RESEARCH PAPER

Questioning the effectiveness of the Natura 2000 Special Areas of Conservation strategy: the case of Crete

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ABSTRACT

Aim This study examines the effectiveness of the selected 'network' of Natura 2000 Special Areas of Conservation (SACs) at a regional scale in Greece, in terms of its representativeness of plant biodiversity.

Location The island of Crete is used as a case study because it is considered to be one of the 10 hotspots for biodiversity in the Mediterranean Basin.

Methods Hotspot analysis and complementarity algorithms are used to define priority areas for conservation and calculate their spatial overlap with the Natura 2000 SACs in Crete.

Results The various categories of hotspots contain subsamples of plant categories, used for their definition. Spatial overlap among different categories of hotspots, areas of complementary diversity and Natura 2000 SCAs is low.

Main conclusions The results show that the Natura 2000 SACs 'network' in Crete seems insufficient to ensure satisfactory representation of the regional plant biodiversity elements.

Keywords

Conservation planning, conservation value, endemism, Greece, hotspots, rarity, reserve selection algorithms.

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INTRODUCTION

In the year 2004, the Member States of the European Union are expected to complete a major step in the implementation of a large and integrated nature conservation policy, the operationalization of the Natura 2000 network of Special Areas of Conservation (N2K). The importance of the N2K policy is fundamental for biodiversity conservation worldwide because it exemplifies an almost thirty-year trans-national (15 Member States were involved) policy-making process at a continental scale (Bromley, 1997).

Technically, the N2K network is based on an 'area-selection' conservation planning strategy that addresses as many as several thousand types of natural habitat, where about 150 species of mammal, 520 species of bird, 180 species of reptile and amphibian, 150 species of fish, 10,000 plant species and over 100,000 species of invertebrate occur (European Environmental Agency, 1995). Several of these species and habitats show a dramatic decline in their densities and extent. The challenge for the European Union's N2K strategy was translated into how to achieve trade-offs among society's needs in land-use allocation, along

with the allocation of funds for the accompanying economic instruments, in an ecologically diverse territory of over 3 million km², and a socially and economically diverse human population of 370 million.

The European Union has opted for a compositionalist approach for the design of the N2K network, based on the idea of preservation of listed species and habitat types qualified as being of 'community interest' (EU Directive 92/43/EEC, http://www.europa.eu.int/comm/environment/nature/natura.htm). Sites are selected for inclusion into the N2K network mostly on the basis of representativeness, quality of the habitat, size and density of listed species, and the degree of their isolation.

Given that there have been few 'real world' applications of such principles for the selection of whole-sets of areas for conservation, it is worth examining the effectiveness, i.e. the ability to achieve conservation targets, of the N2K network because of its exemplary value in biodiversity conservation planning worldwide. In that sense, although it appears legitimate to avoid the use of evaluation criteria that are conceptually external to those used to select N2K sites in a specific region, i.e. functionalist criteria, it seems necessary to adopt compositionalist criteria that go

beyond the ones defined in the N2K site selection process. There are several reasons for that:

• Methodologically, sticking to the N2K criteria would lead to a dangerous conceptual circularity that at best would test the ability of the Environmental Administration to apply them in a given context.

• In several countries, especially the biodiversity-rich ones, the N2K network will certainly be the only nature conservation scheme. For example, in Greece, where approximately 260 sites have been selected, almost 20% of the national territory is included in the N2K scheme. It is reasonable to assume that the N2K network will not be complemented with additional local reserve networks, which could take into account specific biodiversity features that are not listed as being of 'community interest', but do need protection.

• It is questionable whether the inclusion of species and habitats in the list of biodiversity components of 'community interest' has been based on a previous detailed evaluation of regional biodiversity patterns. Rather, the selection of N2K sites was based on the inclusion of pre-existing national *ad hoc* schemes, and available local taxonomic experience (e.g. Sfenthourakis & Legakis, 2001). This is contrary to the scientific consensus that accepts that the conservation value *per se* of such a network (measured within the compositionalist framework as a function of species richness) should be evaluated in terms of representativeness of regional biodiversity, and not on an opportunistic, species-specific and *ad hoc* basis.

