

## **Endemism mapping and biodiversity conservation in western Europe : an Arthropod perspective**

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### **Abstract**

Endemism patterns in Arthropods have been little explored at the West European scale. In this paper, three groups rich in endemics are analysed: Oniscidea Isopoda, Collembola and Staphylinidae Coleoptera. Grid maps (0.2\*0.2°) of endemism richness are presented for each group separately and for the three groups pooled together. These appealing maps are however dependent on local sampling efforts, and we stress the necessity to interpret them with caution under the supervision of group specialists. Most endemics are associated to Mediterranean mountains south of 45°N. Patterns observed in the different groups are roughly congruent for Pyrenees and slightly less for the Iberian peninsula. In southwestern Alps, high endemism areas are clearly not concordant between Collembola, poorly diversified there, and the two other groups, which reach in this area their highest scores. An unexpected low endemism richness is also recorded for Sierra Nevada, in sharp contrast to floristic data. On these grounds, we emphasise the need of a several-group approach for accurately identifying areas of endemism. At the study scale, grid cells with endemics cover a considerable part of southwestern Europe. The presence of endemic taxa cannot therefore be considered as a sufficient criterion for selecting areas for conservation, given existing socio-economical constraints on land-use. To cope with these constraints at a minimal cost for biodiversity, we explored the effects of reducing the dataset to the endemics limited to the smallest mapped unit, i.e. a single grid cell. We obtained a set of grid cells (the one-cell-endemic area subset) which is still very large, occupying in

particular most of the Pyrenees and the southeasternmost part of the Alps. The minimal area including all species of the region, which is the background of area-selection methods, would be necessarily larger than this one-cell-endemic area set. It would be therefore inefficient by itself for area-selection in the regions which host the richest biodiversity of western Europe. For this purpose, it should be accepted that at least some narrow endemic species are not represented in the minimal area. This process of elimination of species for reducing minimal area could be optimised at the lowest cost for biodiversity by combining existing area-selection methods with an evaluation of the biological value of concerned taxa. With the limitations attached to sampling heterogeneity in mind, and at the cost of a few methodological adaptations, endemism mapping associated to area-selection methods will soon provide an essential tool for European policies of biodiversity conservation.

**Keywords :** Isopoda, Collembola, Staphylinidae, hotspots, Mediterranean biodiversity.

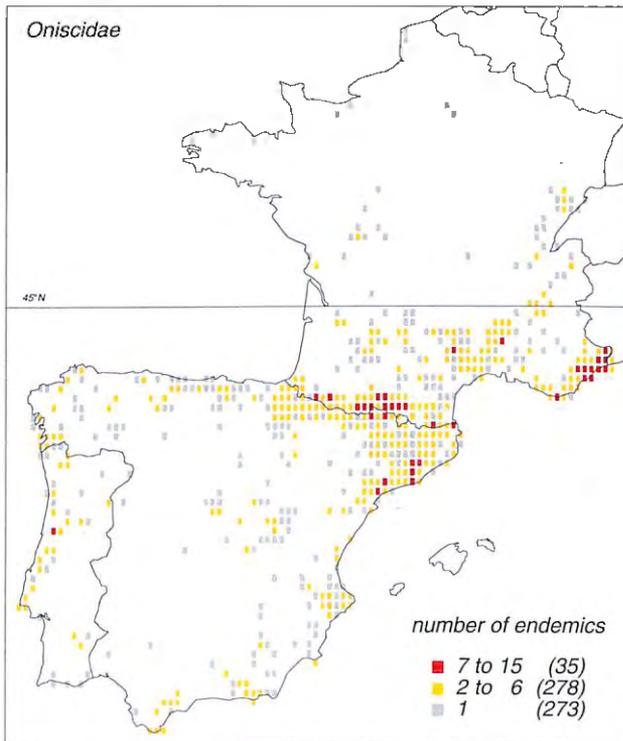


Fig. 1. Map of endemic Oniscidea (woodlice) over Western Europe, on a  $0.2 \times 0.2$  degree grid. Number of grid cells for each class in brackets.

