**“Supplementary Information”**

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

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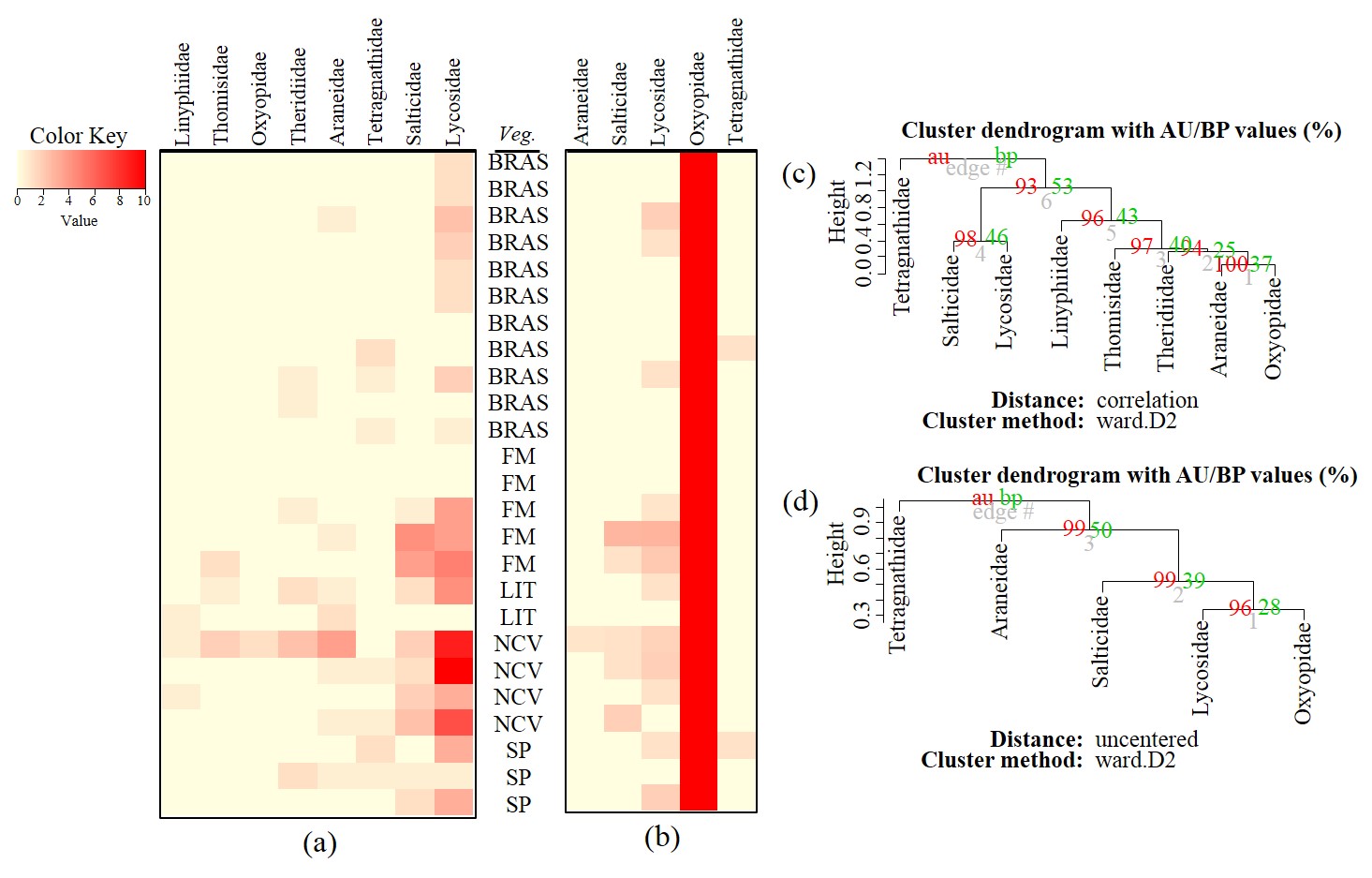
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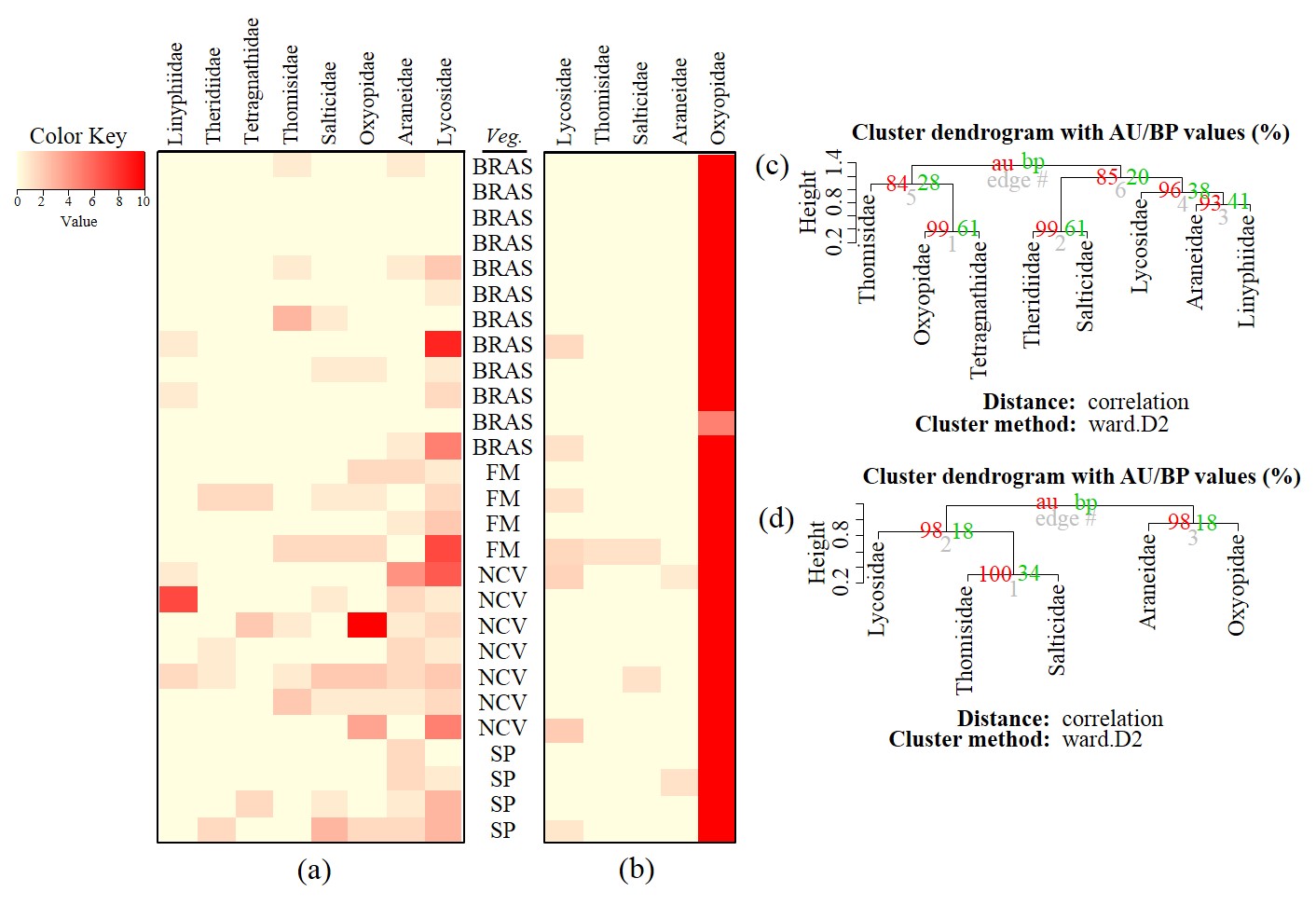
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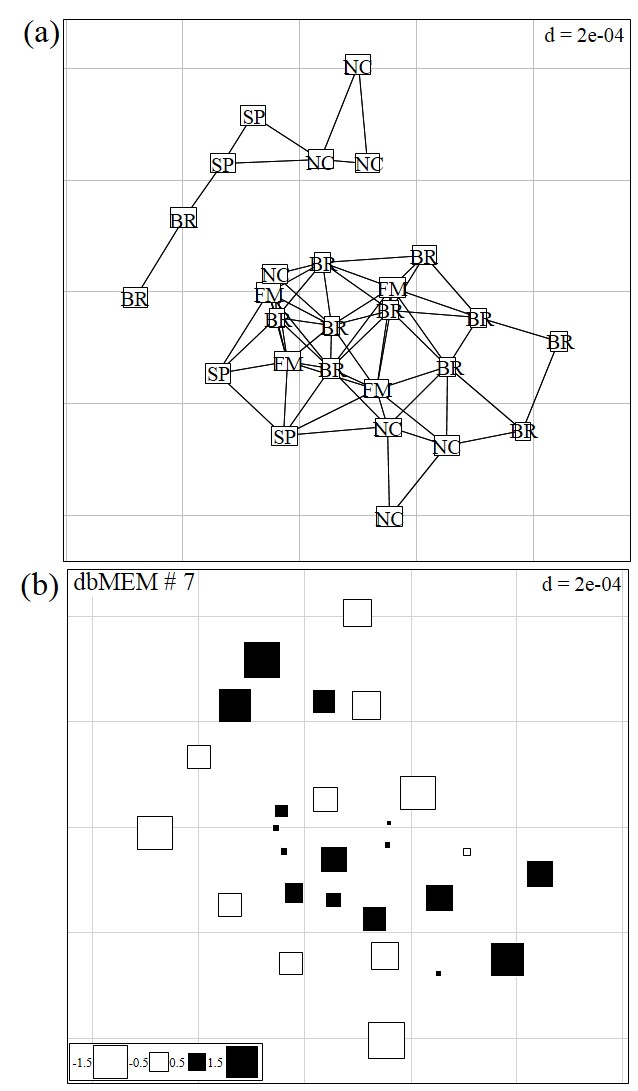
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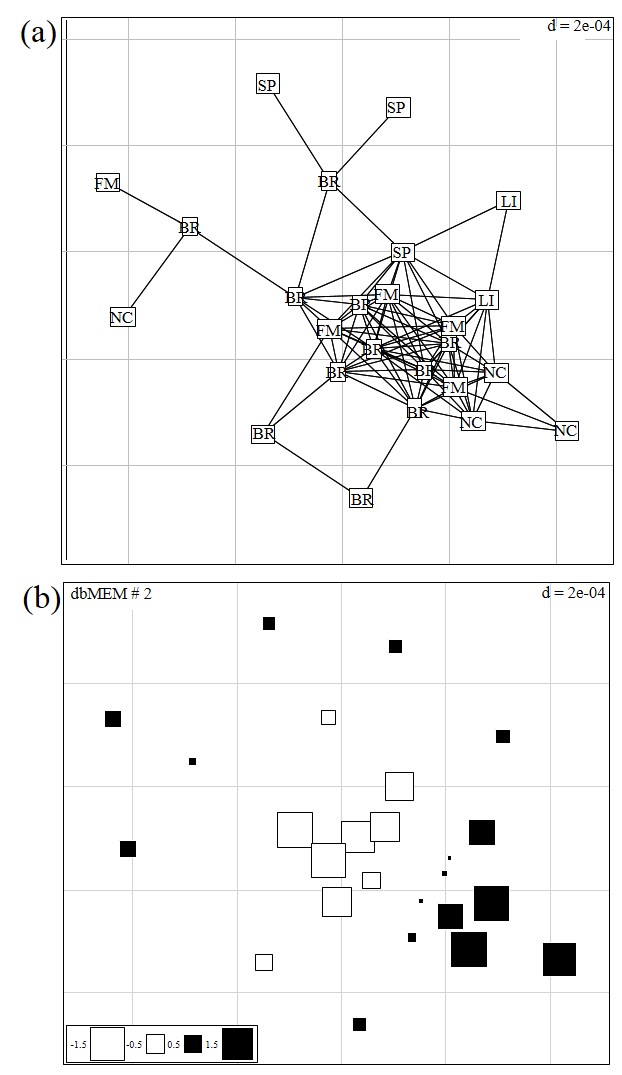
**Figure S1** Heatmaps based onhierarchical clustering using Bray-Curtis resemblance matrix of spider taxa **(a)** abundance and **(b)** diversity (*H*) at Nantong 1, where; “BRAS” = Brassica, “LIT” = litchi, “SP” = sweet potato, “NCV” = Non-crop vegetation and “FM” = Field margins. Cluster plots to test the goodness of hierarchical clustering for **(c)** abundance and **(d)** Shannon diversity of spider families at Nantong 1. 