The purpose of this paper is to examine the effectiveness of the selected 'network' of Natura 2000 SACs at a regional scale in terms of its representativeness of plant biodiversity. We use classic scoring procedures that estimate the conservation value of habitats at a regional scale based on the spatial distribution of plant diversity. The evaluation scheme we adopt follows four steps, i.e. (1) determination of different categories of priority conservation areas; (2) identification of areas of complementary diversity; (3) examination of the geographical coincidence among these areas and the N2K sites; and (4) examination of the complementarity of protected areas in terms of levels of taxonomic resolution. We use Crete as a case study because it is one of the 10 red alert areas of biodiversity or hotspots situated in the Mediterranean Basin, and because of its rich plant diversity and the threats to that diversity (Medail & Quezel, 1997).

METHODS

The island of Crete has a wide variety of biotopes and a long history of human presence. Spared by Quaternary glaciations and isolated for *c.* five millions years, this island has a unique flora (Phitos *et al.*, 1995). The flora of Crete includes many species with eastern Mediterranean or Anatolian distributions (e.g. *Datisca cannabina*), a few species with North African affinity (e.g. *Erodium crassifolium*) and many Tertiary relictual endemics of the Aegean (e.g. *Lomelosia minoana* ssp. *asterusica*). Its vascular flora comprises 1624 native species and 76 species introduced by man within an area of 8700 km[2] (Turland *et al.*, 1993). The endemic taxa *sensu lato* constitute up to 10% of the native vascular flora (Turland *et al.*, 1993).

The main island of Crete and the surrounding small islands and islets were divided into 162 grid cells of 8.25 km[2]. Distribution maps of individual plant species and subspecies, according to Turland *et al.* (1993), were used as background information in the present study. Published information on vegetation (Zohary & Orshan, 1965), land-uses (EEA, 2000), special protected areas (Dafis *et al.*, 1996) and the evolution of landscape (Grove & Rackham, 2001) were also used as additional sources to describe the habitats of Crete. Grid cell adjustments were made in the following cases: (1) when land contained within a coastal grid cell was less than 10%: in this case the square was merged with the adjacent one; (2) small islands and islets near the coast were incorporated into the adjacent coastal square; (3) islands distant from the coast were included in individual squares with boundaries adjusted so that each island falls into one square (Turland *et al.*, 1993).

Biodiversity scoring

Species distribution maps were digitized using Geographic Information System technology (ARCVIEW vs. 3.1). For each cell, plant species richness was calculated as the sum of all taxa, i.e. species and subspecies, occurring in it. Richness hotspots were defined as the top 5% cells among the 162 cells (i.e. 8 cells), ranked by decreasing order of richness (Prendergast *et al.*, 1993). However, because two cells ranked at the 8th position of the decreasing richness scale, nine grid cells were selected as richness hotspots. Endemic hotspots were defined as the top 5% of the cells that contain at least one endemic species (a total of 152 cells) ranked by endemic species richness.

Rarity is calculated for all taxa in a grid cell as the sum of each taxon's inverse number of grid cells records (Usher, 1986; Williams *et al.*, 1996):

$$\text{Rarity index} = \sum (1/c_i) \quad \{i\colon c \neq 0, 1 \leq i \leq n\}$$

where c_i is the number of grid cells where taxon i is present. The top 5% of the cells with the maximum range-size rarity score were defined as rarity hotspots. This index is mainly affected by the species with the most restricted distribution (Williams *et al.*, 1996).