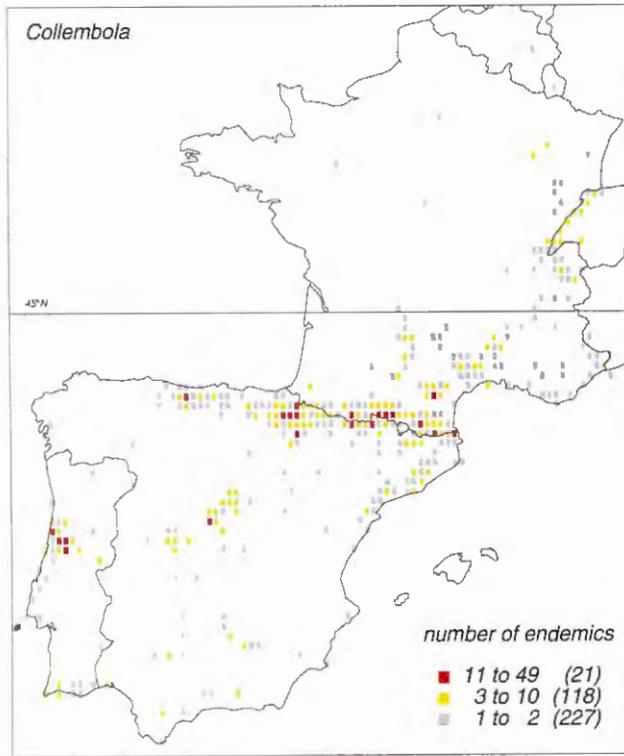


Fig. 2. Map of endemic *Collembola* (springtails) over Western Europe, on a 0.2\*0.2 degree grid. Number of grid cells for each class in brackets.

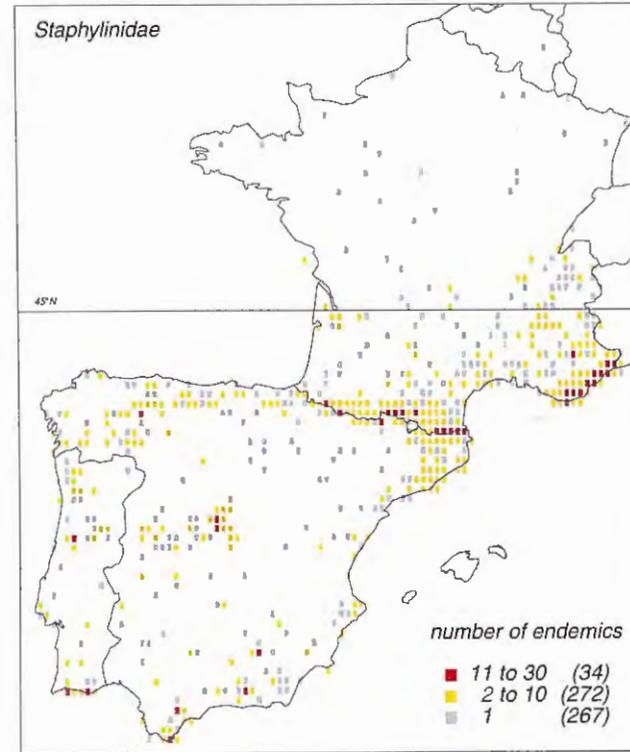


Fig. 3. Map of endemic *Staphylinidae* over Western Europe, on a 0.2\*0.2 degree grid. Number of grid cells for each class in brackets.

## Introduction

Evaluation of biodiversity is the background of conservation policy, and species richness is its most straightforward measure. The importance of Arthropods in this context is clear: with nearly 2/3 of extant species, Arthropods are by far the most diverse of all living groups on earth (KIM, 1993). They also host a contingent of parasitic invertebrates more or less specific or group-specific which may well be altogether only second to them in their contribution to biodiversity. Species count is however a crude and approximate gauge of biodiversity, as repeatedly stated in the literature (WILLIAMS & HUMPHRIES, 1996). For a more accurate representation of biological value, it should be combined to rarity, genetic polymorphism and phyletic isolation, which reflect altogether the uniqueness and the diversity of traits of the species. In this respect, narrow endemic taxa, i.e. those restricted to a limited area, deserve a special attention (GASTON, 1994). Some have survived the successive climatic and geographic upsets which affected the continent, and represent the largest part of oligospecific, phyletically isolated taxa of Europe. Others are poorly differentiated biological entities, narrow endemism being the obligatory status of any incipient species. Most exhibit special patterns of genetic polymorphism (VOGEL *et al.*, 1999). Endemics therefore constitute both the basic material for palaeobiogeographical reconstruction (ROSEN, 1988) and the most important biological values for conservation.

