

Taxonomic Relatedness of Spider and Carabid Assemblages in a Wetland Ecosystem

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Mauro Paschetta, PierMauro Giachino, and Marco Isaia (2012) Taxonomic relatedness of spider and carabid assemblages in a wetland ecosystem. *Zoological Studies* 51(7): 1175-1187. Traditional community indices, i.e. Shannon diversity and Simpson's dominance, are generally used to describe biological assemblages in order to infer ecological trends about the effects of disturbance. Such indices are correlated with species richness and abundance and may be strongly influenced by the sampling effort. Conversely, taxonomic relatedness indices show interesting statistical properties and are independent of the sampling effort. Additionally, high values of taxonomical relatedness indices have proven to reflect habitat functionality in marine ecosystems. Their use in terrestrial ecosystems is rare, and despite their good potential, they have never been used for biodiagnostic purposes. In this paper, we present the 1st application of taxonomic relatedness indices to arthropod assemblages (namely spiders and carabids) and their comparison with several traditional community parameters that are generally used to evaluate environmental disturbances. The study was set in a wetland area within the Natural Reserve of Fondo Toce (northwestern Italy). Four different habitats with different degrees of disturbance (a reed bed, a mown meadow, a riparian wood with mesophilous elements, and a transitional mesohydrophilic area invaded by non-native vegetation) were sampled using pitfall traps. The spider and carabid assemblages occurring in each habitat were characterized by means of multidimensional scaling (MDS) and by several community parameters, including abundance, species richness diversity, taxonomic relatedness indices, and some descriptive functional traits. Differences among habitats were tested with generalized linear models. Correlations among community parameters were evaluated with Spearman's rank correlations. According to the MDS plots, both assemblages were clearly separated in relation to habitat type. When considering the parameters describing the assemblages in relation to disturbance, the taxonomic approach was found to be particularly suitable for spiders, for which the less-disturbed habitat was characterized by higher values of average taxonomic distinctness. Furthermore, functional groups of spiders were more evenly distributed in undisturbed habitats. The functional approach was found particularly appropriate for carabids, which responded to disturbance in terms of a decrease in biomass (average body size) and an increase in the proportional abundance of macropterous individuals. <http://zoolstud.sinica.edu.tw/Journals/51.7/1175.pdf>

Key words: Ecology, Taxonomic distinctness, Diversity, Functional traits, Habitat disturbance.

The potential of arthropods as bioindicators is widely recognized, especially when describing and characterizing different habitats and environmental conditions. The analysis of arthropod communities is traditionally based on characterizing assemblages by means of diversity indices, for example species richness, Shannon

diversity, and Simpson dominance. Such indices are strongly dependent on the sampling effort, and in general terms, they do not take into account any phylogenetic, taxonomic, or functional variability among species within a community (Heino et al. 2005). Work by Warwick and Clarke (1995) proposed several new indices based on taxonomic

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relations between species in a community in order to quantify the average degree to which individuals in an assemblage are related to one another. From this point of view, an assemblage comprising a group of closely related species is less diverse than an assemblage of the same number of more distantly related species, for example belonging to different families. Those new indices show several interesting statistical properties, namely virtual independence from the sampling effort (Clarke and Warwick 1998). Taxonomic diversity (Δ) is the expected path length between any 2 randomly chosen individuals from a sample. Taxonomic distinctness (Δ^*) is a modification of the former index in order to remove some of the overt dependence of Δ on the distribution of species abundances. The average taxonomic distinctness (Δ^+), considers only presence/absence information of each species.

If we assume that taxonomic diversity is closely related to ecological diversity and functionality, it is furthermore evident that evaluating this parameter may be crucial to evaluating the structure and degree of disturbance of a certain ecosystem (Tilman 1996). Taxonomic relatedness indices were suggested to be less sensitive than species richness to intrinsic differences among habitat types, and thereby to be more amenable to detecting degradation due to anthropogenic effects (Warwick and Clarke 1995 1998). Taxonomic relatedness indices have mostly been used in marine and freshwater ecology studies, and there are just a few works that focused on terrestrial ecosystems (von Euler and Svensson 2001, Gresens and Ferrington 2008, Baños-Picón et al. 2009). Furthermore, none of these applied such indices to ground-dwelling arthropods or used them for biodiagnostic purposes.

Ground-dwelling arthropods are small, diverse, and sensitive to environmental variability and can therefore be used as indicators of habitat heterogeneity, ecosystem diversity, and environmental stress (McGeoch 1998). Spiders (Arachnida, Araneae) and ground beetles (Coleoptera, Carabidae), in particular, are widely recommended as bioindicators (Churchill 1997, Rainio and Niemela 2003). The few studies which focused contemporaneously on both groups showed that both are negatively affected by anthropogenic activities (Alarukka et al. 2002, Öberg and Ekbohm 2006, Pearce and Venier 2006, Negro et al. 2009 2010).