A vulnerability index was calculated for each cell. Estimates of species vulnerability are based on Red Data Book categories (IUCN/TPCS, 1982; WCMC, 1992; Phitos *et al.*, 1995). The vulnerability index is the sum of individual weights of the species contained in the cell. Species listed as 'Endangered', 'Vulnerable', 'Rare' and of 'Unidentified Status' were scored as 1.0, 0.75, 0.5 and 0.25, respectively (Freitag & van Jaarsveld, 1997). Taxa with indeterminate status or insufficiently known, e.g. the majority of Orchidaceae, were scored as 'Unidentified Status' species. Non-listed species were given a score of zero. The top 5% among the 153 cells that contain listed species in Crete ranked by the values of the vulnerability index were defined as threatspots (Troumbis & Dimitrakopoulos, 1998).

The conservation value of a species reflecting its taxonomic distinctiveness was calculated using the index proposed by Daniels *et al.* (1991):

Taxonomic distinctiveness index = 1/*ab*

where *a* is the number of genera in the family and *b* is the number of species (including subspecies) in the genus to which a particular species belongs. Therefore, more distinct taxa received higher scores than species in richer taxa. For each cell, taxonomic distinctiveness was calculated as the sum of that index for all species it contained. The top 5% of cells ranked by the values of its taxonomic distinctiveness were defined as taxonomic hotspots.

Estimation of Complementarity of Natura 2000 SACs

Sets of cells that are complementary for plant species, endemic plant species, genera or families, were selected using an algorithm that identifies any collection of grid cells that contain all the corresponding taxonomic units in the data set at least once. The integer linear programming algorithm, known as 'Set Covering Problem', was used to select the minimum number of cells containing all species (or endemic species or families or genera) in the data sets at least once [see Camm *et al.* (1996) for a full description of the set-covering problem]. This algorithm starts with grid cells including unique species (or genera or families) and adds areas progressively based on rarity of unrepresented features. The mixed integer program solver LINGO was used for the selection of complementary sets of the various taxonomic units studied (LINDO Systems Inc., 1999).

In order to assess, through locational criteria, the appropriateness of the 'network' of Natura 2000 SACs in Crete, the degree of spatial overlap between them and the various biodiversity hotspots and complementary sets was calculated using the Jaccard coefficient {[number of grid cells shared / (number of grid cells selected for hotspot category A + number of grid cells selected for hotspot category B − number of grid cells shared)] × 100} (van Jaarsveld *et al.*, 1998).

RESULTS

The correlations among species richness, vulnerability, range-size rarity, endemic species richness and taxonomic distinctiveness in the collection of cells are high in all cases (Table 1), showing that they provide reliable surrogates for one another. In terms of conservation strategy, this result can be misleading if considered without further analysis. For instance, Table 2 presents the percentage of (1) plant species (2) endemic species and (3) red-listed species occurring in the various categories of diversity hotspots. Interestingly, richness hotspots contain fewer species (i.e. 1001 species) than endemic hotspots and threatspots (both 1030 species). Furthermore, the fact that a category of hotspot is defined according to a specific criterion does not mean that the ensemble of these hotspots contains the full set of the taxa corresponding to that criterion. For example, only 80% of all endemic species occur in the endemic hotspots. The percentage of endemics drops to 48% in the richness hotspots. Endemic hotspots and threatspots contain the highest proportion of red-listed species among the different categories of diversity hotspots (i.e. 185 species or 65%).

The majority of the richness- and taxonomic-hotspots are located in the western part of Crete (Fig. 1). Contrary to what is

Table 1 Spearman rank correlation coefficients among scores for species richness, vulnerability, range-size rarity, endemic species richness and taxonomic distinctiveness in the 162 studied cells in Crete

	Species richness	Vulnerability	Range-size rarity score	Endemic species richness	Taxonomic distinctiveness
Species richness	1	0.791	0.939	0.723	0.938
Vulnerability		1	0.825	0.889	0.674
Range-size rarity score			1	0.755	0.841
Endemic species richness				1	0.614
Taxonomic distinctiveness					1

Table 2 Proportion of plant species, endemic plants and red-listed species occurring in hotspots, threatspots, rarity hotspots, endemic hotspots and taxonomic hotspots in Crete

