However, the species richness approach is considered as having variable outcomes due to its dependency on the pairs of taxa under investigation and it provides little insight into overall species representation and composition (Su et al., 2004).

More recently, patterns of congruence derived from community similarity and/or the examination of similarity of community responses to environmental variability have been utilized as approaches to biodiversity surrogacy (Larsen et al., 2012; Paszkowski and Tonn, 2000; Rooney and Azeria, 2015; Rooney and Bayley, 2012; Su et al., 2004). A potential caveat with this method, however, is the effect of spatial scale of observation and habitat differentiation on congruence patterns. Invertebrate diversity may respond to spatial scales not typically considered in conservation strategies (Haslett and Salzburg, 1997; Weaver, 1995), and community composition can be influenced by microhabitat changes across small scales that can have a marked effect on community structures (Cole et al., 2010). In wet grassland habitats, this may be further exacerbated by temporal changes such as periodic inundation in combination with grazing patterns (Carey et al., 2017; Maher et al., 2014; Ryder et al., 2005). Thus, the examination of invertebrate communities may need to be assessed at spatial scales atypical of those employed in conventional biodiversity assessments which are often linked to agri-environmental scheme evaluations at farm or field-level scales (Anderson et al., 2011; Boyle et al., 2015).

The differentiation of habitats into categorical groups has also been shown to affect congruence patterns with anthropogenic disturbance and ecoregion having a noticeable influence on congruence measures (Ekroos et al., 2013; Myšák and Horsák, 2014; Rooney and Azeria, 2015; Rooney and Bayley, 2012). The selection of invertebrate biodiversity surrogates, therefore, needs to carefully consider determinants such as the distribution of the indicator taxa relative to the scale of the observation, response of the indicator to ecological variance, and possible ecological relationships between the indicator and the wider community it is chosen to represent (McGeoch, 1998; Paoletti, 1999).

In wet grassland habitats, adult marsh flies (Diptera: Sciomyzidae) are considered as potential bioindicators owing to their ubiquity and ease of capture (Carey & LeRoy et al., 2015; Knutson and Vala, 2011; Murphy et al., 2012). However, they are known to have highly localised habitat fidelity and exhibit a markedly limited movement (Williams et al., 2010); factors which may restrict their usefulness as surrogates for broader dipteran diversity if the scale of observation utilized is greater than that which accurately reflects the distribution of broader diversity. In contrast to this, adult hoverflies (Diptera: Syrphidae) are considered suitable bioindicators in agricultural systems (Burgio and Sommaggio, 2007) but are vagile in nature with adults capable of foraging over long distances (Sommaggio, 1999). The use of either of these groups as invertebrate biodiversity surrogates is therefore dependent on the similarity of their response to factors such as spatial scale and habitat differentiation relative to the broader invertebrate diversity for which they are selected to represent.

Along with these considerations, the identification of multiple and diverse groups such as Diptera to species level usually requires expertise and time which is not readily available in the context of typical designation or monitoring timeframes. Suggested alternatives to this impediment include attempting to rapidly identify several groups of invertebrates using less traditional taxonomic methods such as non-taxonomic sorting of species or molecular identification methodologies (Cardoso et al., 2011; Emerson et al., 2016; Oliver and Beattie, 1996a; Yu et al., 2012). Rapid biodiversity assessment techniques such as parataxonomy (morphospecies) as described by Oliver and Beattie (1993) utilises an approach whereby individuals with similar external morphological traits are grouped together as typological units or Parataxonomic Units (PUs) without the use of taxonomic keys. This work can be carried out by individuals with minimal taxonomic training and possibly even through public participation initiatives such as citizen science (Casanovas et al., 2014). The main advantage of using PUs in assessments is that it is relatively quick and permits the analysis of a broader suite of groups in limited timeframes. Nevertheless, PU allocation is especially difficult for non-specialists when sibling species are encountered within samples. This can lead to many outwardly similar individuals being erroneously labelled as the same species (lumping), or conversely, the separating out of the same species into two PUs (splitting) (Thorsten-Krell, 2004). Though the method is subject to debate regarding its effectiveness (Thorsten-Krell, 2004; Ward and Stanley, 2004), when executed with caution and subject to some level of taxonomic verification, it can be utilized to give ecologically relevant outcomes (Cotes et al., 2009; Obrist and Duelli, 2010; Oliver and Beattie, 1996a,b; Ward and Stanley, 2004). Studies of Diptera in wet grasslands which have utilised the two approaches (taxonomic and parataxonomic) have generally focused on richness correlations of all Diptera and not examined community similarity (Hayes et al., 2015; Ryder et al., 2005). Though useful patterns can be derived from such data, especially in terms of family richness and abundances, a more in-depth investigation of a smaller number of dipteran families using more prolonged sampling and intensive sorting methods might be more insightful (Frouz, 1999).

Given that Sciomyzidae and Syrphidae fulfil the criteria for suitable bioindicators as outlined by McGeoch (1998), we compared measures of their diversity with a broader assemblage of nine Diptera families identified using parataxonomy. By examining agreement among groups in terms of environmental responses we were able to identify the role that environmental factors play in determining community structure of different dipteran assemblages. We also conducted a hierarchical sampling regime from two wet grassland habitat types (rush dominated and sedge dominated wet grasslands) based on samples from individual traps or samples from traps from the same sample patch pooled together. We investigated the role that spatial scale and habitat type played in determining patterns of congruence among the three assemblages (Sciomyzidae, Syrphidae, and dipteran PUs) using a range of tests.

Our principal objectives were to:

1. Examine patterns of environmental correlation between the groups at two spatial scales (trap level and patch level)
2. Determine whether cross-taxon congruence among groups was affected by scale of observation
3. Investigate the role that habitat type plays in contributing to patterns of cross-assemblage congruence

The results of this investigation are discussed in the context of selecting suitable invertebrate biodiversity indicators within high nature value agri-ecosystems such as wet grasslands.