Since the potential of spiders to act as

bioindicators was highlighted (Allred 1975, Clausen 1986, Marc et al. 1999), several ecologists used spider assemblages to describe and characterize different habitats and different environmental conditions. Spiders proved to be valuable for evaluating anthropic disturbances in several cases (Maelfait et al. 1998, Aakra 2000, Chen and Tso 2004, Negro et al. 2010, Sattler et al. 2010). Their bioindicative potential mostly derives from the peculiar features of these arthropods: they are abundant and ubiquitous, they are obligate predators, they exploit different ecological niches and, according to their diversified and multiple hunting strategies, they may reflect the complexity of an ecosystem (Marc et al. 1999). Alterations in microhabitats may influence several aspects of animal communities, such as the number and diversity of niches, local abundances, and guild compositions (Montaña et al. 2006). Spiders may be particularly suitable for this approach because they can be sorted into “functional groups” (or guilds), according to different hunting strategies. The soundness of this approach was proven in different ecological studies concerning, for example, forests (Huang et al. 2011), perennial agroecosystems (Isaia et al. 2006), and pasture management (Batary et al. 2008).

Carabids are frequently used to indicate habitat alterations. They have been used in grasslands and boreal forests where species number and/or abundances were noted to change along a habitat disturbance gradient (Niemelä et al. 1996). They have also been used in many other habitats; for example, in agroecosystems (Cole et al. 2002), high-elevation areas (Negro et al. 2010, Gobbi et al. 2011), and urban-rural ecosystems (Sadler et al. 2006).

Despite common trends having been found (poorly dispersing specialist species decrease with increased disturbance while small generalist species with good dispersal ability increase; Rushton 1989, Kotze and O’Hara 2003), according to Rainio and Niemela (2003), there is; however, not enough research to determine how suitable carabids are for biodiversity studies, or how well they represent responses of other species. However, Gobbi and Fontaneto (2008) suggested that analyses of ground beetle species assemblages commonly performed in applied ecological studies may be potentially misleading: the species richness approach can be too reductive to characterize different assemblages occurring in different habitats, especially when focusing on their sensitivity to human disturbance.

In response to this, Gobbi and Fontaneto (2008) proposed a taxonomic approach to characterize carabid assemblages in different habitats with different degrees of anthropogenic disturbance. Despite their not explicitly referring to Clarcke and Warwick's indices (Δ , Δ^* , and Δ^+), they calculated phylogenetic distances between species using the branching topology of a taxonomic tree. All pairwise species distances within each assemblage were computed using their topological distances (number of segments separating 2 species in the taxonomic dendrogram, with nodes identified by taxonomic categories from species to family). Such an approach revealed no significant effect of habitat typology on carabid assemblages. On the other hand, in order to better characterize assemblages of different habitats with different degrees of disturbance, several authors (Ribera et al. 2001, Purtauf et al. 2005, Gobbi and Fontaneto 2008), analyzed ecological and functional traits of carabid assemblages like wing morphology (macropterous, full-sized wings, and brachypterous, reduced wings or wingless), diet, body size, and trophic rank. The functional approach proved to be more effective than the taxonomic one, underlining significant differences in habitats with different degrees of disturbances with the minor presence of large, brachypterous, predatory species in more-disturbed habitats (Gobbi and Fontaneto 2008). The species richness of carnivores also proved to be very sensitive to landscape simplification (Purtauf et al. 2005).

In view of future applications of the taxonomic approach, the aim of our study was to test taxonomic relatedness indices on spider and carabid assemblages in order to characterize different habitats with different degrees of environmental disturbance in a wetland ecosystem. Responses of taxonomic relatedness indices to disturbance were also compared to those given by traditional community indices (such as species richness, abundance, Shannon's diversity, and Simpson's dominance) and those given by functional trait parameters (biomass expressed as the average body size of individuals of each assemblage, evenness of functional groups of spiders, and wing morphology of carabids), in order to highlight the potential of taxonomic relatedness in terms of biodiagnostic use.

MATERIALS AND METHODS

Study area

The study was carried out in the Natural Special Reserve of Fondo Toce located on the shore of Lake Maggiore (Verbania, northwestern Italy). The reserve includes the mouth of the Toce River and the alluvial plain of Fondo Toce. Several habitats are included in the protected area: a large bed of reeds (BR), a contiguous transitional mesohygrophilic area invaded by non-native vegetation (MV), a riparian wood with mesophilous elements (RW), and a mown meadow (MM). The reserve is remarkably threatened by the intense human activities around it, including urbanization, tourism, and infrastructure projects such as highways. Furthermore, a large popular campsite is located on the border of the reserve. The BR (adjacent to the latter) covers an area of 28 ha and is dominated by *Phragmites australis*. This is the most endangered habitat in the area, and its conservation represents the main aim for which the reserve was established in 1990. The RW is dominated by *Salix alba* and *Alnus glutinosa* with scattered *Quercus* sp. and *Tilia* sp. The MV (1.3 ha) is infested with goldenrod *Solidago canadensis*, a non-native species introduced to Europe from North America. The invasion of this species was first reported in Europe in 1645 and in China around 1930. Today it is widespread and invasive all over Europe and increasingly in East Asia. Given its broad tolerance to nutrients and humidity, it colonizes a variety of different habitats, including natural habitats as well as derelict land, roadsides, and dry floodplains. At several locations *Sol. canadensis* is considered a threat to biodiversity (Global Invasive Species Database 2005).