What is exactly the proportion of endemic taxa in the actual fauna of western Europe has been loosely documented at a general level, in contrast to the excellent information set available for plants in some countries like in the Iberian peninsula (MORENO SAIZ & SAINZ OLLERO, 1992; MORENO SAIZ *et al.*, 1998). It is well known that large numbers of endemic species exist in many living groups, in first line among Arthropods, but the ratio endemic versus non-endemic species has rarely if ever been measured across a wide range of taxa. At a more limited scale, the evolutionary diversification of lineages into a number of endemic species without clear habitat specialisation often appears as the main support of high biodiversity among non-herbivorous groups. Evidence of that can be drawn for instance from the cave and deep soil Coleoptera, generally differentiated into a huge number of narrow distributed, often parapatric species living in very similar microhabitats. The closely related genera *Aphaenops* and *Hydrapphaenops* (Trechidae beetles), endemics to the Pyrenees, have altogether 44 species in this mountain range, all cave dwellers of very narrow distribution (CASALE & LANEYRIE, 1982). The 119 species of *Leptotyphlus* (Staphylinidae beetles of deep soil layers) known from the Franco-Iberian area are all very narrow endemics as well (DRUGMAND & OUTERELO, 1997). This contribution of narrow endemic taxa to global biodiversity is growing year on year, for the simple reason that most non-endemic species have now been found in Europe, while many narrow-endemic species, particularly among continental Arthropods, are still to be discovered and described. Available evidence, including the present dataset, suggests that the

proportion of endemics defined at a threshold of 20,000 square kilometres is likely to be over 50% of the total number of species for several major Arthropod groups of Europe.

More than marginal, biologically attractive research objects, endemic Arthropods increasingly appear to be the bulk of biodiversity. Yet, this importance is reflected neither in the literature devoted to European biodiversity nor in European biodiversity policy. Such a paradox may stem from two simple facts: first, the very loose use of the word "biodiversity", which has been reshaped to embrace the complete field of traditional ecology and more, from single species physiology to socio-economic analyses; second, the lack of spatial data about endemic Arthropods. It is this last point that we shall address here.

Delimiting areas of endemism is a basic step in biogeography (MORRONE, 1994), and so it is for a sound policy of biodiversity conservation. It has to be admitted first that vertebrates and many winged insects are virtually useless for identifying areas of high endemism in Europe, simply because they include too few endemic species (GROOMBRIDGE, 1992). High endemism areas can only be traced from endemic-rich groups, which include plants, Mollusca and, above all, different groups of Arthropods. A large amount of data is sparse in the literature, which could feed endemism pattern reconstructions in Europe, and direct future field work. Our contribution, using three groups of Arthropods rich in endemics, is a first step in this direction. The present paper aims at (i) displaying endemism patterns and identifying high endemism areas for the studied groups in western continental Europe; (ii) highlighting differences between groups and their implications for biodiversity evaluation and conservation; (iii) exploring the peculiarities attached to endemic-rich datasets in relation to the classical goal of having all species represented in a minimal area for managing biodiversity; (iv) place endemism mapping in the global strategy of biodiversity conservation in Europe.

### Material and methods

Throughout this text, taxa which have a distribution area of less than 500 km in their longest dimension are considered as endemics. Due to the loose sampling coverage of Europe for endemic-rich groups of Arthropods, this linear approach has been found more operational (particularly for aquatic and cave animals) than the grid-based approach used in better sampled groups such as vascular plants. It assumes that the studied taxon may be present between the sampled points where it is known to occur. It is likely to exclude rare or rarely collected species of large distribution. Its major drawback is to be misleading for taxa with highly disjunct distributions.

The regions covered in this study are the continental part of France, the Iberian peninsula, Belgium and Luxembourg. Great Britain, Netherlands and Western Germany do not have endemic species for the studied groups and accordingly have not been included.

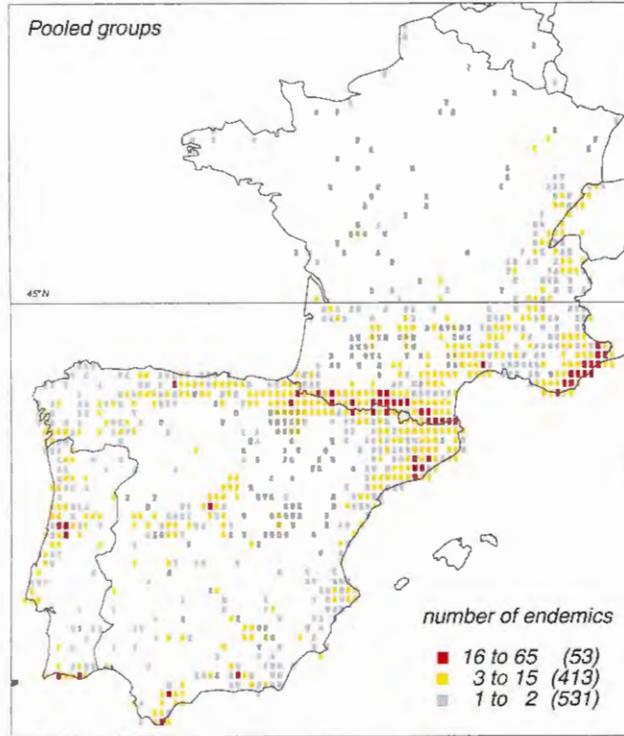


Fig. 4. Map of endemics for the pooled set (Oniscidea+Collembola+Staphylinidae) over Western Europe, on a  $0.2^{\circ} \times 0.2^{\circ}$  degree grid. Number of grid cells for each class in brackets.

