Contents lists available at ScienceDirect

Ecological Indicators

journal homepage: www.elsevier.com/locate/ecolind

Spatial mismatches between plant biodiversity facets and evolutionary legacy in the vicinity of a major Mediterranean city

M. Pouget^{a,*}, S. Youssef^b, P.-J. Dumas^a, T. Baumberger^c, A. San Roman^a, F. Torre^a, L. Affre^a, F. Médail^a, A. Baumel^a

^a Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale (IMBE) Aix Marseille Université, CNRS, IRD, Univ. Avignon, Technopôle Arbois-Méditerranée Bât. Villemin – BP 80, F-13545 Aix-en-Provence Cedex 04, France

^b Faculty of Agriculture and Forestry, University of Duhok, Kurdistan Region, Iraq

^c ECO-MED, Écologie et Médiation, Tour de Méditerrannée, 65 avenue Jules Cantini, 13298 Marseille Cedex 20, France

ARTICLE INFO

Article history: Received 12 June 2014 Received in revised form 17 July 2015 Accepted 20 July 2015

Keywords: Phylogenetic diversity Evolutionary legacy Rocky habitats Surrogate Conservation Arenaria provincialis National Park of Calanques

ABSTRACT

The analyses of congruencies among biodiversity components address the issue of conservation priorities, but previously they have been done at coarse scales with limited relevance for conservation actions. Moreover, these former studies consider only the species level components of biodiversity and not the intra-specific evolutionary legacy that influences future biodiversity. This study represents the first assessment of congruencies between various components of plant biodiversity and the evolutionary legacy of a narrow endemic taxon (*Arenaria provincialis*, Caryophyllaceae). Assessment is conducted in the vicinity of a Mediterranean big city (Marseille, S.E. France) where habitats and flora are threatened by mass tourism and urban sprawl. Our analyses reveal that the different plant biodiversity facets assessed are spatially mismatched and unequally protected. Moreover, by using only species-level components of biodiversity as conservation targets we ignore crucial areas for the evolutionary legacy of this narrow endemic plant. Our results highlight the crucial role of phylogeography as a criterion to target the genetic precursors of future biodiversity in conservation planning.

© 2015 Elsevier Ltd. All rights reserved.

1. Introduction

Conservation biology aims to conserve all components of biodiversity as well as the ecological and evolutionary processes that sustain them (Moritz, 2002; Lankau et al., 2011). To date, conservation strategies have largely focused on taxonomic diversity to protect species or areas at various scales. Evolutionary assessments of biodiversity may reveal serious weaknesses in the network of protected areas, especially where areas with high species richness are not cradles of diversification (Becerra and Venable, 2008) or hotspots of genetic diversity or uniqueness (Taberlet et al., 2012). For example, Davis et al. (2008), who investigated mammal diversity, and Kraft et al. (2010), who focused on plant diversity, demonstrate some spatial discrepancies between simple counts of endemic species richness and ongoing diversification within the California biodiversity hotspot. Other recent studies report robust links between the genetic and specific components of biodiversity (*e.g.*, He et al., 2008; Papadopoulou et al., 2011; Lamy et al., 2013) and support the existence of surrogates of genetic diversity under certain conditions and scales. These results emphasise that, for system-based conservation planning (Whittaker et al., 2005; Rodrigues and Brooks, 2007), and to better understand the future of biodiversity under global change (Lee and Jetz, 2008), we need to improve our knowledge of the relevance and consistency of putative links between the different components of biodiversity. These links question the existence and value of biological and ecological surrogates.

The inclusion of the evolutionary history of populations in conservation planning is an important issue for long-term management of biodiversity (Moritz, 2002; Sechrest et al., 2002; Tucker et al., 2012; Moritz and Potter, 2013). Historically isolated sets of populations are likely to have distinct evolutionary potential (Moritz, 1994): their existence is the consequence of past evolutionary processes that occurred within populations, shaping



^{*} Corresponding author. Current address: Royal Botanic Garden Edinburgh, Centre for Middle Eastern Plants, 20a Inverleith Row, Edinburgh EH3 5LR, Scotland, UK. Tel.: +44 7459790952.