	Plant species	Endemic plants	Red-listed species
Richness Hotspots	61% (1001)	48% (93)	47% (135)
Threatspots	63% (1030)	80% (155)	65% (185)
Rarity Hotspots	67% (1109)	66% (127)	56% (159)
Endemic Hotspots	63% (1030)	80% (155)	65% (185)
Taxonomic Hotspots	55% (908)	33% (63)	37% (104)

The number in parentheses indicates the number of species.
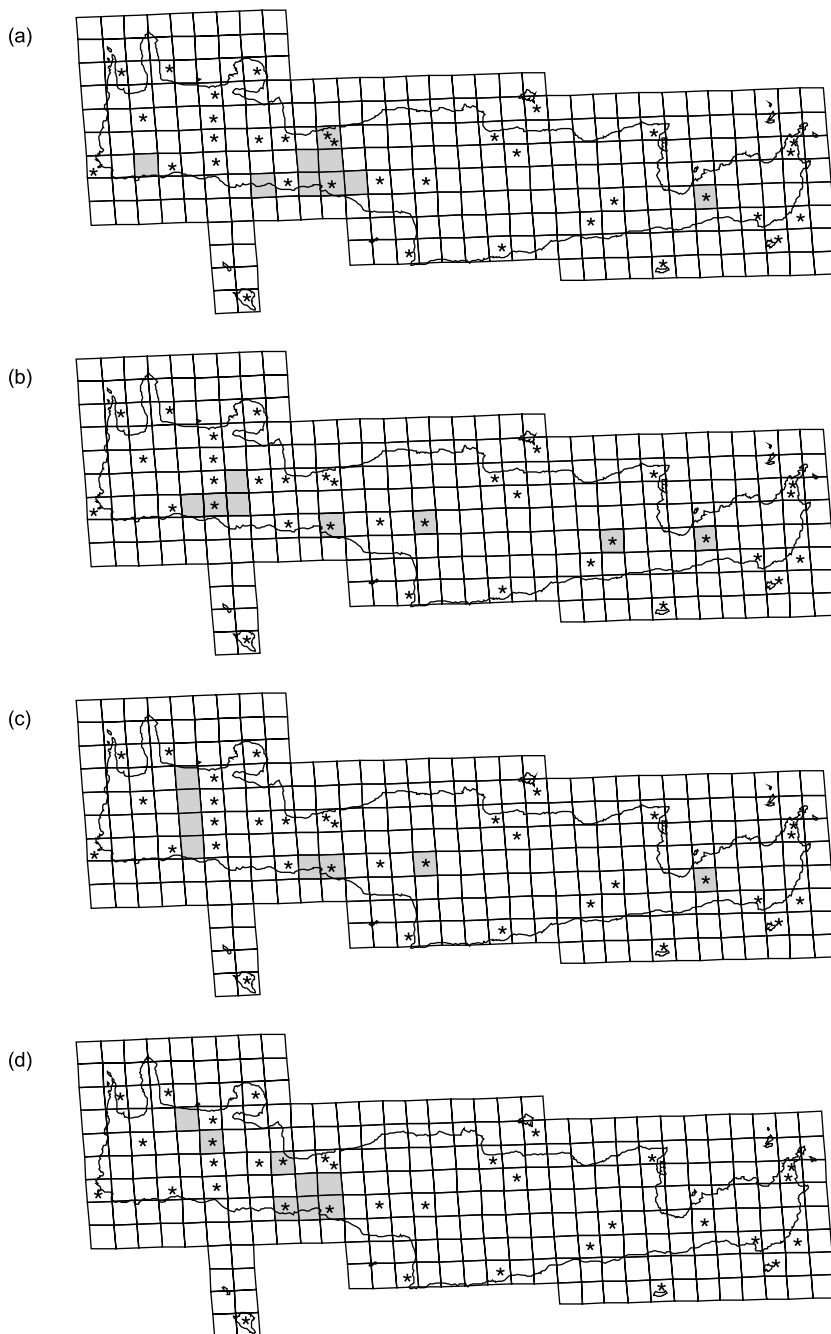
(a)

(b)

(c)

(d)

Figure 1 Maps of location of (a) richness hotspots, (b) threatspots and endemic hotspots, (c) rarity hotspots and (d) taxonomic hotspots of plant diversity of Crete, according to the division of the island into 162 grid cells of 8.25 km². Asterisks indicate Natura 2000 SACs.

traditionally assumed in *ad hoc* conservation practices in Crete, partially reflected in the designation of the Natura 2000 SACs, richness hotspots are not located in the three main massifs of the island (i.e. Lefka Ori, Psiloritis, Dikti). Instead, these mountains are rich in endemics and threatened species (Fig. 1) but not the total number of species.