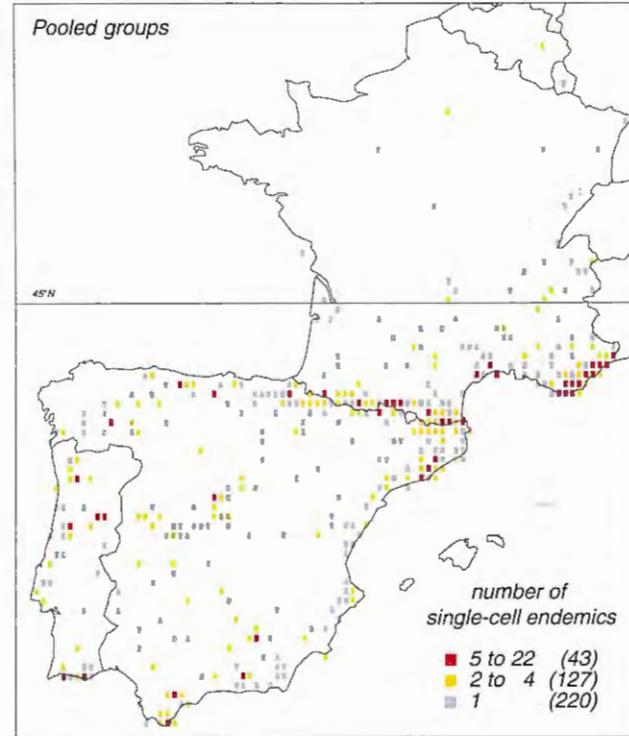


Fig. 5. Map of narrow endemics for the pooled set (Oniscidea+Collembola+Staphylinidae) over Western Europe, on a  $0.2^{\circ} \times 0.2^{\circ}$  degree grid. Only narrow-endemics restricted to a single grid cell have been considered to build this map. Number of grid cells for each class in brackets.

The dataset analysed is based on a compilation of published data. Three groups of Arthropods have been selected, which all bring a substantial contribution to European endemism and biodiversity. We have taken into account all taxonomic (species, subspecies) or parataxonomic ("races", only for woodlice) categories currently recognised as valid entities by the group specialists. For woodlice, data may be considered as exhaustive; they are extracted from VANDEL (1960, 1962) for France, CRUZ (1990) for the Iberian peninsula, and a number of recent faunistic papers. The dataset has been carefully checked for data quality (DEHARVENG, 1998). Detailed specific maps and localisation lists are available on CD-ROM (DALENS *et al.*, in press). Staphylinidae *sensu lato* (including the former Pselaphidae), represent the largest beetle family of the continent. The dataset is nearly as complete as the woodlice one, including probably all described species and the vast majority of the locations cited in the literature and compiled by DRUGMAND & OUTERELO (1997). It has been roughly checked for data quality. The Collembola dataset excludes Symphypleona (a group with a minor contribution to endemism), and is similar to the Staphylinidae dataset for data quality. It is based on a review of the catalogue of JORDANA *et al.* (1990) for the Iberian peninsula, compiled from a number of taxonomic papers for Spain (in particular SELGA, 1971 and SIMON-BENITO, 1979) and for Portugal (in particular GAMA, 1964), and completed for recent data; for France and Benelux, data were gathered from a large number of taxonomic papers, no recent compilation having been published.

Information for reconstructing endemism patterns is extracted from the Endemica database managed by the different specialists involved in the European programme "Endemism" (DEHARVENG, 1998). For the purpose of this work, all data were merged in a larger database under the software 4th Dimension v.5 (RIBARDIERE, 1992). Each localisation was turned into decimal degrees coordinates, taking the centroid of the original geographical units (UTM squares, small administrative units...) when necessary. Vague or ambiguous locations as well as dubious identifications were discarded. Richness by grid cell was calculated in two steps: first, we attached a grid cell number to each species location after exportation into the GIS Mapinfo; second, after re-importation into the database, we calculated the number of endemic species by grid cell using a special procedure implemented for this purpose. Two sets of data were analysed: (i) the full set of endemic species, subspecies and races (distribution area of less than 500 km in its longest dimension), and (ii) a subset of narrow endemics, each restricted to a single 0.2\*0.2 degree grid cell.