E-mail addresses: marine.pouget@imbe.fr

⁽M. Pouget), sami.youssef@hotmail.com

⁽S. Youssef), pierre-jean.dumas@imbe.fr (P.-J. Dumas), teddy.baumberger@yahoo.fr

⁽T. Baumberger), almudenasrs@hotmail.com (A. San Roman), franck.torre@imbe.fr (F. Torre), Laurence.affre@imbe.fr (L. Affre), frederic.medail@imbe.fr (F. Médail), alex.baumel@imbe.fr (A. Baumel).

genome diversity and structuring genetic variation as well as a response to selection in case of environmental change (Lankau et al., 2011). The evolutionary legacy of populations is mostly examined through phylogeographical studies (Avise, 2009) and concerns the structure of distinct evolutionary lineages at the intraspecific level or between closely related species. Their recognition led to the adoption of a dynamic view of biodiversity constituting continuously evolving lineages (*e.g.*, Sgro et al., 2011; Hoffmann et al., 2015) sustaining the potential of future evolution to face environmental changes. As such, giving priority to areas that maximise only species-level diversity may have detrimental consequences for future biodiversity due to the inability to recognise the evolutionary legacy of population histories.

Dealing with pattern and history, biogeography has attached great importance to macrorefugia and microrefugia (Avise, 2009; Mosblech et al., 2011; Hampe and Jump, 2011; Keppel et al., 2012; Mee and Moore, 2013) because of their role in the persistence of the genetic and specific components of biodiversity, notably species endemism (Sandel et al., 2014). In the Mediterranean region, a positive association has been observed between hotspots of plant endemism and phylogeographically defined refugia, designating them as areas requiring special attention for conservation (Médail and Diadema, 2009). More recently several studies have focused on the geographical congruence between the different facets of biodiversity and analysed it at coarse spatial scales (e.g., Kraft et al., 2010; Devictor et al., 2010; Mouquet et al., 2012; Taberlet et al., 2012; Zupan et al., 2014). For example, Devictor et al. (2010) found for bird biodiversity that high taxonomic diversity is better represented in French protected areas than phylogenetic or functional diversities. However, conservation strategies need to consider multiple scales, and assessment of biodiversity components at smaller scales deserves more attention because it represents the practical scale for efficient conservation planning (Schwartz, 1999). Conservation strategies have to deal with human settlement issues and give attention to places where people live (Miller and Hobbs, 2002). Even small protected areas can be impacted by human activities such as mass tourism which can have strong effect on endangered species (Ballantyne and Pickering, 2013). Biodiversity studies focusing on large scale (e.g., Devictor et al., 2010; Zupan et al., 2014) are therefore not sufficient to deal with the difficult issue of conservation planning.

To address the issue of congruence among different components of biodiversity, including evolutionary legacy, at a practical scale for conservation planning, we have used an extensive vegetation survey coupled with phylogeographic knowledge of a Mediterranean narrow endemic threatened plant, *Arenaria provincialis* Chater & Hallid. (Caryophyllaceae). *A. provincialis* occurs on limestone outcrops in Provence (south-eastern France) surrounding the big city of Marseille, and its habitats are threatened by severe urban sprawl, recreation and trampling leading to habitat degradation. Like many other endemic species of the Mediterranean region, *A. provincialis* is high in conservation priorities (Thompson et al., 2005; Hobohm and Tucker, 2014), but seriously threatened by human activities (Hoekstra et al., 2005; Underwood et al., 2009) and particularly by urban sprawl along Mediterranean coastlines in the vicinity of major cities (Médail and Diadema, 2006; Vimal et al., 2012).