The degree of spatial overlap among the different categories of hotspots and Natura 2000 SACs is shown in Table 3. Although (1) Crete is a small territory (area), (2) the grid cell size is comparatively large, and (3) the definition of the various hotspot categories is semantically close, the richness of the Cretan flora and its ecological and taxonomic diversification lead to rather low

spatial overlap between hotspots. For instance, only one cell out of 162 can be classified as a hotspot for all of the categories studied. Further, little overlap is also observed between richness hotspots and rarity hotspots. For example, spatial overlap between rarity hotspots, endemic hotspots and threatspots is *c.* 33%. In contrast, endemic hotspots and threatspots fully coincide (100% overlap) (Fig. 1), although the ranks of individual cells in these two categories are different. This is due to the criteria used for the definition of these two categories of hotspots.

In Crete, 34 sites have been selected for inclusion in the Natura 2000 network, covering an area of 2778 km² — or 32% of the island area (Dafis *et al.*, 1996) — located in 32 grid cells. The spatial

Table 3 Percentage overlap of different categories of diversity hotspots and Natura 2000 SACs with species- and endemic species-based complementary sets and complementary sets representing different taxonomic levels. The overlap was calculated using the Jaccard coefficient

Comparisons	Spatial overlap (%)
Richness hotspots	
vs. threatspots	13.33
vs. rarity hotspots	21.43
vs. endemic hotspots	13.33
vs. taxonomic hotspots	30.77
Threatspots	
vs. rarity hotspots	33.33
vs. endemic hotspots	100.0
vs. taxonomic hotspots	6.67
Rarity hotspots	
vs. endemic hotspots	33.33
vs. taxonomic hotspots	23.08
Endemic hotspots	
vs. taxonomic hotspots	6.67
Species-based complementary sets	
vs. richness hotspots	8.42
vs. threatspots	8.51
vs. rarity hotspots	8.51
vs. endemic hotspots	8.51
vs. taxonomic hotspots	7.37
Endemic species complementary sets	
vs. richness hotspots	2.56
vs. threatspots	21.88
vs. rarity hotspots	11.43
vs. endemic hotspots	21.88
vs. taxonomic hotspots	2.63
Species complementary sets	
vs. endemic species complementary sets	31.58
Genera complementary sets	
vs. species complementary sets	42.71
Family complementary sets	
vs. species complementary sets	10.53
Natura 2000 SACs	
vs. richness hotspots	10.26
vs. threatspots	13.51
vs. rarity hotspots	8.11
vs. endemic hotspots	13.51
vs. taxonomic hotspots	10.53
vs. species-based complementary sets	25.49
vs. endemic species complementary sets	27.45
vs. genera complementary sets	30.5
vs. family complementary sets	9.76

overlap between Natura 2000 SACs and the various diversity hotspot categories actually reaches a maximum of 14% (Table 3).

Using our complementarity criterion, the number of grid cells necessary to contain all the plant taxa of Crete, at least once, covers a very large part of the island (i.e. 94 of 162 grid cells, or 74% of Crete, which corresponds to approximately 6400 km^2). When particular categories are used, this number decreases to 33.7% (or 43 cells) for full genus-level complementarity, to 24.3% (or 31 cells) for full endemics complementarity, and to 8.6% (11 cells) for full family complementarity (Fig. 2).