The 4 habitats within the Reserve are characterized by different degrees and typologies of disturbance: the MM is mowed twice a year during spring and summer; the MV is invaded by non-native vegetation replacing the natural vegetal association of *Molinietum*; and the BR is characterized by natural disturbances related to seasonal variations of water levels. Despite exceptional events of floods (with an average recurrence interval of 5-10 yr), the RW is characterized by the general absence of either anthropogenic or natural disturbance.

Experimental design

We selected 40 sampling plots in the 4 different habitats within the reserve. Ten pitfall traps were placed in each of the 4 habitats and emptied once a month for 4 samplings, from May to Sept. 2009 (112 days of activity in 4 habitats \times 10 traps \times 4 replicates: 160 traps positioned in all).

Traps were filled with 50% ethylene glycol to kill and preserve specimens. All specimens were stored in vials with 70% ethanol and examined under a stereomicroscope at up to 40x. Spiders and carabids were identified whenever possible to species level. Voucher specimens of spiders are stored at the Dipartimento di Biologia Animale e dell'Uomo of Turin Univ, Turin, Italy. Voucher specimens of carabids are stored in Giachino's collection, Turin, Italy. The nomenclature of spiders followed Platnick (2011), and that of carabids followed Fauna Europaea (2011).

Data analysis

Spider and carabid assemblages

An abundance-based richness estimator (ACE) was used to predict the expected species richness in the 4 habitats. Completeness was measured for each site as the percentage of the total number of species predicted by the estimator which we actually observed. The richness estimator was computed using EstimateS 8.0.0 (Colwell 2006). MDS plots (Bray-Curtis distance, 100 random starts) were used to compare spider and carabid assemblages. MDS plots were run with the PRIMER-E vers. 6 software package (Clarke and Gorley 2006).

Comparisons among habitats

In all analyses comparing arthropod assemblages that occurred in each habitat, we considered the mean value of the 4 replicates as the basic sample unit. In total, 40 basic sample units were used. For each basic sample unit, we computed the species richness (S), abundance (N), Shannon diversity (natural logarithmic form, H'), Simpson diversity (1 - lambda' form, $1 - \lambda'$), and Pielou's evenness (natural logarithmic form, J'). Three taxonomic relatedness indices including taxonomic diversity (Δ), taxonomic distinctness (Δ^*), and average taxonomic distinctness (Δ^+) were also calculated using the equations reported in Clarck and Warwick (1998). The taxonomic

matrix used to calculate the taxonomic relatedness indices for spiders (order Araneae) included 3 primary ranks: family, genus, and species. In order to have the same number of ranks (3) for the 2 assemblages, for carabids (family Carabidae), we added a secondary rank of subfamily, considering that only the 2 primary ranks of genus and species were available. PRIMER-E, vers. 6 software package (Clarke and Gorley 2006) was used to calculate all indices.

Some functional traits characterizing the assemblages (values for single basic sample units) were also considered: for spiders, we computed the evenness of functional groups (FGs; assigned by referring to Cardoso et al. 2011) and an estimate of the biomass of the assemblage (average body length from the clypeus to spinnerets in mm weighted according to the abundance, AVG; data gathered from the literature). In accordance with Gobbi and Fontaneto (2008) for carabid assemblages, we computed the wing morphology ratio (number of macropterous specimens among total specimens, MACR) and estimated the biomass of the assemblage (average body length from the clypeus to the posterior margin of the elytra in mm weighted according to the abundance, AVG; data gathered from the literature, Jeannel 1942, Casale et al. 2005).

Given that parametric tests could not be properly employed because several assumptions were not met (homoscedasticity was violated, and error terms were not always normally distributed), generalized linear models (GLMs) were used to test differences between habitats. Link functions were selected according to McIntyre and Lavorel (1994). Tests of the significance of the effects in the models were performed by means of Wald statistics (Dobson 1990). In the parameter estimation analysis, we used the RW as the reference category. Distribution fitting of indices was performed with Easyfit vers. 5.5. The GLMs were calculated using the STATISTICA 6.0 package (StatSoft Italia 2001).

Species richness and abundance of both assemblages were better described by a Poisson distribution; therefore, these distributions of errors were assumed, and community parameters were related to explanatory variables via a logarithmic link function. Taxonomic relatedness indices (Δ , Δ^* , and Δ^+), biomass of both assemblages, and Shannon and Simpson diversity of spider assemblages were better described by gamma distributions, and they were related to explanatory variables via an inverse link function. All other

indices (Pielou's evenness for both assemblages and Shannon and Simpson's diversity for carabids), the evenness of functional groups of spiders, and the macropterous ratio of carabids were better described by a normal distribution and were related to explanatory variables via an identity link function.

Correlations among indices

We used nonparametric Spearman rank-order correlation tests to analyze relationships among indices for both assemblages. Spearman correlations were calculated with STATISTICA 6.0 software package (StatSoft Italia 2001). A level of significance of $\alpha = 0.05$ was used for the analysis.

