

Sensitivity of different taxonomic levels of soil Gamasina to land use and anthropogenic disturbances

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- Abstract**
- 1 The effect of taxonomic level on the sensitivity of bioindicators has been widely investigated in aquatic ecosystems and, to a lesser extent, in terrestrial ecosystems. However, no studies have been conducted on the sensitivity of the different taxonomic levels of soil mites, especially Gamasina, to human activities.
 - 2 The present study aimed to assess the sensitivity of different taxonomic levels of soil Gamasina mites to anthropogenic disturbances in Europe and Argentina. We arranged the data from previous projects in a hierarchical system and conducted a study to identify the critical taxonomical levels that had the highest discriminative potential between sites (Europe and Argentina) or management types (forests, grasslands, fallows, succession, recultivation and agricultural sites).
 - 3 For the Gamasina community, geographical location was by far more important than the influence of any land use type. The analysis including only the European sites demonstrated that communities belonging to sites subjected to different land uses were also significantly different.
 - 4 The species data set provided a clearer separation of sites according to both the geographical and the land-use gradients than the genus and family data sets. The genus and, to a lesser extent, the family approach may be sufficient to elucidate the influence of great geographical differences and also of certain land uses (e.g. grasslands from the forests and arable sites).
 - 5 Species presence/absence data provided valuable information in our analyses, although the use of quantitative data yielded a clearer separation of sites.

Keywords Gamasina, mites, presence/absence data, taxonomic resolution.

Introduction

Changes in soil quality can be assessed by measuring appropriate indicators. To assess the sustainability of natural soil functions and different uses, key indicators should include biological soil parameters (Filip, 2002). Bioindicators integrate environmental information over a certain period of time and represent a practical tool for describing the sustainability of a farm or landscape (van Straalen, 1997; Paoletti, 1999). Bioindicators can be used at various levels of biological integration, from a single organism to communities and biological processes (Linden *et al.*, 1994; Pankhurst, 1997; van Straalen, 1998). In some cases, assessment of high-level taxa can provide

enough detailed information to compare communities from different systems. One alternative is to define parameters that pool species by taxonomic groups, life-history tactics, dispersal strategies or feeding guilds. These parameters are less variable and are more predictable at the site level, where soils are similar.

The predatory mite fauna is considered to be a good indicator of forest soil quality. In a hierarchical multi-taxon classification system, Gamasina is one of the groups most sensitive to changes in the ecological quality of soil (Römbke *et al.*, 1996). Gamasina fulfil the essential criteria usually suggested for the selection of bioindicators. They are species-rich and reach high densities in soil. They are relatively easy to collect undamaged and to identify. They are also sensitive to environmental conditions and have significant ecological functions in soil ecosystems.

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At present, Gamasina mites are used as soil quality bioindicators in Europe; for example, within the German Soil Biological Site Classification (BBSK) (Ruf *et al.*, 2003). This classification relies heavily on knowledge of appropriate environmental quality preferences or thresholds for different faunal taxa; in general, however, information on soil microarthropod species is scarce. Therefore, other higher, integrating levels must be sought to better exploit these extremely species-rich fauna useful for ecological indication (Ruf, 1998).

The predatory mite fauna of European soils is relatively well known. Comprehensive taxonomic keys and ecological information are available. This situation largely contrasts with the very poor knowledge of these mites in Argentina, where there are no experts and taxonomic tools or data on Gamasina species available, and where no surveys below suborder level (Bedano & Cantú, 2003) have been conducted.

The effect of taxonomic level on the sensitivity of biomonitoring programmes has been widely discussed for aquatic ecosystems; however, there is no broad consensus among researchers. Some researchers emphasize species-level identifications, others recommend using higher taxa under some circumstances, whereas yet others suggest using both, depending on the objectives of the study (Taylor, 1997).

In terrestrial ecosystems, Nahmani *et al.* (2006) evaluated different levels of taxonomic resolution of soil macrofauna for use as indicators of metal pollution. They found different answers for different groups. In the case of the family Lumbricidae, pooling of species to higher taxonomical groups led to a loss of information, whereas, in the case of Formicidae, grouping species in families yielded good results.

No studies have been conducted on the sensitivity of taxonomic level of soil Acari, especially Gamasina, to detect disturbances by human activities, such as different land uses.

The present study aimed to assess the sensitivity of different taxonomic levels of soil Gamasina mites to anthropogenic disturbances in soil ecosystems of central Europe and central Argentina. We investigated the effects of taxonomic resolution (from species to families) on the assessment of differences between land uses, and between geographical locations. We hypothesize that the loss of information entailed in the use of higher taxonomic level databases would result in a reduced ability to detect significant effects of land uses or experimental treatments. We also investigated the importance of including density values in the analysis compared with using binary (presence/absence) data. From a practical point of view, the use of presence/absence data instead of dominance data can prove to be more efficient. For marine ecosystems, it has been suggested that ecological patterns would still be clear after reducing dominance data to presence/absence data (Moore, 1974).