The spatial overlap between the complementary sets of cells calculated for the full list of species and the different categories of hotspots is less than 9% at best (Table 3). When only endemic species are taken into account, the overlap between complementary sets of cells and endemic hotspots is *c.* 22% (Table 3). The coincidence between the full list of species- and the endemic species-complementary sets is also low (32%). When complementary species sets of cells are compared with complementary genus- and family sets, the degree of overlap falls from 43% to 11%, respectively (Table 3). Overlap between Natura 2000 SACs and species- and endemic species-complementary sets is also low (25.5% and 27.5%, respectively). Natura 2000 SACs overlap poorly with complementary genus- and family sets (30.5% and 10%, respectively; Table 3).

To conclude, the diversity hotspot analysis demonstrates that (1) any category of hotspot contains only subsamples of the other hotspot categories, and (2) there is little spatial overlap among the various categories of hotspots and the Natura 2000 SACs.

DISCUSSION

First of all, it is necessary to elaborate on the validity of two elements of the methodology we used, in order to evaluate the effectiveness of the N2K network in Crete: (1) the criterion of complementarity, and (2) the comparison of the N2K site selection process to the solution of a minimum-set problem, i.e. the selection of the minimum number of areas to represent plant species at least once.

N2K sites in Crete were selected in order to ensure persistence of a specific subsample of its native biodiversity, i.e. a collection of species considered as of European 'community interest'. Most evidently in Crete, as in every rapidly transforming rural space with intense competition over land-use allocation, the core problem for conservation is not the identification of key-areas through the use of some 'robust' biodiversity indicator(s); rather, it is related to the adoption and implementation of a process of allocation and regulation of land use. In such a natural and socio-economic context, dominated by the 'old tradition' of nature protection on an *ad hoc* basis (i.e. selection based on scenery, recreation value, or hunting preserves) and the conflicts over land-uses, the 'real-world' conservation process is ultimately subordinate to societal perceptions and local political distortions (e.g. Lombard *et al.*, 1997). Under these circumstances, it is legitimate to assume that the N2K network will be the only biodiversity conservation scheme that has a 'political' chance to be implemented on the island. To put it more explicitly, the N2K network should be viewed as a starting point for negotiations with stakeholders, through 'scheduling' work (see predictions by Pressey, 1998; Margules & Pressey, 2000; Margules *et al.*, 2002). In that sense, the actual importance of the N2K network would
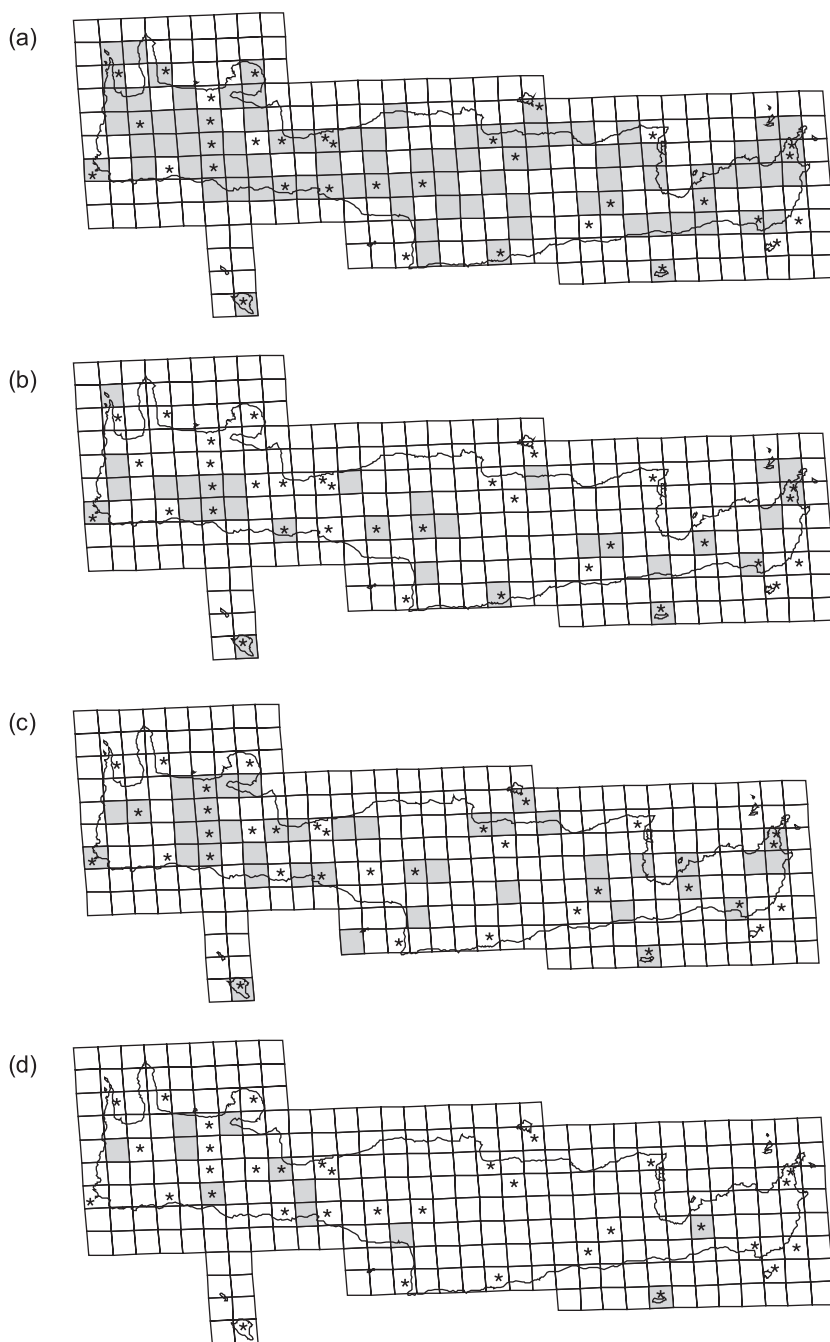
(a)