RESULTS

Spider and carabid assemblages

In total, 559 spiders and 1480 carabids were collected. Spiders belonged to 10 families and 35 species, while 32 species (9 subfamilies) of carabids were identified. The Lycosidae was the most abundant spider family, followed by the Thomisidae, Tetragnathidae, and Linyphiidae. The most abundant species were *Pardosa prativaga*, *Trochosa ruricola*, and *Ozyptila praticola*. According to Cardoso et al. (2011), we identified 5 different functional groups in our dataset: ground hunters, ambush hunters, orb web weavers, sheet web weavers, and other hunters. Most of the spiders belonged to ground hunters (69.6%), followed by ambush hunters (10.8%). The most abundant carabid species was *Amara aenea*

followed by *Harpalus luteicornis*. Most individuals (77.7%) were macropterous (for the complete list of spiders and carabids species see Appendices 1 and 2).

Sampling of spiders was adequate for 3 habitats (RW, MM, and BR) given that most of the expected species were effectively caught. For carabids, all habitats were sampled adequately. Given this result, for spider assemblages, we considered only the RW, MM, and BR, while for carabids, all habitats were considered in the analysis (Table 1).

MDS plots (Figs. 1, 2) revealed that both spider and carabid assemblages well characterized the 4 different habitats (stress for the Araneae was 0.088 and that for Carabidae was 0.01).

Comparisons among habitats

GLM estimates of spider indices (Table 2) showed that mean values of Shannon diversity were significantly lower in the MM with respect to the reference category (RW, $p < 0.05$), while Pielou's evenness and Simpson diversity were significantly higher. All taxonomic relatedness indices (Δ , Δ^* , and Δ^+) showed the same trend: the MM had significantly lower values ($p < 0.05$) while the BR showed significantly higher values than the RW ($p < 0.01$). No significant differences between the reference category and other habitats were found with respect to the biomass of spiders, while a significantly lower evenness of functional groups was observed for the MM ($p < 0.05$).

GLM estimates of carabid assemblages (Table 3) show that compared to the reference category (RW), species richness was significantly higher in the transitional MV ($p < 0.05$) and significantly

Table 1. Results of the abundance-based richness estimator (ACE) for the Araneae and Carabidae in each habitat

Taxa	Habitat	Observed species	ACE	Percent of estimated species
Araneae	RW	10	10.799	92.6
	BR	9	9.802	91.8
	MV	12	30.487	39.4
	MM	17	21.487	79.1
Carabidae	RW	19	19.937	95.3
	BR	7	7.831	89.4
	MV	18	19.457	92.5
	MM	16	20.486	78.1

RW, riparian wood with mesophilous elements; BR, bed of reeds; MV, transitional mesohydrophilic area; MM, mown meadow.

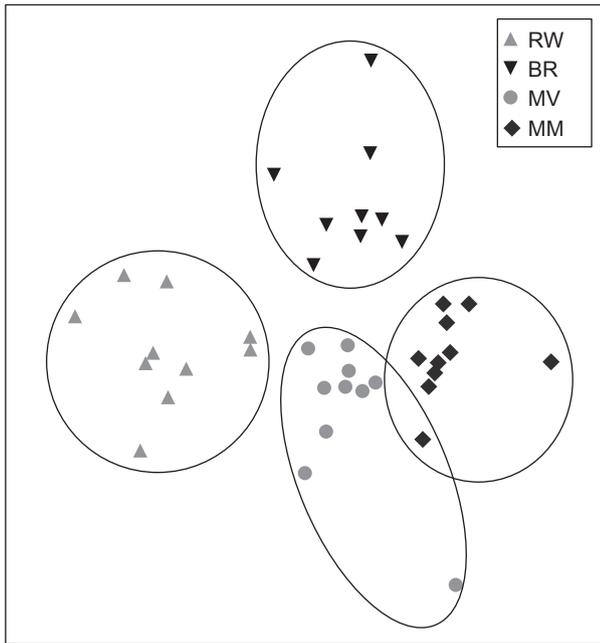


Fig. 1. Two-dimensional multidimensional scaling plot of spider assemblages (with a stress values of 0.088). Each point describes a single basic sample unit. RW, riparian wood with mesophilous elements; BR, bed of reeds; MV, transitional mesohydrophilic area; MM, mown meadow.

lower in the BR ($p < 0.01$). No significant differences occurred between the RW and MM in terms of species richness. Abundances showed the same trends as species richness, but in this case, the MM had a significantly lower value than the RW ($p < 0.01$). Pielou's evenness was

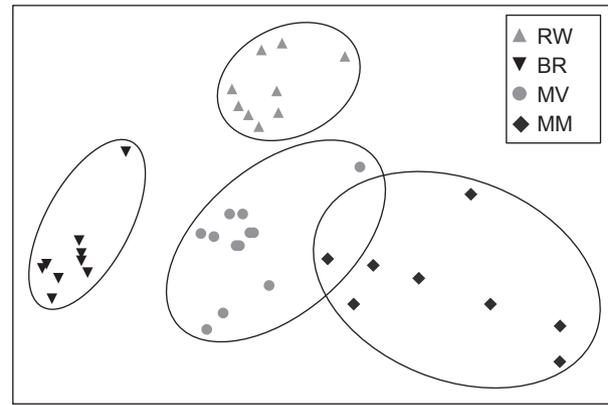


Fig. 2. Two-dimensional multidimensional scaling plot of carabid assemblages (with a stress value of 0.01). Each point describes a single basic sample unit. RW, riparian wood with mesophilous elements; BR, bed of reeds; MV, transitional mesohydrophilic area; MM, mown meadow.