Materials and methods

Data sources

The information presented in the present study originates from a number of data sources but relies predominantly on data collected by the authors between 1990 and 2001 in their different research projects. Other important sources of

Table 1 Data sources

Location	Land use types	N sites	Reference
Córdoba, Argentina	Uncultivated grasslands, cattle-raising, conventional agriculture and mixed production systems	4	Bedano and Ruf (2007)
Germany	Forests, grasslands and arable lands	4	Karg (1967)
Germany	Forests, fallows and arable lands	5	Schulz (1991)
Southern Germany	Forests	12	Römbke <i>et al.</i> (2001)
Germany	Forests, grasslands and arable lands	23	Römbke <i>et al.</i> (2000)
Northern Germany	Forests	7	Wegener (2002)
Austria	Forests	5	Coja and Bruckner (2005)
Latvia	Forests	3	Salmāne (2000)
Northern Germany	Succession and recultivation sites	2	Koehler and Müller (2002)

information include data from both published and unpublished studies (Table 1).

We analysed data representing two different geographical regions: central Europe and central Argentina. The main database contains information on 73 sites and 306 species distributed in Europe and South America. The data from central Europe include forests, grasslands, fallows, succession, recultivation and agricultural sites. The data from Argentina include a natural grassland, a cattle-raising site, a mixed production site (cattle-raising and agriculture) and an agricultural site.

In all cases, the sampling method consisted in extracting a soil core from 0 to 8–10 cm in depth with a core sampler, according to the ISO standard (ISO Guideline 23611–23612, 2006). The extraction of mites from soil was in all cases developed by means of a Berlese–Tullgren funnel system.

Data analysis

To conduct the analyses, we collated all the information from both regions in a single database. From this database, two types of data sets were derived: one including information on the abundance of organisms (in terms of dominance) and the second comprising presence/absence data (binary data). The dominance database was then divided into three sub-databases: the family, genus and species level databases. Separate analyses were performed with data sets for each level of taxonomic resolution.

For all the data sets, we conducted a detrended correspondence analysis (DCA) (Hill, 1979; Hill & Gauch, 1980). This indirect gradient analysis maximizes the separation between sites along ordination axes based on species composition, and has proven to be a powerful tool for detecting patterns in communities that reflect underlying environmental gradients (Hill & Gauch, 1980; Peet *et al.*, 1988). In DCA, gradient length is expressed in standard deviation (SD) units of species turnover,

where an equal distance of ordination corresponds to an equal difference in species composition. DCA was detrended by segments with no transformation of species dominance data, no weighting of species or samples and no downweighting of rare species. For each site group, the centre was calculated using the mean of the scores for both axes and a confidence area after having calculated the SD of the scores for each group of sites.

To test for significance of differences between land use types, we performed an analysis of variance (ANOVA) [*a posteriori* least significant difference (LSD) Fisher's tests] on DCA scores of sites grouped according to land use type and geographical location. Non-normal distributed data were transformed before the analysis. The DCA was conducted using CANOCO, version 4.53 (ter Braak & Smilauer, 2004) and the ANOVA using INFOSAT (Universidad Nacional de Córdoba, 2004).

Results

Site specific community

According to the first axis of the DCA ordination of sites, the Argentine sites were separated from all the European sites by a mean distance of 17 SD (Table 2) and the differences were statistically significant. The second axis reflected the land use gradient in the European data. Five groups were well defined, corresponding to the forest, grassland, fallow, succession and recultivation sites, respectively, whereas the arable sites did not form a definite group. The results of the ANOVA showed that forest scores were different from scores of the other sites, and also that the succession and recultivation sites differed from the remaining sites (Table 2).

To analyse the influence of land use on soil Gamasina in European sites, we conducted a DCA excluding the Argentine sites (Figure 1). The first axis was linked to the gradient of land use. The DCA ordination identified five groups of sites. The mean of forest sites and the mean of recultivation sites were different from all the other site means and the mean of succession sites also differed from the mean arable lands (Table 3). The arable sites were not clearly separated from the grasslands but both groups were located between forests and successional sites. There was no evident trend in the succession and recultivation sites that allowed us to identify how Gamasina communities changed over time. Succession and recultivation samples were taken from two experimental plots: one left

Table 2 Distances (in SD units) between the different groups of European and Argentine sites according to the detrended correspondence analysis conducted using the species dominance data

	Argentina	Forest	Arable	Grassland
Forest	17.4	—	—	—
Arable	17.4	1.6	—	—
Grassland	17.4	2.4	—	—
Succession	17.3	3.6	2.0	1.3
Recultivation	17.3	4.5	2.9	2.1

Significance of difference between distances; one-way analysis of variance: $F_{6,58} = 36.45$, $P < 0.0001$. Only significant ($P \leq 0.05$) distances in least significant difference Fisher's tests are listed.

for undisturbed succession and the other managed as a lawn. Consequently, the sites represent a chronosequence and are not true replicates.

