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Multivariate ordination identifies vegetation types associated with spider conservation in brassica crops

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Conservation biological control emphasizes the importance of vegetation other than the focal crop for providing natural enemies with refuge and shelter against disturbance. There is an unmet need for better methods to identify types of vegetation that are optimal to support specific natural enemies that may colonize into crops. Here we explore the commonality of the spider fauna of brassica crops with that of adjacent crops of other species and non-crop vegetation, employing spatial-based multivariate ordination approaches, hierarchical clustering and spatial eigenvector analysis. The small-scale mixed cropping and high disturbance frequency of southern Chinese vegetation farming offered a setting to test the role of alternate vegetation for spider conservation. Our findings indicate that spider families differ markedly in occurrence with respect to vegetation type. Grassy field margins, non-crop vegetation, taro and sweetpotato offer the best opportunity for promoting spider taxa that are also brassica-active species. In contrast, pumpkin and litchi contain species not found in brassicas, and so may have little benefit for conservation biological control services for brassicas. Our findings also illustrate the potential utility of advanced statistical approaches for identifying spatial relationships of species and identify the land uses most likely to offer alternative habitats for spider conservation biological control efforts and generates testable hypotheses for future studies.
Multivariate ordination identifies vegetation types associated with spider conservation in brassica crops

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ABSTRACT

Conservation biological control emphasizes the importance of vegetation other than the focal crop for providing natural enemies with refuge and shelter against disturbance. There is an unmet need for better methods to identify types of vegetation that are optimal to support specific natural enemies that may colonize into crops. Here we explore the commonality of the spider fauna of brassica crops with that of adjacent crops of other species and non-crop vegetation, employing spatial-based multivariate ordination approaches, hierarchical clustering and spatial eigenvector analysis. The small-scale mixed cropping and high disturbance frequency of southern Chinese vegetation farming offered a setting to test the role of alternate vegetation for spider conservation. Our findings indicate that spider families differ markedly in occurrence with respect to vegetation type. Grassy field margins, non-crop vegetation, taro and sweetpotato offer the best opportunity for promoting spider taxa that are also brassica-active species. In contrast, pumpkin and litchi contain species not found in brassicas, and so may have little benefit for conservation biological
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hypotheses for future studies.

Subjects: Agricultural Sciences, Entomology, Applied ecology and pest management

Keywords: Conservation Biological Control, Ecological Engineering, Ecosystem Service, Spatial
Autocorrelation, Hierarchical Clustering, Variance Partitioning, principle coordinates of neighbor
matrices (PCNM), Distance Based Moran’s Eigenvector Maps (dbMEM)

INTRODUCTION

Anthropogenic activities – such as land clearing, environmental pollution and agricultural
intensification – have led to adverse effects on the occurrence, diversity and evenness (Bengtsson
et al. 2005; Benton et al. 2003; Landis et al. 2000; Sunderland & Samu 2000; Thies et al. 2011;
Thies & Tscharntke 1999), and even the outright extinction of numerous species (Thomas et al.
2004). Biodiversity loss due to agricultural intensification is not merely driven by increases in the
non-judicious use of hazardous fertilizers and pesticides (Geiger et al. 2010; Roubos et al. 2014),
but also the landscape simplification and fragmentation, and the loss of habitat on which many
species rely. To limit the use of chemical inputs and to fulfill the food demands of a growing
worldwide population, researchers and growers have shifted their attention to the development of
effective integrated pest management (IPM) tactics by manipulating the cultural and mechanical
farming practices (Gurr et al. 2016; Gurr et al. 2017; Landis et al. 2000), including attempts to
conserve biological control agents (Fiedler et al. 2008; Liu et al. 2014; Pedigo & Rice 2014).
Habitat management has long been used to promote beneficial arthropods in agroecosystem for the delivery of ecosystem services, particularly biological pest control (Gurr et al. 2017). The addition of non-crop vegetation to a crop system is effective in enhancing local densities of predators and parasitoids but is often not readily compatible with farming practices and may reduce yields by reducing the area sown to the crop (Letourneau et al. 2011). An alternative approach is to manipulate the availability of nearby donor habitat in field margins or adjacent fields and uncropped zones. There is a need, however, to develop approaches that will help understand specific interactions between crop, adjacent vegetation types and natural enemies (predators and parasitoids) (Furlong 2015; Furlong et al. 2008; Furlong & Zalucki 2010; Szendrei et al. 2014; Tscharntke et al. 2012).