Table 2. General linear model results for spider assemblages. Riparian wood (RW) was the reference category (BR, bed of reeds; MM, mown meadow). Distribution models and link functions are indicated in brackets

	Habitat	Estimate	Standard error	Wald statistic	p
S	BR	-0.047	0.130	0.903	0.499
(Poisson, log link)	MM	0.202	0.122	27284	0.099
N	BR	-0.237	0.076	9617	0.001**
(Poisson, log link)	MM	0.084	0.070	1440	0.230
J'	BR	-0.006	0.030	0.040	0.841
(Normal, identity link)	MM	0.055	0.027	408235	0.043*
H'	BR	-0.072	0.123	0.339	0.560
(Gamma, inverse link)	MM	0.221	0.108	421883	0.039*
1 - λ'	BR	-0.066	0.057	1361	0.243
(Gamma, inverse link)	MM	-0.121	0.053	5291	0.021*
Δ	BR	-0.003	0.001	72658	0.007**
(Gamma, inverse link)	MM	0.002	0.001	38165	0.051
Δ^*	BR	-0.001	0.000	12890	0.000**
(Gamma, inverse link)	MM	0.003	0.000	57490	0.000**
Δ^+	BR	-0.001	0.000	14377	0.000**
(Gamma, inverse link)	MM	0.003	0.000	48208	0.000**
AVG	BR	-0.355	0.395	0.811	0.368
(Gamma, inverse link)	MM	0.504	0.395	1.630	0.202
J'FG	BR	0.277	0.146	3.605	0.057
(Normal, identity link)	MM	-0.501	0.239	4.417	0.035*

* $p < 0.05$; ** $p < 0.01$.

significantly higher in the MM ($p < 0.05$) and BR ($p < 0.01$). The Shannon diversity index showed no differences among habitats, while a higher value for the Simpson diversity index was found in the MM ($p < 0.05$). No significant differences among habitats were found for carabids with respect to taxonomic relatedness indices (Δ , Δ^* , and Δ^+).

The biomass of carabids was significantly lower in the MM ($p < 0.01$) and significantly higher in the BR ($p < 0.01$) with respect to the reference category (RW). In addition, the macropterous ratio in the reference category (RW) was consistently lower with respect to all other habitats ($p < 0.01$).

Correlations among indices

Results of nonparametric Spearman rank-order correlations showed similar results for spider and carabid assemblages (Tables 4, 5). Pielou's evenness (J') and Shannon diversity (H') showed significant correlations (negative for J' and positive for H') with species richness (S) and abundance (N) for both assemblages, proving the dependence of these indices on the sampling effort. A similar trend was also found for Simpson's diversity ($1 - \lambda'$) of spiders, showing a positive correlation with S . Taxonomic relatedness indices (Δ , Δ^* , and Δ^+) showed no correlations with S or N , but proved to

Table 3. General linear model results for carabid assemblages. Riparian wood (RW) was the reference category (BR, bed of reeds; MV, mesohydrophilic vegetation area; MM, mown meadow). Distribution models and link functions are indicated in brackets

	Habitat	Estimate	Standard error	Wald statistic	p
S (Poisson, log link)	BR	-0.433	0.146	87519	0.003**
	MV	0.236	0.109	47120	0.029*
	MM	-0.216	0.140	23901	0.122
N (Poisson, log link)	BR	-0.642	0.074	74239	0.000**
	MV	0.224	0.052	18238	0.000**
	MM	-0.709	0.079	80050	0.000**
J' (Normal, identity link)	BR	0.093	0.035	6699176	0.008**
	MV	-0.003	0.036	0.007	0.931
	MM	0.080	0.040	396536	0.046*
H' (Normal, identity link)	BR	-0.079	0.173	0.208	0.648
	MV	0.137	0.135	101932	0.313
	MM	-0.144	0.175	0.671	0.413
$1 - \lambda'$ (Normal, identity link)	BR	-0.065	0.100	0.420	0.5170
	MV	0.022	0.092	0.060	0.806
	MM	0.193	0.098	391422	0.047*
Δ (Gamma, inverse link)	BR	-0.001	0.001	0.238	0.626
	MV	-0.001	0.001	1,213	0.271
	MM	0.001	0.001	0.329	0.566
Δ^* (Gamma, inverse link)	BR	0.001	0.001	1,106	0.293
	MV	0.000	0.001	0.029	0.864
	MM	0.000	0.001	0.249	0.618
Δ^+ (Gamma, inverse link)	BR	0.001	0.001	1,181	0.277
	MV	0.000	0.001	0.290	0.590
	MM	0.001	0.001	0.469	0.493
AVG (Gamma, inverse link)	BR	-0.041	0.002	271.794	0.000**
	MV	-0.005	0.003	2.749	0.097
	MM	0.024	0.004	37.644	0.000**
MACR (Normal, identity link)	BR	0.408	0.059	48.364	0.000**
	MV	0.311	0.060	26.927	0.000**
	MM	0.416	0.060	48.051	0.000**

* $p < 0.05$; ** $p < 0.01$.

be correlated with each other. Regarding spider assemblages, Δ and Δ^* were correlated with H' and $1 - \lambda'$, and Δ was also correlated with J' . In carabid assemblages, Δ was correlated with J' , H' , and $1 - \lambda'$.