The synthetic maps, produced using the GIS Mapinfo, illustrate endemism richness at a grid scale of 0.2 per 0.2 degrees, but virtually any kind of grid or projection could have been produced, as coordinates of data locations are stored in the database. The surface of a grid cell varies with latitude from 312 square km at 50.8-51°N to 400 square km at 35.8-36°N. Each grid cell is coloured according to three levels of richness in endemics: red for the 10% (map of single cell endemics) or 5% (map of larger endemics) richest grid cells, yellow for the cells of intermediate richness, and grey for the poorest

cells. These last two sets of grid cells have been made as equal as possible in number (35 to 55% each).

## Results and discussion

### A. Endemism statistics

Table 1. Endemism among the studied Arthropod groups in Western Europe. For Oniscidea, races, a category used but poorly defined by the authors, corresponding to ill-defined subspecies, are also included in addition to species and subspecies.

	Oniscidea	Collembola	Staphylinidae
Total number of species or subspecies in the studied area (endemics + non-endemics)	333	about 1000	about 3000
Number of citations of endemics	3051	2610	2445
Number of endemic species or subspecies	231	438	976
Number of genera or subgenera with endemic species or subspecies	48	86	208
Number of species or subspecies known from a single site	44	167	655
Number of species or subspecies known from a single grid cell (0.2*0.2 degrees)	51	195	685
Ratio endemics / total (species or subspecies)	0.7	0.44	0.33
Ratio single site endemics / endemics (species or subspecies)	0.19	0.38	0.67
Ratio endemic genera or subgenera / endemic species or subspecies	0.21	0.2	0.21

Endemism among the studied groups reaches remarkably high levels (Table 1), of the magnitude of those found for vascular plants on isolated islands. The number of endemics ranges from 33 to 70 percent of the total number of species, subspecies or races recognised by the specialists for each group. These values are increasing each year, because the new taxa which are still frequently described from Europe, particularly among Collembola and Staphylinidae, are mostly endemics. For the studied groups, this trend has so far not been significantly counteracted by the extension of the distribution ranges of known endemics resulting from recent faunistic works.

Down to a finer grain, the number of species only known from a single grid cell or even from a single location (a few square kilometres or less) remains considerable with respect to the total species numbers. Some groups like Staphylinidae even approach the extremely narrow endemism documented for Diplomatinae snails by VERMEULEN (1998) in Borneo.

Endemism statistics have however to be taken with caution as the taxonomy of endemic-rich groups is changing rapidly. Several "polymorphic" taxa have recently been split into a number of smaller, often narrow endemic species or subspecies, such as the epigeal *Oritoniscus* woodlice (DALENS *et al.*, 1996, 1997) or the springtail *Monobella grassei* (BEDOS & DEHARVENG, 1998), both in the Pyrenees. Conversely, the number of species recognised in the extremely diverse Leptotyphlinae beetles (Staphylinidae) has been challenged for some species-groups (THELOT, 1984). As for now, the overall effect of such

taxonomic revisions still results in an increase of European endemism levels for the studied groups.

Highly contrasted values have been found from one group to another when comparing the numerical proportion of single site endemics relative to endemics, and of endemics relative to non-endemics (Table 1). These discrepancies may point to significant differences in the speciation process underlying endemism patterns, though the species concept of specialists and the level of knowledge of the groups concerned certainly play a role. Endemics are proportionally less frequent among Staphylinidae than among woodlice, but if winged Staphylinidae are left aside, the proportion would reverse, with probably 90% of non-winged Staphylinidae being endemics. The nearly 100% narrow-endemism rate among cave Isopoda is another clear-cut fact. On the whole, natural history traits linked to dispersal ability and habitat specialisation are likely to explain much of the observed differences and this certainly needs more thorough investigation.

## B. Spatial patterns of sampling effort

Accumulations of endemics in limited areas and over a large range of living groups is more or less familiar to taxonomists, and is largely supported by our maps (Figs 1-5). This may reflect the real endemism patterns of the studied area, but is also dependent on non-biological parameters, i.e. sampling effort and data quality. Data quality, which embraces data validity, data coherence and mapping precision, is a complex question, neglected in most biodiversity mapping approaches (DEHARVENG, 1998). It is however likely to bring only local changes in the results as it will tend to be statistically smoothed over large datasets. Heterogeneity in sampling effort (COLWELL & CODDINGTON, 1994; WILLIAMS & GASTON, 1994; WILLIAMS, HUMPHRIES & ARAUJO, 1999) is more familiar to taxonomists and may introduce very serious bias interesting large groups of taxa, because the data compiled to make the maps have rarely been collected for mapping purpose. Data accumulation on limited areas may result of three processes. (i) Endemic species richness recorded at a given site for whatever reason will foster further collecting, which in turn will bring new discoveries of endemic taxa. Many sites of eastern Pyrenees and southern Alps are concerned by this auto-catalytic process which run lower as we approach the near-zero slope of the cumulative curve of endemic species richness. (ii) Areas located near group-specialist working places are, as a rule, more documented. There is evidence that several hot-spots of endemism among springtails (Madrid, Coimbra and Pamplona areas), though indicating a real high richness in endemics, also correspond to sites which have been most actively sampled by local collembologists during the last decades. (iii) Areas selected for special studies similarly result in data-accumulations which substantially contribute to sampling heterogeneity. The highest hot-spot of Pyrenees for Collembola (a grid with 47 endemic species corresponding to the Neouvielle Massif) has been the target of repeated investigations, because of special field facilities (aside its long recognised biological interest).