Population and community ecology has entered an exciting phase of pattern unification (Blanchet et al. 2008; Legendre & Gauthier 2014). As the importance of spatial ecological models has become better understood (Legendre & Fortin 1989; Legendre & Gauthier 2014), it has become increasing clear that ecologists need to incorporate spatial distribution patterns into their models. There have been a number of methodological developments in ecology to investigate the influence of environmental gradients on species spatial distribution patterns (Legendre & Gauthier 2014). For example, incorporation of geostatistical tools to explain geographical variation of species (Peterson et al. 2007). However, spatial eigenvector analysis investigations are more robust and forgiving of lower sample sizes and missing data that often accompany agroecological studies, as compared to the classical geostatistical approaches (e.g. semivariograms) (Blanchet et al. 2008; Legendre & Gauthier 2014).

Spiders (Araneida) are an invariably abundant and dominant, species-rich guild of predators in crop fields (Marc et al. 1999; Nyffeler & Sunderland 2003; Schmidt et al. 2003; Schmidt &
Tscharntke 2005). Characteristically, few spider taxa achieve distinct dominance on agricultural lands, and they have been known as the “agrobionts” (Marc et al. 1999; Samu & Szinetár 2002). It is however not clear if these spider species prefer agricultural habitat in general or exhibit specificity to crop and non-crop habitats on farms. This has clear and important ramifications for the extent to which they utilize a diversity of crop types and non-crop vegetation as an source habitat when colonizing a focal crop of interest. This study was designed to explore the extent of similarity between spider assemblages in brassica crops and different types of adjacent crop and non-crop vegetation, and to explore the influence of various adjacent vegetation types on the spatial distribution of spiders. Specifically, we hypothesized that different vegetation communities would share the spider fauna of brassica fields to varying degrees and that this would indicate the potential value of these as donor habitats from which spiders could move to colonise a newly planted brassica crop or to repopulate after a disturbance event.

**MATERIALS AND METHODS**

**Experimental Design and Sampling**

Spiders were sampled in brassica crops and surrounding vegetation in three sites in Fujian Province, China. Two sites were located in the Nantong district (25°55'13.97"N, 119°15'42.15"E & 25°55'0.25" N, 119°15'39.46"E, respectively) and a third in the Minqing district (26°10'4.72" N- 118°46'18.08" E), of greater Fuzhou City. Each site comprised a focal brassica field and the surrounding crop and non-crop vegetation within an approximate 50 x 50 m grid. Other crop vegetation types included litchi, pumpkin, sweetpotato and taro crops; whilst non-crop vegetation consisted of adjacent field margins and fallow fields (both containing a variety of grasses and forbs and some bare ground) as well as uncultivated areas with small woody perennials. Sites were
typical of smallholder farming in southeastern China and not uncommon in other agricultural systems globally. All of the agronomic practices – including fertilizer inputs and (frequent) pesticide application – were carried out as per normal by the host farmers.

At each site, spiders were sampled from 25 to 29 grid points (Minqing n=29 points, Nantong 1 n=25 points, Nantong 2 n=27 points) (at least 10 m apart) extending across all vegetation types. Samples were collected on five occasions from August and December of 2015, using a motorized vacuum sampler with a removable net bag mounted in the inlet (Lee et al. 2014; Lin et al. 2016; Whitehouse et al. 2005). A major typhoon in October completely flooded fields, which severely affected the population dynamics of spiders. Samples collected after the typhoon were not considered in the analysis of present study, as spider abundances were very low. Samples were collected at each grid point by running the vacuum sampler for 2 minutes within an area of 2 m². Sample bags were labeled and transferred to an ice box to prevent predation and sample degradation, and taken to the laboratory for sorting and identification under a stereo microscope. Adults and immatures were identified to family level (genus in some cases) and assigned to morphospecies.