Two special groups of sites were also included in the analysis: one corresponding to a soil litter removal experiment (Karg, 1967) and the other to a succession experiment (Schulz, 1991). The sites from Karg's experiment were plotted in the upper part of the diagram (Figure 1, indicated by K). The forest without litter (the uppermost site in the diagram) was not situated near the control forests, nor was it close to the grassland or the arable site. This indicates that the community changes dramatically after litter removal.

The succession sites from Schulz's experiment (Schulz, 1991) were arranged in a manner that is compatible with the succession trajectory: from the arable site through the fallows (4 and 11 year fallows), the early succession forest, and the mature forest (Figure 1). Interestingly, the appearance of trees in the system (in the early succession forest) produced an important change in the predatory mite community. The community was closer to the mature forests than to the fallows or grasslands.

There were no identifiable differences between sites with the same land use according to Schulz (1991), which means that the taxonomic system is robust.

Taxonomic resolution

The analysis using the genus level database produced a separation of sites according to the geographical gradient and land use type (Figure 2). The gradient length was shorter (5 SD) than that produced by the species level database. The scores of the Argentine sites were significantly different from the European ones (Table 4), except for the recultivation sites. Grasslands scores were different from the scores of forests and arable sites. At the genus level, it was not possible to identify a succession gradient in the sites from Schulz's succession experiment Schulz (1991). The ordination obtained with the family level database was similar to that of the genus level, although the gradient length was shorter (3.5 SD) and overlapping of forest, grassland and arable sites was greater (Figure 3). As in the species and genus level analysis, Argentine sites were different from the European sites (Table 5). There were also significant differences in axis 1 scores between forest sites and grassland and recultivation sites and also between succession sites and grassland and recultivation sites (Table 5).

The species data set more powerfully separated the sites according to the geographical and the land use gradients than the genus and family data sets. The genus and, to a lesser extent, the family data set were also useful for discriminating between the sites according to geographical location. Some of the patterns observed in the species data set ordination were not detected with the higher taxonomic level data sets. Moreover, the effects of experimental manipulation were better detected by the species level analysis.

Presence/absence data

The DCA performed with presence/absence data produced a clear separation of sites according to geographical location