Conversely, cold-spots of endemism richness may reflect poor biodiversity or poor sampling, with no simple way to discriminate for the non-specialist.

Indeed, using directly biodiversity maps as a background for biogeographical interpretation or for area-selection in conservation policies could be strongly misleading. It requires that a minimum set of assumptions about sampling representativeness are associated to the maps, with the assistance of group-specialists. The central Amazonia example, where presumed hot-spots of biodiversity were shown to merely reflect sampling density (NELSON *et al.*, 1990) should be kept in mind in this respect.

Partiallying out sampling heterogeneity should be therefore a prime objective of future works, both in the field and on the maps. It could be made in different complementary ways:

(i) by detecting probable artifacts. Cell undersampling may be suspected when empty cells are surrounded by endemic-rich cells, for instance in the Pyrenees southwest of Andorra (Fig. 4). Cell oversampling is likely when isolated rich cell is surrounded by less rich or empty ones, in the absence of special geographical feature, for instance in central Portugal (Figs 1, 3).

(ii) by attaching a measure of sampling effort to each grid cell, in order to put in perspective the crude count of endemic species. One way to achieve this goal is to map the whole set of endemic and non-endemic species, with the drawback associated to this approach, i.e. a considerable increase in census effort. The number of published faunistic lists per grid cell may constitute a lighter surrogate to this approach.

(iii) by correcting crude species counts using, when applicable, mathematical methods based on putative models of species distribution, like rarefaction (MAGURRAN, 1988), or on cumulative curves of endemic species richness (COLWELL & CODDINGTON, 1994).

(iv) by making every effort to restore data homogeneity through appropriate design of future field studies, for instance by targeting the samples towards major spatial gaps or poorly sampled areas with a rich biological potential.

(v) by developing predictive models of endemism richness, which might help increasing the efficiency of sampling design. In particular, exploring more of the links between the patterns of endemism and the historical determinism of present-day living group distribution, i.e. glaciation in first line, should provide useful predictive models for detecting potential high endemism areas, and facilitate the process of biodiversity assessment.

(vi) by smoothing the specialist-dependent sampling heterogeneity. As done here or in the vertebrate-plants biodiversity map of WILLIAMS, HUMPHRIES & ARAUJO (1999), the combined use of different taxonomic groups of significant contribution to endemism richness, may work in this respect.

### C. Spatial patterns of endemism in western Europe

Spatial patterns of endemism in the Franco-Iberian region are synthesised on five maps (Figs 1-5). They will be interpreted keeping in mind all the limitations listed above. As a rule, we shall comment on general patterns (clusters of endemic-rich cells) rather than on isolated hot-spots.

Endemic woodlice are mainly present in the Mediterranean mountains and along the coastal areas, with three high endemism areas: Pyrenees, South-western Alps and southern Catalonia (Fig. 1). The largest number of endemic-rich cells are in southwestern Alps (7 among the 11 richest cells, including the highest score per cell, i.e. 15 endemics). It should be stressed that woodlice sampling is relatively homogeneous on the whole studied area except central and southern Iberian peninsula.

Collembola are more distinctly clustered, with a major area of high endemism from the Pyrenean to the central Cantabrian ranges. As stated above, the secondary hot-spots in the Madrid region (Spain) and the Coimbra region (Portugal), are linked to high local sampling effort. In fact, they probably belong to much larger high endemism areas which remain to be delineated (Fig. 2). The low richness of southwestern Alps is partly due to under-sampling, but recent sampling campaigns seem to confirm that this area is definitely poorest in endemics than Pyrenees. The largest number of hot cells are in central Pyrenees (6 among the 11 richest cells, including the highest score per cell, i.e. 47 endemics).

Staphylinid beetles have nearly one thousand endemics in the studied area. The pattern of endemism recalls that of woodlice, with several Iberian hot-spots (NW Spain, Coimbra, Madrid area, Algarve and Cordillera Betica), and the highest endemism areas in Pyrenees and southwestern Alps (Fig. 3), where the largest number of hot cells are recorded (respectively 4 and 3 among the 11 richest cells, including the highest score per cell, i.e. 30 species in the eastern part of Oriental Pyrenees).