(b)

(c)

(d)

Figure 2 Maps of distribution of grid cells chosen to represent (a) all the plant species, (b) all the endemic plant species, (c) all the genera and (d) all the families at least once, according to the division of the Crete into 162 grid cells of 8.25 km². Natura 2000 SACs are indicated with asterisks.

largely surpass the original goals of a European-level conservation of the collection of 'interesting' species and habitats. In terms of biodiversity conservation planning, the N2K network should be evaluated in terms of broader long-term goals and success indicators, especially at its current early implementation stage. Therefore, the question: 'how close are the results of the N2K site-selection process to the policy expectations of regional biodiversity representativeness?' becomes central to the evaluation methodology. At the network level, representativeness is intrinsically related to complementarity, being viewed as the gain in biodiversity representation when an area is added to an 'existing' set of protected-areas (Margules *et al.*, 1988; Vane-Wright *et al.*, 1991; Faith *et al.*, 2003).

N2K is a compositionalist strategy for biodiversity conservation through site or habitat selection. But, how are areas added to the set of SACs? The fundamental concept is to allow for persistence of a given collection of species, without a *priori* setting an upper limit of land allocated to conservation. The number of sites and their individual and total surface result in the listed species of 'community interest' occurring in Crete being represented at least once in the regional N2K. From a methodological point of view, this process can be assimilated technically to a computer-based

selection algorithm of a minimum set of protected areas. In other words, it corresponds to the problem of selecting the minimum number of areas to represent biodiversity attributes at least once.

Ought we to have fixed an upper limit of complementary cells representing SACs equal to the number of N2K sites in Crete, in order to evaluate its effectiveness? The answer is no, because this would correspond to a maximum-covering problem, i.e. selecting a set of areas that maximizes the representation of biodiversity attributes for a given area, and that was certainly not the N2K approach; in Crete at least.