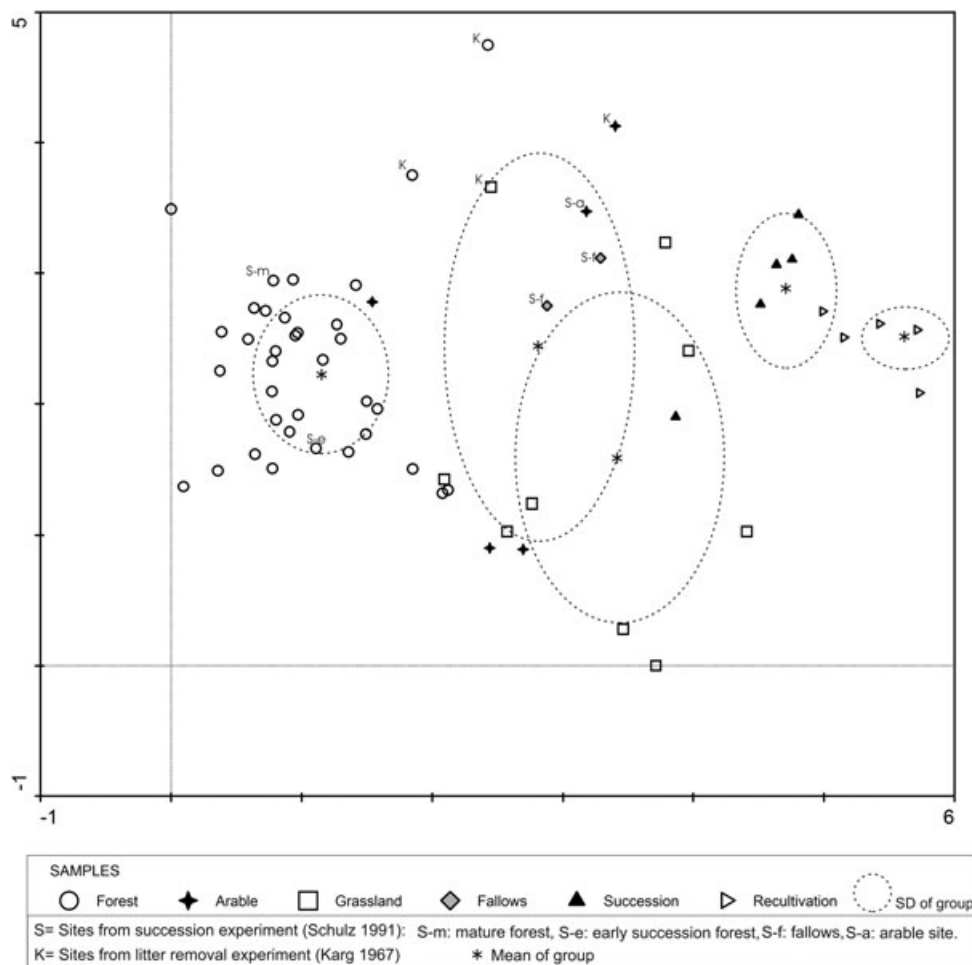


Figure 1 Plot of the first two axes of detrended correspondence analysis conducted using the Gamasina species dominance data (254 species) showing the ordination of European sites (61 sites). Sites are labelled according to the six different land uses. Total inertia 12.89; eigenvalue first axis 0.78; second axis 0.61. The mean \pm SD of the scores in both axes for each land use group are indicated by an asterisk and a circle, respectively.

Table 3 Distances (in SD units) between the different land uses in Europe according to the detrended correspondence analysis conducted using the species dominance data

	Forest	Arable	Grassland
Forest	—	—	—
Arable	1.6	—	—
Grassland	2.2	—	—
Succession	3.5	1.9	—
Recultivation	4.4	2.8	2.2

Significance of difference between distances; one-way analysis of variance: $F_{5,54} = 44.31$, $P < 0.0001$. Only significant ($P \leq 0.05$) distances in least significant difference Fisher's tests are listed.

and the results did not differ significantly from the ordination obtained with the species dominance values. Sites from Argentina differed from the European sites in 6.7 SD. European sites were separated on axis 2 according to land use. Forest sites were different from the other sites, and succession and recultivation sites were different from the remaining ones.

We also conducted a DCA excluding the sites from Argentina to analyse the power of the presence/absence data set to discriminate between the different land uses in the European sites (Figure 4). Sites were separated in three groups. As revealed by the dominance data (Figure 1), the forests were clearly separated from the other sites and the arable sites were plotted near the grasslands. In this case, the recultivation and the succession groups of sites were not separated from each other but they formed a single group. The scores of the forest sites on axis 1 were different from the other sites (Table 6). The recultivation and the succession sites differed from the arable lands. The sites from the two experiments previously described were plotted in a manner that could not be clearly interpreted.

Finally, we have included in the analysis, data on faunistical lists from five Austrian and three Latvian sites, arranged in a presence/absence database (Figure 5). The DCA produced an ordination that was broadly consistent with the land use. A separation of sites according to altitudinal differences was also evident among the forests from Austria; the four alpine forests were plotted at the right end of axis 1, separated from the floodplain forest that was located closer to the other European

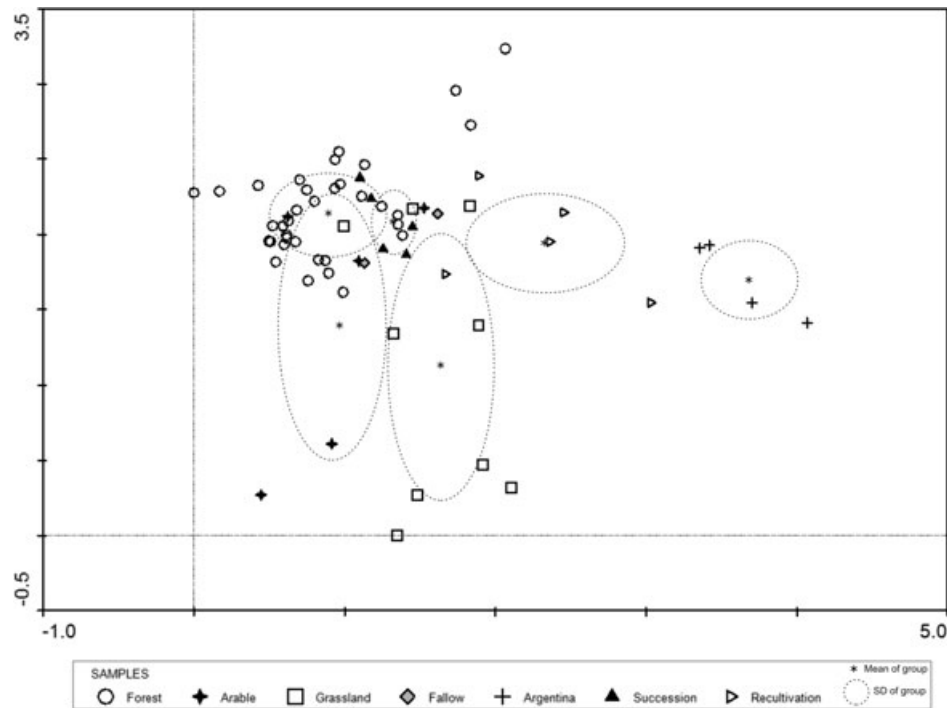


Figure 2 Plot of the first two axes of detrended correspondence analysis conducted using the Gamasina genus dominance data (52 genera), showing the ordination of European and Argentine sites (65 sites). European sites are labelled according to the six different land uses. Total inertia 5.02; eigenvalue first axis 0.571; second axis 0.411. The mean \pm SD of the scores in both axes for each land use group are indicated by an asterisk and a circle, respectively.