Statistical Analysis

To test the importance of vegetation identity on spider assemblages in brassica fields and the influence of those vegetation types on the spatial distribution of spider species, we applied variance partitioning, hierarchical clustering (for community’s similarities or dissimilarities) and spatial eigenvector analysis for spider abundance and diversity data. Abundance “n”, Shannon-Wiener index “H” (Shannon et al. 1949) were calculated using the vegan package (vegan 2.4-0) (Oksanen et al. 2016), in R statistical software (R version 3.3.1), then data was Hellinger transformed to
obtain normality and adjust variance prior to multivariate analysis. The Hellinger transformation has good statistical properties to test for relationships among explanatory variables and draw biplots in constrained or unconstrained multivariate ordination (e.g. redundancy analysis RDA) without resorting to the Euclidean distances (Legendre & Gallagher 2001). We identified the response of spider abundance and α-diversity (H) against differing vegetation types and principle coordinates of neighbor matrices (PCNM) (Borcard & Legendre 2002; Borcard et al. 2004; Dray et al. 2006) using “varpart” function of vegan package in R-software, which allowed variance partitioning to separate the effects of distance and vegetation type on species turnover (Peres-Neto et al. 2006). Additionally, “rda” function was used to test the significance of fractions of spider families abundance and diversity, and triplots were constructed to visualize the vegetation types associated to different spider families. All analysis were carried out separately for each of the three experimental sites because of differences in adjacent land cover to the brassica field.

To measure community dissimilarities of spiders in different vegetation types, hierarchical clustering was carried out for the abundance and Shannon diversity for each experimental site. A quantitative version of the Sørensen index, Bray-Curtis dissimilarity was used to measure the percentage differences and to construct dissimilarity matrices for abundance and diversity of spider families in different crop and non-crop vegetation types using “vegdist” function with “method = “bray”” (Aanderud et al. 2015; Jeremy 2013). We visualized the β-dissimilarity matrix using heatmap for the abundance and α-diversity (H) of spider families at each of experimental site (Aanderud et al. 2015; Jeremy 2013; Murtagh & Legendre 2014). An assessment of the uncertainty in the cluster delineation was done through multiscale nonparametric bootstrap resampling tests (Shimodaira 2002). This helps to determine p-values (two types: approximately unbiased (AU) p-
value and bootstrap probability (BP) value) of each cluster in the hierarchy (Suzuki & Shimodaira 2006).

Spatial eigenvector analysis is particularly well suited to data with low spatial or temporal replication, rather than using classical geostatistical analysis (e.g. semivariograms) (Peres-Neto & Legendre 2010; Perović & Gurr 2012), which was the case in our data after post-typhoon samples had been removed from analysis due to low abundances. We were interested in calculating the spatial variation in the occurrence of spiders, mapping it, and analyzing its relationship with the adjacent vegetation of the focal brassica field. Distance-based MEM (dbMEM) (Borcard et al. 2004; Legendre & Gauthier 2014) was used to control for spatial correlation in tests of abundance and α-diversity (H) of spider-vegetation relationships, as in Griffith & Peres-Neto (2006). We identified total of 11 spatial variation maps for Minqing, seven for Nantong 1 and nine for Nantong 2. Significant spatial variation maps for each of the experimental sites were identified with forward selection using double stop criterion (Blanchet et al. 2008), α= 0.05 and R² values (for abundance; R²= 0.45 in Minqing, R²= 0.37 in Nantong 1 and R²= 0.34 in Nantong 2, and for α-diversity; R²= 0.46 in Minqing, R²= 0.34 in Nantong 1 and R²= 0.23 in Nantong 2). We identified one significant spatial variation map for spider abundance out of total 11 in Minqing and nine for Nantong 2. While for α-diversity (H); we identified two significant spatial variation maps out of total 11 in Minqing and one significant spatial variation map out of nine for Nantong 2. Furthermore, canonical analysis (RDA) was performed to compute the dbMEM spatial model and “anova” function was used to test the significance of these models. And all of spatial models were found to be highly significant (p-value<0.00). All analyses were carried out using vegan, adespatial, ade4, adegraphics, Heatplus, RColorBrewer, pvclust, ComplexHeatmap and gplots packages in R software (R version 3.3.1). R-codes and datasets are attached as Supplementary data 1.
RESULTS

A total of 919 spider individuals were captured, representing 48 morphospecies across nine families. Variance partitioning showed that abundance of spider families was vegetation type-dependent in Minqing (Fig 1a). Whilst variance for diversity of spiders was dependent on spatial distance only in Nantong 1 (Fig S1a) and the intercept between vegetation type and spatial distance in Minqing and Nantong 1 (Fig 1b, S1b). RDA analysis (for testing the significance of each variance fraction) revealed strong effects of vegetation types and spatial correlation on the abundance of different spider families in Minqing (df = 5, F = 1.56, p-value = 0.07) (Fig 2), similarly, for spider diversity in Minqing (df = 5, F = 1.22, p-value = 0.28) (Fig 3), Nantong 1 (df = 4, F = 1.75, p-value = 0.11) (Fig S2a) and Nantong 2 (df = 3, F = 0.83, p-value = 0.57) (Fig S2b).