DISCUSSION

Understanding patterns of biological diversity and their underlying causes using diversity indices is one of the most important challenges in ecological studies (Begon et al. 1996). As community indices are abstractions that may be useful when making comparisons among different habitats (Begon et al. 1996), we used both the traditional approach of community indices and the less-conventional one of taxonomic

relatedness in order to assess the responses of carabid and spider assemblages to different degrees and typologies of habitat disturbance. In accordance with the literature, we also used a functional approach that proved to be useful for characterizing arthropod assemblages (particularly carabids) in terms of evaluating disturbance (Ribera et al. 2001, Purtauf et al. 2005, Gobbi and Fontaneto 2008).

The suitability of carabids and spider assemblages for characterizing different habitats was first observed using MDS plots (Figs. 1, 2), indicating that spider and carabid assemblages were well differentiated in the 4 habitats and confirming the strong relation of spiders and carabids with their habitat (Marc et al. 1999, Entling et al. 2007, Schirmel and Buchholz 2011).

Habitat comparisons provided some inte-

Table 4. Correlations among spider assemblages. The asterisk indicates a correlation ($p < 0.05$). RW, riparian wood with mesophilous elements; BR, bed of reeds; MV, transitional mesohydrophilic area; MM, mown meadow; S, species richness; N, abundance; H' , Shannon diversity (natural logarithmic form); $1 - \lambda'$, Simpson diversity; J' , Pielou's evenness (natural logarithmic form); Δ , taxonomic diversity; Δ^* , taxonomic distinctness; $\Delta+$, average taxonomic distinctness

	S	N	J'	H' (loge)	$1 - \lambda'$	Δ	Δ^*	$\Delta+$
S								
N	0.741*							
J'	-0.361*	-0.538*						
H' (loge)	0.922*	0.585*	-0.085					
$1 - \lambda'$	0.574*	0.155	0.440*	0.807*				
Δ	0.312	0.011	0.346*	0.487*	0.674*			
Δ^*	-0.271	-0.175	-0.096	-0.332*	-0.353*	0.445*		
$\Delta+$	-0.148	-0.054	-0.154	-0.222	-0.308	0.460*	0.957*	

Table 5. Correlations among carabid assemblages. The asterisk indicates a correlation ($p < 0.05$). RW, riparian wood with mesophilous elements; BR, bed of reeds; MV, transitional mesohydrophilic area; MM, mown meadow; S, species richness; N, abundance; H' , Shannon diversity (natural logarithmic form); $1 - \lambda'$, Simpson diversity; J' , Pielou's evenness (natural logarithmic form); Δ , taxonomic diversity; Δ^* , taxonomic distinctness; $\Delta+$, average taxonomic distinctness

	S	N	J'	H' (loge)	$1 - \lambda'$	Δ	Δ^*	$\Delta+$
S								
N	0.825*							
J'	-0.592*	-0.683*						
H' (loge)	0.808*	0.443*	-0.142					
$1 - \lambda'$	0.024	-0.182	0.634*	0.388*				
Δ	0.147	-0.091	0.490*	0.508*	0.846*			
Δ^*	0.228	0.174	-0.281	0.205	-0.290	0.262		
$\Delta+$	0.091	0.016	-0.079	0.174	-0.181	0.333*	0.938*	

resting results in terms of evaluating environmental disturbances. The most “undisturbed” habitat (riparian wood with mesophilous elements, RW) was characterized by lower values of Pielou’s evenness and Simpson diversity for both assemblages compared to the most disturbed habitat (mown meadow, MM). Furthermore, spider assemblages showed higher values of Shannon diversity in the disturbed habitat (MM). These results are in accordance with the Intermediate Disturbance Hypothesis (Sasaki et al. 2009, Svensson et al. 2009), which assumes that intermediate levels of disturbance are associated with higher diversity values. The transitional mesohydrophilic area infested by non-native goldenrods (MV) and the MM may be regarded as example of intermediate disturbance: the 1st represents a perturbation of the natural evolution of the bed of reeds but with massive colonization by non-native plants, while the latter is characterized by constant physical disturbance derived from human activities. Regardless of whether mowing proved to be efficient in maintaining plant diversity (Buttler 1992, Cowie et al. 1992, Güsewell et al. 1998), the effect on ground-dwelling arthropods is less understood and may differ for different groups. Concerning spiders, for example, it was proven that less-mobile species and ones living in litter, including rare species, are negatively influenced by mowing (Cattin et al. 2003), while for carabids, significant effects were proven according to the mowing techniques (Humbert et al. 2008). In addition, Schirmel (2010) reported that with mowing in a heathlands preserve, carabid assemblages find suitable habitat conditions shortly after management.