Table 4 Distances (in SD units) between the different groups of European and Argentine sites according to the detrended correspondence analysis conducted using the genus dominance data

	Argentina	Forest	Arable
Forest	2.7	—	—
Arable	2.7	—	—
Grassland	2.0	0.75	0.67
Succession	2.3	—	—

Significance of difference between distances; one-way analysis of variance: $F_{6,56} = 14.72$, $P < 0.0001$. Only significant ($P \leq 0.05$) distances in least significant difference Fisher's tests are listed.

non-alpine forests. The distance between Austrian forest mean and the other forest mean was 2.7 SD, which indicates a species turnover of approximately 75%. This suggests a unique Gamasina species composition in Austrian alpine forests. Latvian forests did not form a separate group, neither did they fall within the SD area of the other forests.

Discussion

Site specific community

DCA results at the species level clearly revealed strong differences in species composition in the communities of soil Gamasina from Argentina and from central Europe.

It has been suggested that sites differing by 4 SD in DCA scores would tend to have no species in common (Gauch, 1982; Jongman *et al.*, 1995). The results obtained in the present study showed a substantial distance between the European and the Argentine sites (17 SD), which means that the Gamasina communities had almost no species in common (Gauch, 1982). However, we know that they shared three species. Therefore, the differences lay in other parameters, such as dominance, abundance or distribution.

Also, the communities under each of the six land uses in central Europe were different from each other. In the DCA, site location on axis 2 was consistent with the land use explanation. Few exceptions to this interpretation were found, such as some grassland sites that were unexpectedly close to some forest sites.

It is obvious from this analysis that the geographical location factor was much more important to the Gamasina mites than the influence of any of the land uses considered.

The analysis of European sites alone (Figure 1) revealed strong differences in land use. The results obtained in the present study show a marked difference in Gamasina community structure between forests and the other land uses. Differences between the communities of grasslands and arable land were not so noticeable, because arable lands were plotted among the grassland sites rather than forming a separate group. The analyses also showed great variation among arable sites. We included sites encompassing a broad range of agricultural practices. It has been suggested that predatory mites are differentially affected by different tillage methods (Lagerlöf &