Good congruence exists in the spatial patterns of endemism of the three studied groups. Because data have been collected by a number of independent specialists, this can be interpreted as a strong support to the validity of the recognised high endemism areas. This congruence does not however hold at any scale nor for any region. The most puzzling area of discrepancy is southwestern Alps, remarkably rich in endemic woodlice and Staphylinidae, but not in springtails (Figs 1-3). An even stronger difference exists with vascular plants: the moderate Arthropod richness of Sierra Nevada for the studied groups (the richest grid cell has 18 endemics, of which 13 are Staphylinidae) is in sharp contrast with its outstanding floristic richness (SAINZ OLLERO & MORENO SAIZ, in press). It is worth noting that more xero-resistant Arthropods not included in the present analysis, like Orthoptera (DEFAULT, personal comm.; DEHARVENG, 1998) or weevils (MARTIN *et al.*, this volume), exhibit high richness in Sierra Nevada, suggesting that a single group approach may

lead to a misleading evaluation of the biological interest of a site, with serious implications for conservation.

When all three groups are pooled and mapped together, the high density of cells in southern Europe offers a strong contrast with their sparse occurrence north of the latitude 45°N (only 9% of the 1509 grid cells of the studied area contain endemics in this last area, fig. 4), presumably in relation to the extent of quaternary glaciers and associated climatic changes. Endemics which appear beyond this northern limit therefore deserve special attention, as they might indicate some micro-refugia status of the concerned spots. The Belgium spot (Figs 2-5) is specially puzzling in this respect, as home of one of the two species of the Collembolan genus *Gisinea* MASSOUD, 1965, the other one having been recently described from Siberia.

South of 45°N, the number of grid cells with endemics reaches 865 from a total number of 2245 for the area (39%). Many lowland areas host a few endemic taxa, but areas of highest endemism are mainly clustered on and around mountainous ranges (Pyrenees, Southeastern Alps, Catalonia, and to a lesser extent Cordillera Cantabrica, Sistema Central and Cordillera Betica). Portugal with hotspots in the lowlands (around Coimbra and on the littoral of Algarve) is an exception. The very dense coverage of mountain areas is illustrated by the (Pyrenees + Catalonia) region where only 4 cells from a total of 154 do not have any recorded endemic. In this area, the presence of an endemic taxon would be a poor discriminant criterion for selecting a grid cell. Given the existing socio-economic constraints in the region, it would be unrealistic to propose for conservation the whole area where endemics occur (Fig. 4), which implies that the number of grid cells should be significantly reduced to make a map operational at this scale. The most efficient way to achieve this task would be to use the complementarity approach (WILLIAMS *et al.*, 1996), aimed at determining the minimal set of grid cells embracing the whole set of endemic species.

Our dataset is however unusual compared to the literature data (DOMMANGET, 1994 about French Odonata, WILLIAMS *et al.*, 1996 about British birds, GASC *et al.*, 1997 about European amphibians and reptiles) in that it contains a large number of species of very limited range. We represent on figure 5 the grid cells which contain only those species limited to a single 0.2\*0.2 degree cell, i.e. the smallest spatial unit at the scale of our maps. This one-cell-endemic area is made of 390 grid cells on the 998 which host endemics. It is a subset of the minimal area: any grid cell removed from this one-cell-endemic area is removed from the minimal area which would no more contain the complete set of regional species. The problem is that, even for this one-cell-endemic area alone, grid cells tend to cluster so densely that they nearly cover Pyrenees and southwestern Alps. It is very likely that the remaining endemic and non endemic species are not all represented in the one-cell-endemic area, and would require additional grid cells, increasing the proportion of the region included in the minimal area. In such endemic-rich regions of Europe where the minimal area tends to equate the whole surface of the area, minimal area

would be of little help for directing biodiversity policy. The problem will grow when more endemic-rich groups will be added to the datasets (higher plants, millipedes, mites, weevils, Carabidae beetles ....). It would not be unexpected, given the very high level of endemism in some of these groups and the low sampling coverage of the area, that virtually any  $0.2 \times 0.2$  degree grid cell of the western Mediterranean basin is home of at least one single cell endemic. To make complementarity approach operational in such a configuration, the number of cells of the minimal area, and even of the one-cell-endemic area, have to be imperatively reduced, and we must accept that some taxa are not represented in the final "minimal" set of grid cells.

### Conclusion

With the evoked limitations in mind, our results have nevertheless several implications for biodiversity conservation issues that we shall briefly summarised below.