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 S2** Heatmaps based onhierarchical clustering using Bray-Curtis resemblance matrix of spider taxa **(a)** abundance and **(b)** diversity (*H*) at Nantong 2, where; “BRAS” = Brassica, “SP” = sweet potato, “NCV” = Non-crop vegetation and “FM” = Field margins. Cluster plots to test the goodness of hierarchical clustering for **(c)** abundance and **(d)** Shannon diversity of spider families at Nantong 2. 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 S3** **(a)** Rough map showing the 27 sampling points (~10m apart) at Nantong 1 computed using geographical sampling distance matrix. **(b)** Bubble plot map based on theforward selection to identify the significant dbMEM spatial model among all dbMEM eigenfunction models of spider’s abundance; showing the relative importance of spider’s abundance along with their spatial distribution; The size of the square box representing spider’s abundance in each eigenvector, ranging from white (largest negative value) to black (largest positive value).



**Figure S4** **(a)** Rough map showing the 25 sampling points (~10m apart) at Nantong 2 computed using geographical sampling distance matrix. **(b)** Bubble plot map based on theforward selection to identify the significant dbMEM spatial model among all dbMEM eigenfunction models of spider’s diversity (*H*); showing the relative importance of spider’s Shannon diversity along with their spatial distribution; The size of the square box representing spider’s diversity in each eigenvector, ranging from white (largest negative value) to black (largest positive value).