With respect to carabid assemblages, significantly higher values of S and N were found in the goldenrod-invaded habitat (MV), while conversely, the MM showed significantly lower values of abundance. The interpretation of these results is unclear, in accordance with the fact that the community is largely dominated by macropterous carabids, with contrasting ecological requirements (Negro et al. 2010). Furthermore, in accordance with Gobbi and Fontaneto (2008), the species richness was too reductive for interpreting the sensitivity of carabid assemblages to human disturbances.

On the other hand, the functional approach proved to be effective for carabids, with a higher ratio of macropterous carabids in disturbed habitats, like the MM. Similar conclusions were reported by Gobbi and Fontaneto (2008). In

relation to the high dispersal power and high potential to colonize disturbed habitats (Ribera et al. 2001), winged carabids prove to be more abundant in disturbed habitats. In accordance with Gobbi and Fontaneto (2008), minor biomass was found in the most disturbed habitat (MM). Considering that big species are generally linked to stable environments, the higher biomass in the bed of reeds (BR) suggests that this habitat is more stable with respect to the reference category (RW). This result could have been biased due to the fact that we used the average body size weighted on individuals rather than species; on the other hand, the higher average body size found in this habitat may reflect the absence of anthropogenic disturbance.

The biomass of spiders showed no significant differences among habitats. As far as we know, the biomass of spiders is rarely applied in ecological studies to evaluate impacts of disturbances. On the other hand, in some cases, using functional groups of spiders gave interesting results. Huang et al. (2011) found that spider guilds respond differently to forest management practices; Isaia et al. (2006) reported an increase in the ratio of sheet web weavers in intensive vineyards located in homogeneous agricultural landscapes. In our case, a decrease in the evenness of functional groups per basic sampling unit was observed in disturbed habitats, namely the MM, attesting to the reliability of using functional groups of spiders for biodiagnostic purposes.

Indices of taxonomic relatedness of an assemblage could reflect the functionality of the habitat (Warwick and Clarke 1998). In our case, the most undisturbed habitats, like the RW and the BR, were characterized by highly taxonomically diverse spider assemblages. These results are in accordance with Gallardo et al. (2011), suggesting that lower and average values of taxonomic distinctness are associated with higher levels of disturbance. Furthermore, their low values may reflect the absence of a variety of ecological niches that may support complex biological assemblages. Compared to spiders, carabid assemblages seemed to be less suitable for evaluating environmental disturbance through the application of taxonomic relatedness indices.

As pointed out by Clarke and Warwick (1998), one of the most interesting features of the taxonomic approach is its independence of the sampling effort. The study of correlations among indices confirms this property: taxonomic diversity, taxonomic distinctness, and average taxonomic

distinctness (Δ , Δ^* and Δ^+) for both assemblages were not correlated with the abundance (N), which reflects the sampling effort. Additionally, Δ^+ showed no correlations with any of the traditional community indices, suggesting that it provides different kinds of information for characterizing the assemblage. This observation is in accordance with a study by Gallardo et al. (2011), in which it was found that while Shannon diversity (H') increased, variations in both taxonomic distinctness and average taxonomic distinctness (Δ^* and Δ^+) scores remained low.

In view of their taxonomic hierarchy (Order level), the relative stability of their systematics, their sensitivity to habitat disturbances, and most of all, their huge ecological diversification (for example in terms of hunting strategies and belonging to different guilds, see Cardoso et al. 2011), the taxonomic approach applied to spider assemblages seems to provide a suitable way to characterize habitat disturbance. In addition, independence from the sampling effort may provide reliable results when dealing with small datasets or presence/absence data. In particular, in view of future studies, the average taxonomic distinctness (Δ^+) of spider assemblages seems to provide an effective measure for biodiagnostic purposes: it is not correlated with any of the other traditional community indices and detects significant differences among habitats with different degrees of disturbance.

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Appendix 1. Spider species listed in systematic order (nomenclature follows Platnick 2011) and abundance (N)

