

## Assemblage structure of wolf spiders in south Hungarian grasslands

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### Abstract

The natural and quasi-natural habitat patches surrounded by agricultural fields and other areas, influenced and governed by human activities, form a typical mosaic-like landscape pattern of the southern Hungarian Great Plain. Fifteen ridges, belonging to seven grasslands, were sampled with pitfall traps, five times in 1999 and 2000. A total of 15 wolf spider species were collected and on the basis of the sample – cumulative species number function no more species could be expected even if more similar ridges were involved. A positive correlation was observed across species between the mean local density and the number of occupied ridges. The spider assemblages are classified into three groups, based on their dominance-diversity function. The absolute predominance of one species is characteristic for the first group, the predominance of two or three species for the second, whereas the distribution of species frequencies is more even in the third. No definite trend of spatial segregation was found among the species belonging to the same genus according to the results of the correspondence analysis of the species. The similarities of spider assemblages, by the same ordination technique showed no correlation with the geographical distances of the corresponding sites.

**Key words:** Lycosidae, scale, distribution, diversity

### INTRODUCTION

Grasslands, which comprised the largest part of the Hungarian Great Plain, mainly disappeared and their former sites are largely used as arable lands. The remnants of the wet grasslands are relatively small patches, used as haylands or pastures, which form the typical mosaic-like landscape pattern of the southern Hungarian Great Plain together with surrounding agricultural fields. These grassland patches are of conservation importance and this gives reason to their preservation and ecological survey (Margóczy 2001).

The arachnological knowledge of the south-eastern part of Hungary is relatively poor in general (e.g. Bugyi et al. 1965; Kerekes 1988; Szita et al. 1998), and no former studies

on spiders were carried out on these wet grasslands.

The aims of present research were to reveal in the studied habitat patches:

1. the species composition of the wolf spider fauna and the assessment of the reliability of faunistical survey;
2. the properties of species' distribution (i.e. the relationship between local density and regional distribution and the distribution of taxonomically related species);
3. the structure and the diversity of the wolf spider assemblages at different spatial scales;
4. the effect of between-habitat distances on the similarity of the wolf spider assemblages.

## MATERIAL AND METHODS

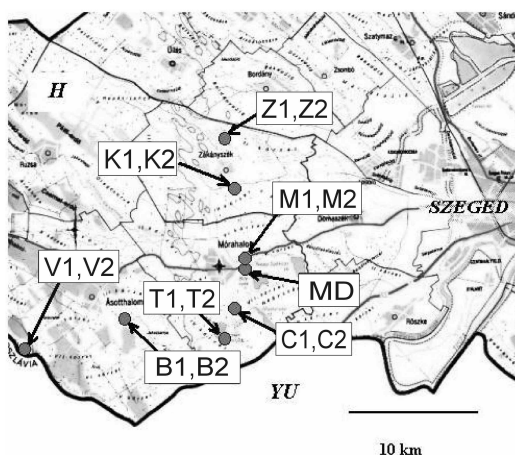
Wolf spider assemblages were studied in seven grasslands, which are situated in the south-eastern part of Hungary in an area of 600 sq. km (Fig. 1). The grasslands ("sites" hereafter) consist of an archipelago of small ridges (approximately 500 sq. m.; sampling plots hereafter) separated by wetlands. The grasslands were botanically very similar. The dominant plant species were *Chrysopogon gryllus*, *Festuca rupicola*, *Galium verum*, *Salvia pratensis*. In each grassland two or three, altogether 15, samplig plots were sampled. The distances between the samplig plots and the percentage dissimilarities of the vegetation, using Renkonen index (Podani 1997) were calculated. I used pitfall trap sampling, as it appears to be the most suitable method for collecting epigeic spiders (Uetz & Unzicker 1976; Samu & Sárospataki 1995). Twelve traps were placed at each samplig plot, with distances between traps of five meters in a 3x4 grid. The traps were plastic jars (6 cm in diameter) filled with ethylene-glycol as preservative and detergent was added to minimise the surface tension. The sites were sampled in 1999 11-26 March; 10-24 April; 08-23 June; 29 July-16 August; 07-21 October.