Our diversity hotspot analysis of the Cretan flora has shown that the answer to the question 'how close are the results of the N2K site-selection process to the policy expectations of regional biodiversity representativeness?' should be considered rather cautiously. The Cretan flora is characterized by a high number of species with restricted distribution range. Two hundred and forty of 1648 censused plant species (i.e. 15%) have been recorded only once in a grid cell and they are present in 89 of the 162 grid cells. This fact along with the peculiarities of the spatial distribution of the full list of Cretan species would, in practice, require another five additional cells in order to have all the species represented at least once. Consequently, the use of the maximum-covering approach would equate to accepting the exclusion of a large percentage of rare species from the network of protected areas. In other words, the evaluation of the effectiveness of the N2K would exclude fundamental criteria of conservation planning such as the representativeness and irreplaceability of included biodiversity features. Furthermore, in theory, the first step in any analysis of area complementarity is the selection of the sites (grid cells in our case) where species are recorded once (e.g. Williams *et al.*, 1996; Hopkinson *et al.*, 2001). This also means that the advantage of complementarity algorithms producing flexible results is limited when large numbers of irreplaceable species are found in the data sets of a small-sized geographical region.

The richness of the present-day Cretan flora can been explained within the general explanatory scheme of biological diversification in the Mediterranean Basin, especially in its south-eastern part, which combines elements of both structural and dynamic biogeographical theories (Turner *et al.*, 1996); and which focuses on many ecological processes of immigration, extinction, sorting processes and regional differentiation (Blondel & Aronson, 1999). Such processes explain the high level of α-diversity on the island, while the ecological heterogeneity and the complex mosaic of habitats, on this scale, explain the high level of β-diversity among cells. The results obtained confirm that the various categories of hotspot contain only subsamples of the other categories. Similar findings have repeatedly been reported in literature from other biogeographical areas and from various scales of analysis. This has led to the growing criticism of the hotspot approach in the design of representative nature reserve systems (see review by Reid, 1998). In fact, it has been shown that there is often little congruency among hotspots for different taxa and that many species, especially the rare ones, are not present at all (e.g. Prendergast *et al.*, 1993; Curnutt *et al.*, 1994; Lombard, 1995; Gaston, 1996; Williams *et al.*, 1996; Kerr, 1997; Troumbis & Dimitrakopoulos,

1998; Reyers *et al.*, 2000). It is known that planning procedures, based on the umbrella-species concept, do not provide adequate conservation for many species, which belong to separate taxonomic groups (Kerr, 1997). What makes the Cretan example interesting in this sense is that the congruence within the same taxonomic group, i.e. of various plant categories, is low. In Crete, because of the high plant richness and heterogeneous distribution, it seems that this concept cannot be applied even within the same taxonomic group. Furthermore, even the distribution of higher taxonomic levels (e.g. genus or family) seems inappropriate to predict distributions at the species level in Crete. On coarse geographical scales, the diversity of genera and families can be correlated with species diversity in some taxonomic groups (e.g. Williams & Gaston, 1994; Balmford *et al.*, 1996a,b), but on finer, regional scales this pattern seems not to be upheld (van Jaarsveld *et al.*, 1998).

The analysis of spatial overlap between the various categories of hotspots and the Natura 2000 SACs in Crete shows that in absolute terms the overlap does not exceed 30% even at its best (in the case of the genera complementary set of cells and SACs). Is this sufficient to ensure the long-term persistence of the biodiversity elements for which the network has been designed? It is obvious that our measure of overlap is simplistic, since it considers that an entire cell corresponds to the actual size of a SAC. At the same time, a cell is taken as a proxy for the unitary distribution of a species. Both assumptions are only approximations of reality, so the results should be cautiously considered as indicative. Under these circumstances, it is questionable whether the Natura 2000 'network' in Crete is adequate to fulfil its major goals. Even if one assumes that the design (i.e. location, size, shape, connectivity, etc.) and the management plan (i.e. demographic and genetic conservation measures, control plans for catastrophic events, ecosystemic process (– es) management, etc.) of individual SACs are technically correct, it is legitimate to predict that the limitation, control or regulation of certain human activities in areas outside the sites is essential to facilitate biodiversity within a SAC, and to maintain the populations of species not contained in the SACs at viable and functional levels.

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