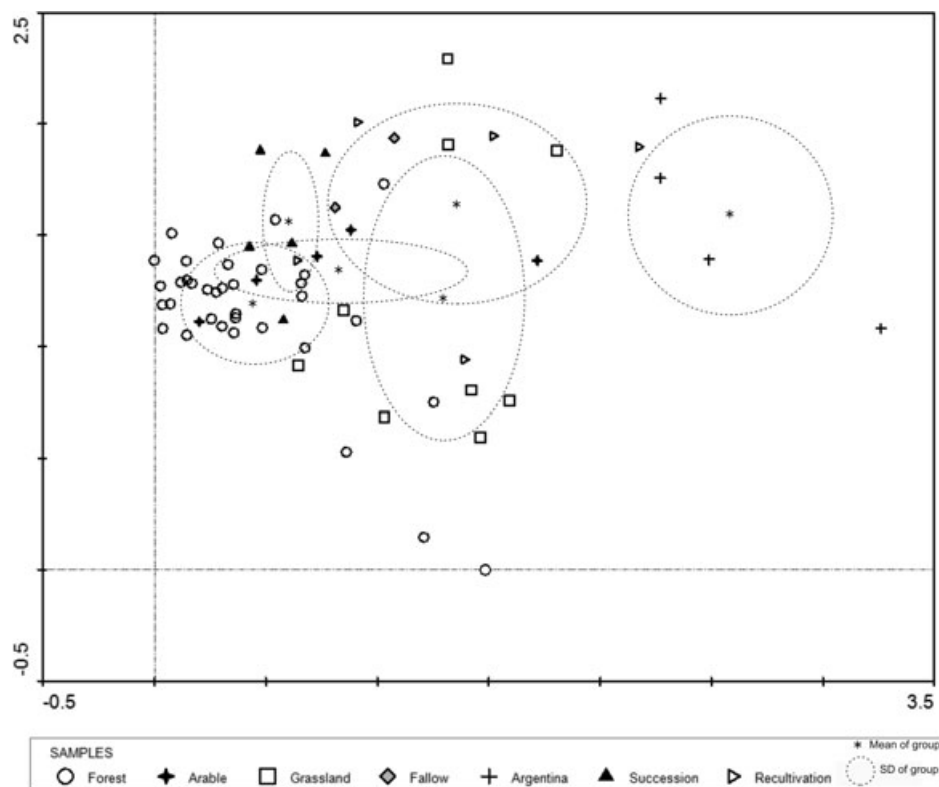


Figure 3 Plot of the first two axes of detrended correspondence analysis conducted using the Gamasina family dominance data (15 families) showing the ordination of European and Argentine sites (65 sites). European sites are labelled according to the six different land uses. Total inertia 1.84; eigenvalue first axis 0.431; second axis 0.193. The mean \pm SD of the scores in both axes for each land use group are indicated by an asterisk and a circle, respectively.

Table 5 Distances (in SD units) between the different groups of European and Argentine sites according to the detrended correspondence analysis conducted using the family dominance data

	Argentina	Forest	Grassland	Succession
Forest	2.10	—	—	—
Arable	1.70	—	—	—
Grassland	1.30	0.86	—	—
Succession	2.00	—	0.7	—
Recultivation	1.20	0.92	—	0.75

Significance of difference between distances; one-way analysis of variance: $F_{6,57} = 15.49$, $P < 0.0001$. Only significant ($P \leq 0.05$) distances in least significant difference Fisher's tests are listed.

Andr n, 1988; Wardle, 1995; Koehler, 1999). Therefore, differences in management strategies should be taken into account in future analyses of arable sites; in addition, more arable sites should be included to better characterize the communities and assess the differences with grasslands. Unfortunately, data on Gamasina from arable lands are scarce (Ruf & Beck, 2005).

The groups of succession and recultivation sites were located closer to each other than either was to the other sites, suggesting that their communities were unique. When the succession and the recultivation sites were analysed alone, they showed a successional trend (Koehler, 2000), although a different result

was obtained when these sites were analysed together with the other land use sites in the present study. This means that there was no development of the predatory mite community towards grasslands or even forests, or that succession is still at an early stage, despite the 20-year progression. This is consistent with the results obtained for mites on tailings from nickel/copper mines where, despite a history of up to 40 years of succession, tailings–mite communities were strikingly different from the surrounding control areas (St. John *et al.*, 2002).

Taxonomic resolution

The use of family and genus rather than species level data can be more efficient for discrimination between sites because the specific identification of soil Gamasina takes significantly more time and resources and also requires more taxonomic expertise. The results obtained, however, suggest that the use of species-level data provides a clearer discrimination between sites. The species approach appeared to be more appropriate than the genus and family approach for discriminating sites according to geographical location and land use. The species-level analysis was also useful for evaluating the effects of experimental manipulation, such as the succession and litter removal experiments that we analysed. Neither the genus nor the family approach was useful for evaluating these manipulations.