Previous studies (Youssef et al., 2011; Imbert et al., 2011; Pouget et al., 2013) have demonstrated that *A. provincialis* evolved throughout the Pleistocene, acquiring very specific adaptations to persist in its highly stressful habitats. A recent phylogeographical study demonstrated highly structured genetic diversity from the centre towards the margins of its distribution and a high distinctness of its populations at the genetic and ecological levels (Pouget et al., 2013). One of the main striking points of the phylogeography of *A. provincialis*, revealed by the study of Pouget et al. (2013), is that the core area of its distribution has the highest level of genetic

diversity. Any efficient conservation planning of *A. provincialis* should, at least, target this core area. Here, we use our knowledge on *A. provincialis* as a natural experiment to test the efficiency of various biodiversity components as indicators for conservation planning. The theoretical threshold of 17% of areas to be designated as protected areas (proposed by the "2020" goal of the Convention for Biological Diversity, CBD, 2012), was used to compare the capacity of the various components of biodiversity and environmental heterogeneity to be surrogates of the evolutionary legacy of *A. provincialis*.

Our aims were: (i) to examine the congruencies between different components of plant biodiversity (species and phylogenetic diversity), and the evolutionary legacy of *A. provincialis*. (ii) To compare the relevance of the various components of biodiversity to be surrogates of the evolutionary legacy of *A. provincialis* and to recognise the core area of the distribution of *A. provincialis* as a prime conservation goal.

2. Materials and methods

2.1. Study area, ecological and floristic data

The study area is located in Southern Provence (South-East of France: see Fig. 1) with a strongly seasonal Mediterranean climate, in an area characterised by several limestone outcrops (up to 1150 m above sea level). The landscapes of these outcrops are characterised by a mosaic of low matorrals ("garrigues") mainly dominated by Quercus coccifera with open rocky spaces and a low vegetation cover formed by herbaceous plants. Along with an increase in the human population density occurring in Mediterranean lowlands near the coast, the naturally open habitats of Provence are affected by a combination of urban sprawl, habitat fragmentation, trampling and direct or indirect pollution (Barbero et al., 1990; Médail and Vidal, 1998; Tatoni et al., 2004; Dumas et al., 2008; Baumberger et al., 2012; Vimal et al., 2012). In parallel, the rocky habitats of Southern Provence shelter many rare or endemic plant taxa that make this area a priority for biodiversity conservation assessment and management. Since 2012, the southern part of the focus area and the islands between Marseille and La Ciotat have been included into the National Park of Calanques (NPCal: see Fig. 1). This study focused on the rocky open habitats of these outcrops situated at the periphery of Marseille, which also encompasses the small islands and islets situated less than five kilometres off the coast (Fig. 1).

2.2. Assessment of the different components of biodiversity

2.2.1. Assessment of species taxonomic and phylogenetic diversity

The study area has been surveyed by the Mediterranean Institute for Biodiversity and Ecology (IMBE), resulting in a database of 1132 floristic and mesologic relevés established for 100 m² circular areas. This method is relevant when comparing the ecology of plants inhabiting rocky habitats in southern Provence (Youssef et al., 2010, 2011; Baumberger et al., 2012). Plant diversity was measured at the taxonomic and phylogenetic levels. Five indices of biodiversity were computed: the alpha species diversity (ASD), the beta species diversity (BSD), the floristic dissimilarity between relevés (FD), the gamma species diversity (GSD) and the phylogenetic species diversity (PSD). ASD, BSD and GSD were computed according to Jost (2007) using the "H" function of the "vegetarian" package in R (R Development Core Team, 2012). The floristic dissimilarity (FD) was measured according to the Jaccard distance ("dist.binary" function and "ade4" package in R).

The phylogeny of the 565 plant species encountered inside the 1132 relevés was constructed in two steps. A preliminary Download English Version:

https://daneshyari.com/en/article/6294144

Download Persian Version:

https://daneshyari.com/article/6294144

Daneshyari.com