In order to assess the reliability of the faunistical survey, the cumulative number of species (S) against the number of sampling plots (n) relationship (Uetz 1976) was analysed by fitting a saturation curve. To calculate the number of species sampled at one site, I chose a site randomly, counted the number of species, repeated this procedure 100 times and calculated the average number of species. In the case of two sites, pairs of sites were chosen randomly 100 times, the catches were pooled and the number of species were counted (Samu & Lövei 1995) and the same procedure was repeated for 3, 4, ... 15 sites. The saturation level of the curve was assessed with the non-parametric first order jackknife estimator (Burnham & Overton 1978; Heltshe & Forrester 1983).

The relationship between the local frequency and the regional distribution of wolf spider species was investigated with the correlation between the averaged local density and the number of habitats occupied on a semilog scale (Hanski 1982, 1999). An exponential curve was fitted to the data. The function of the local frequency of the species against the their numerical rank (dominance-diversity or rank abundance curves; Southwood & Henderson 2000) was employed to classify the wolf spider assemblages on the basis of their numerical composition.

Correspondence analysis (CA; Pilou 1984) was applied to reveal the distributional patterns of taxonomically related species and to delineate possible assemblages on the basis of species co-occurrences. I also used this technique to estimate the effect of between-habitat distances on the similarity of the wolf spider assemblages. Mantel test was applied to decide how the vegetation structure between the samplig plots influence the wolf spider assemblages.

To study scale dependence, the medians of Shannon diversity (Shannon & Weaver 1949) and species numbers were computed for the



**Fig. 1.** The map of sampled grasslands. B – Ásotthalom, Királyrét bővítés; C – Csipak semlyék; K – Zákányszéki gye; M – Mórahalmi gye; T – Tanaszi semlyék; Z – Üllési gye; V – Tőzegebánya.

agricultural field on one side and with a wet meadow on the other. Therefore the high density of these species presumably indicates the influence of the neighbouring habitats on the spider assemblages of the sampling plot.

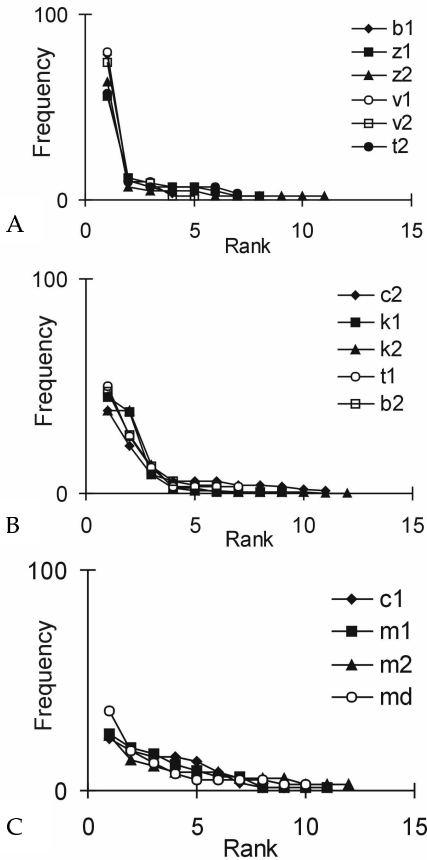
The dominance-diversity curves show three types of community structure (Fig. 2): (A) absolute dominance of one species; (B) two highly dominant species and (C) smooth transition between dominant and less frequent species.

The CA of the species on the basis of their distribution, showed that the species of the same genus differ in their occurrences, suggesting a slight segregation tendency. A discrete group of four species (*Arctosa luteitana* (Simon, 1888), *Pirata latitans* (Blackwall, 1841) *Pardosa agrestis* and *Pardosa palustris*), is clearly visible on the scatterplot (Fig. 3), which is due to their co-occurrence from plot K/2.

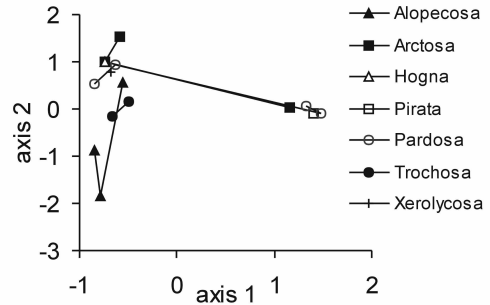
The scale-dependence of cumulative species number and Shannon diversity showed a nonsignificant increasing trend towards the largest scaling level ( $R=0.46$ ,  $t_{21}=1.16$ , NS;  $R=0.38$ ,  $t_{21}=0.73$ , NS respectively). The similarity metrics had a significant maximum (Kruskal-Wallis test:  $H_2=32.8$ ,  $P<0.001$ ) at the plot level (Fig. 4).