(i) Mediterranean areas host by far the largest proportion of West European endemic taxa. The overall species richness of Europe would be probably less reduced by the defaunation of the whole western Europe north of  $50^\circ$  latitude than by the defaunation of a single 350 square kilometre area in the Pyrenees or Guadarrama range. There is an urgent need to massively re-direct the bulk of European efforts for biodiversity conservation towards these Mediterranean regions, as already explicitly suggested by OOSTERBROEK (1994).

(ii) Identification and delimitation of endemism areas should be accelerated in this perspective, keeping in mind that they may be heavily dependent on the group used as indicator, a case well illustrated in Sierra Nevada. To what relative extent the differences observed between regions are due to differences in evolutionary history and to differences in sampling efforts should be evaluated as far as possible. Using a range of taxonomic and functional groups that is as large as possible for identifying areas of endemism is perhaps the best practical approach to limit the sampling effort bias, but other methods have to be explored in complement: artifact detecting, measure of sampling effort, mathematical corrections, complementary field sampling and endemism richness modelling.

(iii) The ideal target of conserving all extant species living on earth, and even in Europe, is unfortunately less tenable as soon as endemic-rich groups of Arthropods and Mediterranean areas are concerned. Using a  $0.2 \times 0.2$  degree grid for representing biodiversity patterns of western Europe, we argue that a minimal area even truncated to accommodate only the single cell endemics (the one-cell-endemic area) would probably cover by itself most of the surface of the Mediterranean mountain ranges. The spatial flexibility needed to cope with socio-economic constraints and to develop a sound conservation policy would be dramatically limited. Working at a larger scale (i.e. finer grain) might bring some improvement (i.e. a smaller one-cell-endemic area), at the cost of increased gaps on the map given the low density of data for Arthropod

endemics. This way has to be explored, but would almost certainly lead to the conclusion that additional sampling has to be made, which we already know, and that the gridding scale has to be adapted to the density of narrow endemics in the areas where they occur in large quantities.

When one-cell-endemic area and minimal area tends to equate the entire area of the studied region, a more affordable and immediate strategy may consist in lowering the one-cell-endemic area to the upper limit of socio-economical acceptability, and in reaching the required number of grid cell by a process of grid cell elimination. In order to minimise species loss, the simplest way would be to discard first the grid cells which are less rich in single cell endemics. However, because non-endemics or large endemics are also present in the one-cell-endemic area, they will be affected by the elimination process. In fact, optimising cell elimination for minimising species loss will be preferable as soon as more than 1 grid cell of the one-cell-endemic area is eliminated. The use of area-selection methods like those implemented in Worldmap (WILLIAMS, 1996) would be necessary here, not for selecting the smallest set of grid cells containing the whole set of regional species, but for eliminating grid cells in high endemism areas at the lowest cost for biodiversity.

(iv) Integrating biological value in the elimination process is of prime importance where endemics are concerned, because this category of taxa involve a particularly large range of biological status, from clusters of closely related species to ancient, isolated, relictual taxa. An estimation of the biological interest and vulnerability of endemic taxa will be increasingly required for better precision in valuing areas. Conceptual tools for attaching biological value to taxa have been emerging for a few years, based on phylogenetic or phenetic bases (HUMPHRIES *et al.*, 1995; KRAJEWSKI, 1994), while arbitrary empirical methods are available for evaluating vulnerability. Both categories of weighting tools could be used on endemic-rich groups, in association with optimisation tools like Worldmap, for exploring the best combinations of minimal areas and minimal cost for biodiversity.

(v) By chance, high endemism areas and protected areas are congruent in several areas of Europe, but there are also serious gaps and mismatches. For instance, the hills of southwestern Alps, among the richest endemism hotspots of Europe, are under considerable human pressure with minimal protection status, while one of the biologically poorest spot of Western Alps, the Pelvoux Massif (SAINTE-CLAIRE DEVILLE, 1928), has benefited from protection for decades. In spite of significant progress in recent years (BOUCHET, 1990), areas proposed for protection in several of the richest regions of Europe, like the Pyrenees, continue to be selected on very loose grounds regarding their biological interest, often without any explicit reference to endemism. There is concern that this incongruence might even increase in some regions with the implementation of the new European policy of biodiversity conservation, which relies heavily on a small set of patrimonial species that are strongly biased taxonomically, and which do not consider endemism as a biological criterion by itself (see STOCH, this volume).

There is obviously a balance to restore on these points. As an emerging tool of biological evaluation, in combination with flexible optimisation tools like Worldmap, and with the involvement of relevant specialists for interpreting patterns, endemism mapping could easily and rapidly improve the biological basis and efficiency of site selection for biodiversity conservation in Europe.

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