RDA ordination showed that the non-crop vegetation strongly supports the abundance of Linyphiidae and Salticidae at Minqing, while taro had particularly high in abundance of Araneidae, Oxyopidae, Tetragnathidae, Theridiidae and Thomisidae (Fig 2). RDA ordination for α-diversity illustrated strong association of Salticidae, Thomisidae and Lycosidae with non-crop vegetation and fallow land in Minqing. Taro, in contrast, had high diversity of Araneidae, Tetragnathidae and Theridiidae, while pumpkin showed strong association with Oxyopidae (Fig 3). However, non-crop vegetation held a greater diversity of Araneidae in Nantong 1 (Fig S2a), and Oxyopidae in Nantong 2 (Fig S2b). Sweetpotato exhibited greater diversity of Tetragnathidae and Lycosidae at Nantong 1 (Fig S2a), and Araneidae at Nantong 2 (Fig Sb). Oxyopidae showed strong positive association with Litchi in Nantong 1 (Fig 2a). The field margins of brassica fields supported high diversity of Salticidae at Nantong 1 (Fig S2a) and of Salticidae, Thomisidae and Lycosidae at Nantong 2 (Fig 2b).
Community similarity/dissimilarity analyses between vegetation types, showed that brassicas share most of the spider families with other surrounding vegetation types in terms of abundance (Fig 4a, S3a, S4a) and diversity (Fig 5a, S3b, S4b) (same colour in heatmap). Lycosidae, however, showed strong differences in abundance between different vegetation types in all experimental sites (Fig 4a, S3a, S4a). Both Lycosidae and Oxyopidae depicted strong differences in diversity among different vegetation types in all three experimental sites (different colour, Fig 5a, S3b, S4b). Additionally, to assess the level of uncertainty in each cluster, the $p$-values for each of the hierarchical clusters were calculated using bootstrap resampling techniques. For example, abundance of spider in Minqing, the cluster labelled 4 in Fig 4b the observed AU-values are 90, 96, 81 and 77, whilst, observed BP values are 44, 40, 43, and 37, respectively. The $p$-values for each of the hierarchical clusters for the abundance and diversity in all experimental sites are shown in Figs 4b, 5b, S3c, S3d, S4c, S4d.

Spatial autocorrelation patterns were found to be highly significant for abundance of spiders in Minqing and Natong 2, and for diversity in Minqing and Nantong 1. Significant spatial correlation model for Minqing, indicated that brassicas, non-crop vegetation, field margins, fallow land and taro were the vegetation types spatially associated with greater spider abundance (Fig 6b) and diversity (Fig 6c). Similarly, for Nantong 2; brassica, field margin, sweetpotato and non-crop vegetation were spatially associated with greater spider abundance (Fig S5b). Moreover, significant spatial correlation was found only for spider diversity in Nantong 1; where litchi, sweetpotato and non-crop vegetation depicted exhibited strong positive spatial correlation with the diversity of spiders (Fig S6b). The spatial weighting matrix maps associated with the dbMEM eigenfunctions for Minqing, Nantong 1 and Nantong 2 are shown in Fig 6a, S6a and S5a, respectively.
Mixed cropping systems that include perennial crops, and non-cropped and non-sprayed zones, offer a relatively stable environment and increase potential for alternative and source habitat for the conservation of spiders and related biocontrol of various pests in modern agroecosystem (Blitzer et al. 2012; Rypstra et al. 1999; Schmidt & Tscharntke 2005). Non-crop vegetation especially can have strong effects on suppressing pest populations by promoting the abundance of functionally different groups of natural enemies (Bianchi et al. 2006; Boller et al. 2004; Gurr et al. 2017; Thies & Tscharntke 1999). Using the right types of adjacent vegetation requires the empirical identification of optimal vegetation types and has tended to require extremely labour intensive surveys with associated laboratory sorting. Such work cannot always be logistically supported in research projects and efforts can be stymied by unexpected events such as floods that lead to small sample sizes that can be difficult to analyze with conventional statistical approaches. Our results suggest that more advanced statistical approaches offer scope to deal with such challenges.