**Table 1.** The list of collected wolf spider species. The presence/absence of species is shown.

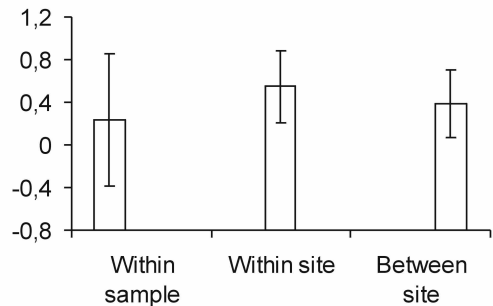
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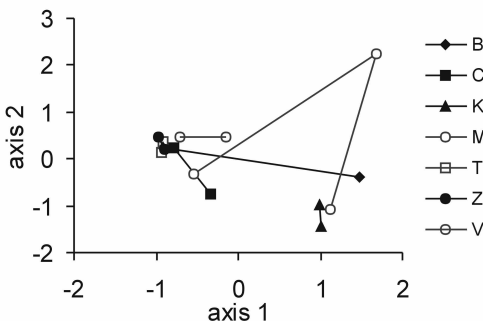
**Fig. 2.** Species abundance against their rank. The following three types of assemblage structure can be distinguished on the basis of their dominance-diversity properties: **(A)** absolute dominance of one species; **(B)** two highly dominant species, **(C)** smooth transition between dominant and less frequent species.



**Fig. 3.** Correspondence Analysis scatterplot of species. Those which belong to the same genus are connected. The cumulative eigenvalues of the two axes represented 65.62 %.



**Fig. 4.** Properties of the structure and the diversity of the wolf spider assemblages at different spatial scales. The medians of Czekanowski similarity function were calculated for the three spatial scales.



**Fig. 5.** Correspondence Analysis scatterplot of sampling plots. Those which belong to the same site are connected. The cumulative eigenvalue of the two axes was 57.62 %.

belonging to the same site are connected in the CA scatterplot (Fig 5). Although the sampling plots of the same site were placed close together, as a rule, in most of the cases they were even nearer to the sampling plots of other sites. In some cases, e.g. in the case of grassland B and M, the sampling plots of some sites were situated far from each other in the scatterplot.

The results of the Mantel test of sampling plots on the basis of Czekanowski similarity index showed no significant correlation between the composition of the wolf spider assemblages and the vegetation structure (Mantel test:  $R=0.165$ ,  $N=15$ , NS).

## DISCUSSION

It is concluded that the range of the grasslands involved into this study was sufficient to give a reliable faunistical survey-result. The sampling effort was probably large enough to catch all wolf spider species of the sampled ridges. Both parametric and non-parametric methods gave the same estimation for the number of species. Presumably it was caused by the lack of species occurring on one samplig plot only.

Positive correlation was observed between the local frequency and the regional distribution of the wolf spider species. This is in accordance with Hanski's (1982) results, who published positive correlations between these parameters on several groups (e.g. bumblebees, leafhoppers, oribatid mites) and which correlation was also found in ants (Gallé 1986). There are several hypotheses and speculations on the reasons of these relationships, although in the opinion of some authors it does not need explanation (cf. Kunin & Gaston 1997). One possible explanation of this positive correlation is that the habitat patches have different carrying capacities for different species, therefore the size of certain local populations are smaller. The extinction risk increases with decreasing population size, and so the number of occupied habitat patches also decreases. This

could explain the narrower distribution of locally less abundant species (Nee et al. 1991). In another opinion, this relationship is a sampling artefact (McArdle 1990; Hanski et al. 1993), because the locally rare species are more difficult to detect.

Moving between the micro-habitat patches within a habitat is part of the foraging strategy of wandering spiders (Ford 1978). Moving on the surface of the ground has a relatively low risk, as the spider can rapidly leave the unsuitable micro-habitat patch (Samu 1999), spending more time in than suitable ones. Presumably this phenomenon resulted in the low value of similarity at the pitfall scale, which is levelled out at the next larger scaling level. The lower similarities at the sites level could be caused by relatively large distance between study sites and the slightly different habitat properties of the sites (Rushton 1987).

The segregation tendency of congeneric and presumably also ecologically more similar species, may be brought about by intraspecific competition (cf. Diamond 1975; and the subsequent debates). But as the distributional data gave very weak evidence for the existence of competition, we cannot keep a competition hypothesis without detailed and directed future research.

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