FAMILY/Species	RW	BR	MV	MM
THERIDIIDAE				
<i>Euryopis flavomaculata</i> (C.L. Koch, 1836)	7	0	0	0
<i>Robertus lividus</i> (Blackwall, 1836)	1	0	0	0
LINYPHIIDAE				
<i>Bathypantes gracilis</i> (Blackwall, 1841)	0	10	0	0
<i>Ceratinella brevis</i> (Wider, 1834)	0	0	3	1
<i>Diplostyla concolor</i> (Wider, 1834)	1	0	0	0
<i>Erigone dentipalpis</i> (Wider, 1834)	0	0	0	2
<i>Gnathonarium dentatum</i> (Wider, 1834)	0	13	0	1
<i>Gongylidiellum murcidum</i> Simon, 1884	0	1	0	0
<i>Nematogmus sanguinolentus</i> (Walckenaer, 1842)	0	2	0	0
<i>Oedothorax retusus</i> (Westring, 1851)	0	0	0	2
<i>Walckenaeria antica</i> (Wider, 1834)	0	0	1	0
TETRAGNATHIDAE				
<i>Pachygnatha clercki</i> Sundevall, 1823	0	8	0	0
<i>Pachygnatha terilis</i> Thaler, 1991	5	0	35	0
<i>Tetragnatha nigrita</i> Lendl, 1886	0	0	2	0
ARANEIDAE				
<i>Argiope bruennichi</i> Scopoli, 1772	0	0	0	1
LYCOSIDAE				
<i>Arctosa leopardus</i> (Sundevall, 1833)	0	2	1	19
<i>Pardosa alacris</i> (C.L. Koch, 1833)	10	0	0	0
<i>Pardosa cribrata</i> Simon, 1876	0	0	0	3
<i>Pardosa prativaga</i> (L. Koch, 1870)	0	2	62	14
<i>Pardosa proxima</i> (C.L. Koch, 1847)	0	0	0	40
<i>Pardosa torrentum</i> Simon, 1876	0	0	1	6
<i>Pirata hygrophilus</i> Thorell, 1872	9	0	0	0
<i>Pirata piraticus</i> (Clerck, 1757)	0	37	1	0
<i>Trochosa hispanica</i> Simon, 1870	55	0	0	0
<i>Trochosa rucicola</i> (De Geer, 1778)	6	17	42	38
<i>Xerolycosa miniata</i> (C.L. Koch, 1834)	0	0	0	6
HAHNIIDAE				
<i>Antistea elegans</i> (Blackwall, 1841)	0	13	1	0
LIOCRANIDAE				
<i>Liocranoeca striata</i> (Kulczyński, 1882)	10	0	1	0
CORINNIDAE				
<i>Phrurolitus festivus</i> (C.L. Koch, 1835)	0	0	0	3
GNAPHOSIDAE				
<i>Drassyllus pusillus</i> (C.L. Koch, 1833)	0	1	0	0
<i>Micaria pulicaria</i> (Sundevall, 1831)	0	0	0	1
THOMISIDAE				
<i>Ozyptila praticola</i> (C.L. Koch, 1837)	48	0	0	0
<i>Ozyptila trux</i> (Blackwall, 1846)	0	0	0	2
<i>Ozyptila simplex</i> (O.P. Cambridge, 1862)	0	0	9	1
SALTICIDAE				
<i>Myrmarachne formicaria</i> (De Geer, 1778)	0	0	0	2

Appendix 2. Carabid species in systematic order (nomenclature follows Fauna Europaea vers. 2.4, 2011) and abundance (N)

SUBFAMILY/Species	RW	BR	MV	MM
CARABINAE				
<i>Carabus granulatus interstitialis</i> Duftschmid, 1812	88	0	51	3
NEBRINAE				
<i>Nebria (Boreonebria) rufescens</i> (Stroem, 1768)	17	0	0	0
ELAPHRINAE				
<i>Elaphrus (Elaphroterus) aureus</i> P. Muller, 1821	2	0	0	1
TRECHINAE				
<i>Asaphidion flavipes</i> (Linnaeus, 1761)	3	0	0	7
<i>Metallina (Metallina) properans</i> (Stephens, 1828)	1	0	0	0
PTEROSTICHINAE				
<i>Poecilus versicolor</i> (Sturm, 1824)	9	8	95	3
<i>Pterostichus (Argutor) vernalis</i> Panzer, 1796	5	1	2	0
<i>Pterostichus (Phonias) strenuus</i> (Panzer, 1796)	107	2	6	2
<i>Pterostichus (Platysma) niger</i> (Schaller, 1783)	9	0	6	0
<i>Pterostichus (Morphnosoma) melanarius</i> (Illiger, 1798)	2	0	4	0
<i>Pterostichus (Pseudomaseus) nigrita</i> (Paykull, 1790)	15	0	0	0
<i>Pterostichus (Pterostichus) pedemontanus</i> Ganglbauer, 1891	1	0	6	0
<i>Abax continuus</i> Baudi, 1876	52	0	76	8
<i>Amara (Amara) aenea</i> (De Geer, 1774)	253	0	12	1
<i>Amara (Amara) familiaris</i> (Duftschmid, 1812)	0	0	10	6
CHLAENIINAE				
<i>Chlaeniellus nitidulus</i> (Schrank, 1781)	0	2	10	6
OODINAE				
<i>Oodes helopioides</i> (Fabricius, 1792)	3	19	19	2
HARPALINAE				
<i>Anisodactylus binotatus</i> (Fabricius, 1787)	1	0	36	0
<i>Anisodactylus nemorivagus</i> (Duftschmid, 1812)	2	0	2	0
<i>Diachromus germanus</i> (Linnaeus, 1758)	0	0	0	2
<i>Stenolophus teutonius</i> (Schrank, 1781)	3	0	20	10
<i>Ophonus (Pseudophonus) rufipes</i> (Degeer, 1774)	0	0	1	2
<i>Harpalus (Harpalus) luteicornis</i> (Duftschmid, 1812)	213	0	2	0
PLATYNINAE				
<i>Calathus fuscipes graecus</i> Dejean, 1831	0	33	0	0
<i>Agonum (Agonum) muelleri</i> (Herbst, 1784)	5	45	2	0
<i>Agonum (Melanagonum) lugens</i> (Duftschmid, 1812)	0	7	0	48
<i>Agonum (Punctagonum) sexpunctatum</i> (Linnaeus, 1758)	37	3	1	0
<i>Agonum (Europhilus) thoreyi</i> Dejean, 1828	1	0	0	0
<i>Limodromus assimilis</i> (Paykull, 1790)	66	0	2	1