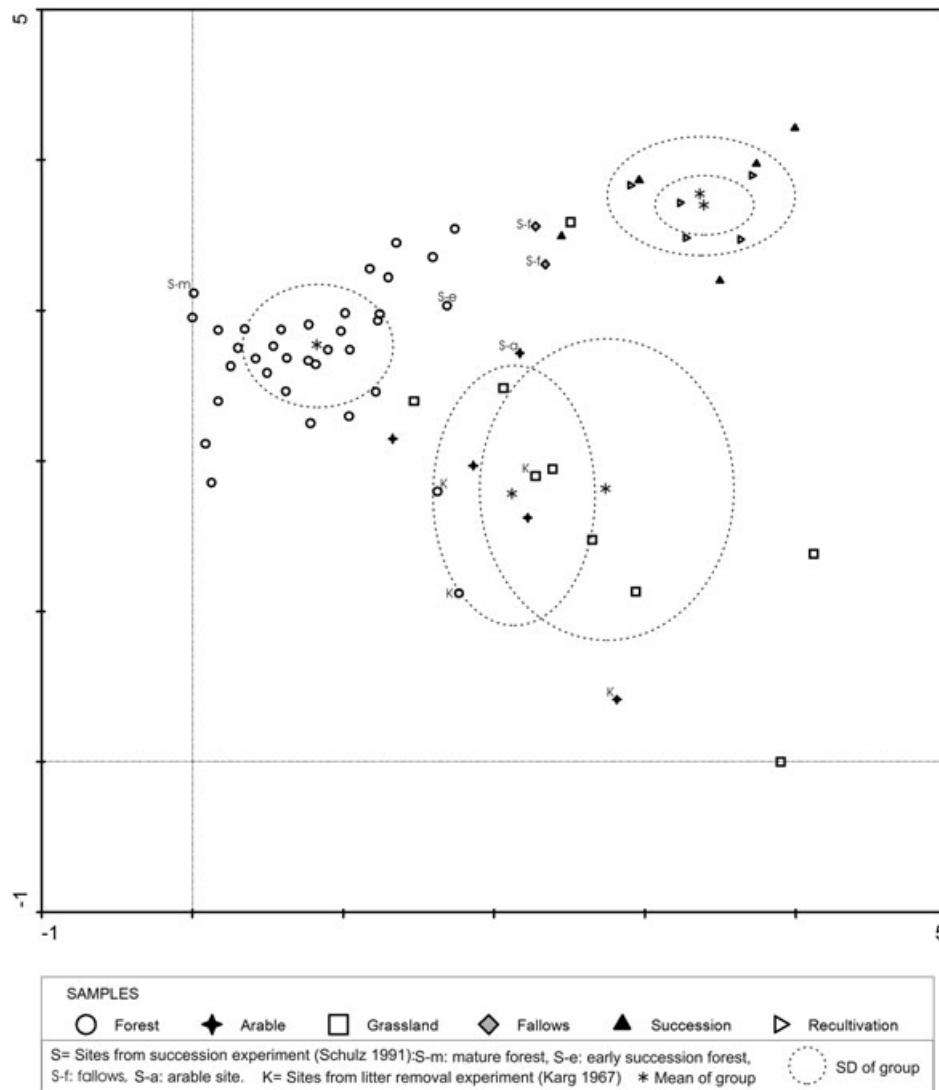


Figure 4 Plot of the first two axes of detrended correspondence analysis conducted using the Gamasina species presence/absence data (254 species) showing the ordination of European sites (61 sites). Total inertia 9.5; eigenvalue first axis 0.902; second axis 0.628. The mean \pm SD of the scores in both axes for each land use group are indicated by an asterisk and a circle, respectively.

Table 6 Distances (in SD units) between the different land uses in Europe according to the detrended correspondence analysis conducted using the species presence/absence data

	Forest	Arable
Forest	—	—
Arable	1.30	—
Grassland	1.90	—
Succession	2.50	1.3
Recultivation	2.60	1.3

Significance of difference between distances; one-way analysis of variance: $F_{5,54} = 24.57$, $P < 0.0001$. Only significant ($P \leq 0.05$) distances in least significant difference Fisher's tests are listed.

The genus-level approach was also valuable for differentiating sites according to geographical location as well as some of

the land uses (e.g. grasslands from the forests and arable sites). The family approach was appropriate for distinguishing the Argentine sites from the European ones, although the picture was not as clear as that obtained using the genus level approach, and sites were separated by a shorter SD distance. This shows that soil dwelling predatory mite families are cosmopolitan and exhibit no specific continental-scale effects. Therefore, no detailed taxonomic work is necessary to detect the effect of major geographical differences or of differences between certain land uses. However, minor differences among sites are better detected using species taxonomic level databases. This is in agreement with results reported by Basset *et al.* (2004), who evaluated the discriminatory power of different arthropod data sets at 12 sites of increasing anthropogenic disturbance in the tropics. They also found that the species-level data sets were more powerful than those including any higher taxa to