In our study, spider community structure was clearly shown to vary among vegetation types. There was high variance observed for spider abundance, species richness and composition among the different vegetation types at the scale of a few meters from the brassica crops in Minqing, whilst spider diversity was mostly a function of spatial distance and its intercept with adjacent crop and non-crop habitats. This emphasizes the patchiness of spider distribution in brassica production systems and was much stronger for cursorial families (Lycosidae and Thomisidae) as compared with web-builders (Araneidae, Linyphiidae, Tetragnathidae), as observed (Blitzer et al. 2012; Schmidt et al. 2003). Vegetation identity had an influence on abundance of spiders in our study; however, diversity was less obviously influenced by nearby vegetation types and affected by the
spatial distance. These results suggest that surrounding vegetation nearby the cabbage field affects
the spider abundance at a meso-scale. This may relate to the structure and cropping duration of
these vegetation types, which provides alternative food or shelter resources and drive the
assemblage of spider species in different vegetation at different times of the growing season
according to their life history and different niche requirements (Langellotto & Denno 2004;
Schmidt & Tscharntke 2005; Thies & Tscharntke 1999).

Spiders are important generalist predators of insect pests in agroecosystems. Some spider species
tend to dominate predator communities in crop fields and are considered as “agrobionts” (Samu &
Szinétár 2002). It is, however, not clear if these species generally prefer agricultural crop fields
and to what degree they associate with other adjacent crop types. Specifically, in brassica
agroecosystems, with a short growing season, adjacent crop and non-crop vegetation can play a
vital role in conserving spiders. Our results illustrate that, for most of the spider families, the
abundance is strongly associated with the perennial or bushy vegetation types (taro, non-crop
vegetation and pumpkin) nearby the brassica fields (Schmidt et al. 2003; Schmidt & Tscharntke
2005). This may be because these vegetation types offer alternative food sources and a place where
spider have time and space to build up population numbers, away from hazards such as low
chemical inputs and less disturbance (Halley et al. 1996; Topping 1999; Topping & Sunderland
1994). On the other hand, the patterns of spider diversity in our study demonstrate strong
association of non-web building spiders (Lycosidae, Salticidae, Thomisidae and Oxyopidae) with
fallow land and brassica fields. This may be a consequence of their mode of hunting, since such
habitats have relatively large areas of open ground for hunting prey (Schmidt & Tscharntke 2005).
In contrast, the diversity of the web building spiders (Theridiidae, Araneidae, Tetragnathidae and
Linyphiidae) showed a strong association with the taro, sweetpotato and non-crop vegetation, this
may be because of the availability of more extensive plant structures for building webs or may also be because of low disturbance regimes in fallow land (Schmidt & Tscharntke 2005; Thies & Tscharntke 1999; Topping 1999). These results suggested different habitat requirement for these two functional groups of spiders, further driving resource differentiation. Distinct preferences, in terms of niche requirements for particular habitat – composed of certain plant diversity – are known for spiders, (e.g. Bonte et al. (2002); Griffin et al. (2008)). Such preferences offer scope for manipulative use in modern agroecosystems to promote ecosystem services of biological control.

These results give a foundation for the future research to unravel the underlying mechanisms for the patterns observed here; for example, distribution and assemblage of spider species caused as a result of plant structural diversity in various cover types or caused by various agronomic practices and the role of broader landscape in aerial dispersion of spiders.

Hierarchical clustering is a powerful clustering method, as it can use ecologically meaningful ways of measuring community dissimilarities. In this study, we move beyond the measuring of \( \alpha \)-diversity within the sites and we investigated the \( \beta \)-diversity, by finding how similarity of the spider assemblages vary in space (Aanderud et al. 2015; Warnes et al. 2009). Results of \( \beta \)-diversity analysis showed commonality in most of the spider taxa abundance and diversity between brassica and adjacent crop and non-crop vegetation types. These results suggested that certain adjacent crop and non-crop vegetation types share spider taxa with brassica fields so these may provide refuge and serve as donor habitat for spiders spilling over into brassica crops following a disturbance event such as replanting, insecticide use or flood.

The statistical approaches used in the present study show utility for extracting, from data sets of modest size, testable hypotheses that can explore underlying mechanistic phenomena related to movement patterns and confirm the relative importance of difference vegetation types as source
habitat for a given focal crop type. It is becoming necessary that ecologists incorporate spatial correlation patterns into ecological models, and analysis of the population dynamics, and species distribution (Blanchet et al. 2008). Our results detected the significant spatial correlation patterns between the numbers of spider individuals at each of sampling point, and revealed highly significant spatial correlations between the numbers of the spiders with various vegetation types. The spatial eigenvectors method proved to be sensitive for detecting spatial patterns in the present data despite it being constrained as a result of the typhoon that occurred during the sampling period. Accordingly, our study also expands the methodological foundation for agroecological studies of ecosystem providers for future research.

During the last few decades, the loss of biodiversity and ecosystem function in modern agroecosystems is a major and growing concern of agroecological researchers (Bommarco et al. 2013; Ecosystem 2005; IPES-Food 2016; Potts et al. 2016). Our study illustrates the likely importance of non-crop plants nearby to crop fields to promote conservational biological control strategies by serving as alternative source habitat for beneficial arthropods and generates testable hypotheses for future studies. For example, the need to measure and track actual rates of spider movement between the habitat types used in the present study in order to determine if the predicted habitat types really are key donors of spider colonization and recolonization for brassica crops. Further, patterns of spider movement need to be studied in relation to disturbance events. More generally, future research should extend to testing the temporal effects of farm management practices (i.e. cropping patterns, chemical inputs) interacting with agricultural landscapes heterogeneity (compositional and configurational) on organizational and functional levels of agroecosystem. These are the major factors which drive the distribution, structure and composition of spider community in agroecosystems.
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Author Contributions

H.S.A.S, G.M.G. and M.S.Y. conceived and designed the study, H.S.A.S. performed the field and laboratory work, H.S.A.S. analysed the data. All authors prepared the manuscript.

Competing financial interests:

The authors declare no competing financial interests.

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Figure legends

**Figure 1** Venn diagram for the fractions of variation obtained at Minqing, by variance partitioning of a response data set; “Y” = Hellinger transformed spider taxa (a) abundance and (b) Shannon diversity matrices against two explanatory environmental variable matrices; “X1” = Vegetation type surrounding the brassica field and “X2” = Principle Coordinates of Neighborhood Matrix (PCNM) and their intercept.

**Figure 2** RDA Triplot (RDA on a covariance matrix) of the spatial correlation between Hellinger transformed abundance of spider families and vegetation types surrounding the brassica field using PCNM as distance matrix. The arrow length and direction correspond to the variance that can be explained by the environmental and response variables. The direction of an arrow indicates the extent to which the given factor is influenced by each RDA variable. The perpendicular distance between abundance of spider families and environmental variable axes in the plot reflects their correlations. The smaller the distance, the stronger the correlation. Numbers represents the sampling points in figure.

**Figure 3** RDA Triplot (RDA on a covariance matrix) of the spatial correlation between Hellinger transformed Shannon diversity of spider families and vegetation types surrounding the brassica field using PCNM as distance matrix. The arrow length and direction corresponds to the variance that can be explained by the environmental and response variables. The direction of an arrow indicates the extent to which the given factor is influenced by each RDA variable. The perpendicular distance between abundance of spider families and environmental variable axes in the plot reflects their correlations. The smaller the distance, the stronger the correlation. Numbers represents the sampling points in figure.

**Figure 4 (a)** Heatmap based on hierarchical clustering using Bray-Curtis resemblance matrix of spider taxa abundance at Minqing, where; “BRAS” = Brassica, “PUMP” = pumpkin, “FAL” = fallow land, “TA” = taro, “NCV” = Non-crop vegetation, and “FM” = Field margin. (b) Cluster plot to test the goodness of hierarchical clustering for abundance of spider families at Minqing. Values at branches are approximately unbiased (AU) p-values (left), bootstrap probability (BP) values (right), and cluster labels (bottom). Clusters with AU > 95 are consider to be significant.
**Figure 5 (a)** Heatmap based on hierarchical clustering using Bray-Curtis resemblance matrix of spider taxa Shannon diversity at Minqing, where; “BRAS” = Brassica, “PUMP” = pumpkin, “FAL” = fallow land, “TA” = taro, “NCV” = Non-crop vegetation, and “FM” = Field margin. (b) Cluster plot to test the goodness of hierarchical clustering for Shannon diversity of spider families at Minqing. Values at branches are approximately unbiased (AU) p-values (left), bootstrap probability (BP) values (right), and cluster labels (bottom). Clusters with AU > 95 are consider to be significant.

**Figure 6 (a)** Map showing the 29 sampling points (~10m apart) in Minqing computed using geographical sampling distance matrix. Bubble plot maps based on the forward selection to identify the significant dbMEM spatial model among all dbMEM eigenfunction models of spider’s (b) abundance and (c) Shannon diversity; showing the relative importance of spider’s abundance and diversity along with their spatial distribution; The size of the square box representing spider’s abundance and diversity in each eigenvector, ranging from white (largest negative value) to black (largest positive value).
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