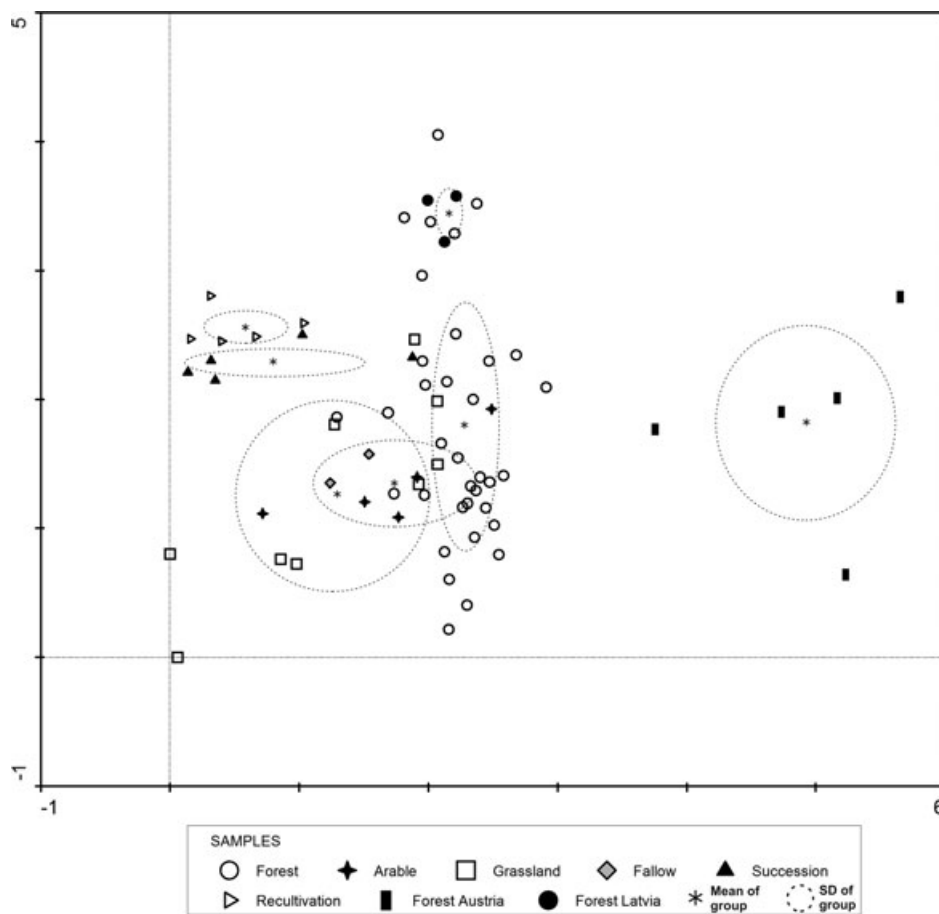


Figure 5 Plot of the first two axes of detrended correspondence analysis conducted using the Gamasina species presence/absence data (303 species) showing the ordination of European sites, including sites from Latvia and Austria (69 sites). Total inertia 11.91; eigenvalue first axis 0.675; second axis 0.453. The mean \pm SD of the scores in both axes for each land use group are indicated by an asterisk and a circle, respectively.

discriminate against the disturbance gradient. Nahmani *et al.* (2006) suggested that grouping species of macrofauna into a single group can lead to a loss of interesting information if the species behave differently towards a given perturbation.

The results obtained in the present study also agree with the results obtained by stream macro-invertebrate analysis, where identification at the family level was as effective as the genus and species level in multivariate analysis across a region, although the species-level approach allowed a more sensitive and responsive assessment at smaller scales or detection of finer levels of impairments (Marchant, 1990; Taylor, 1997; Davies & Cook, 2003).

Presence/absence data

It is often assumed that quantitative data can provide more information than presence/absence data. In agreement with observations made in other ecosystems (Davies & Cook, 2003), the present study showed that the inclusion of quantitative data (species dominance) in the analysis yielded a clearer separation of sites than the presence/absence data analysis, and a greater SD distance between ecologically different sites.

From a practical point of view, the presence/absence of species also provides valuable information in this type of analysis. Two important advantages of presence/absence data over dominance data are consistency and reproducibility. Variation of arable and grassland sites was lower with presence/absence data. However, the forest, succession and recultivation sites showed almost the same variation, independently of the type of data used. The presence/absence approach also permits the use of faunistic lists, allowing a temporal comparison of results and the identification of temporal trends in the communities. However, the use of presence/absence data only shows the loss of species in Gamasina community, and may mask changes in abundance or dominance. For example, some management practices, particularly in agroecosystems (ploughing, pesticide application), affect the density and/or dominance of some species (Lagerlöf & Andrén, 1988; Koehler, 1992; Koehler, 1999) and not the species composition as such.

Conclusions

DCA provided an ordination that reflected differences in species composition of the Gamasina communities between

Argentine and European sites, as well as differences between land use types in the European sites. It should be noted that more data from arable lands are needed to characterize the communities better because there was high variation between arable sites. The predatory mite community of the succession and recultivation sites was different from those of the other land uses, although does not appear to be developing towards grassland or forest communities.

The level of taxonomic resolution needed to obtain an adequate classification depends on the objectives of the assessment and the spatial scale. The species data set (i.e. the highest taxonomic resolution) provided a clearer separation of sites according to both geographical and land use gradients than the genus and family data sets. This confirms our hypothesis proposing that the loss of information resulting from the higher taxonomic level databases would result in a loss of the ability to detect significant effects of land uses or experimental treatments. The data obtained in the present study showed that the genus and, to a lesser extent, the family approach should be sufficient to elucidate the influence of great geographical differences and also certain land uses. However, the species approach provided a more sensitive assessment of the management effects.

Presence/absence data on species provided valuable information in our analyses, although the use of quantitative data yielded a clearer separation of sites. Moreover, the use of dominance data was more suitable for evaluating the effects of experimental manipulations. The use of presence/absence data may be preferred when species abundance data are difficult to obtain; for example, when the aim is to use historical data in the form of species list to compare with the present status or to evaluate historical trends.

The effectiveness of DCA in the distribution of sites along the ordination axis and the compatibility of sites with ecological interpretations is supported by the present application. By including the mean of the scores for each land use group on both axes and the SD circles, the differences and the land use overlap can be observed more clearly. We consider that our approach can contribute to the assessment of the sensitivity of soil mites in the detection of anthropogenic disturbances in soil ecosystems.

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