



Native, alien, endemic, threatened, and extinct species diversity in European countries



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ABSTRACT

While species diversity patterns at large scales (continental to global) have been increasingly studied recently for a few well-known taxa, only a few studies have included less well-known groups, and analysed congruence patterns between taxa. By using data from nine taxonomic groups (vascular plants, bryophytes, mammals, birds, reptiles, freshwater fish, amphibians, butterflies, dragonflies) from 38 European countries and Israel, we analysed the diversity of five diversity subsets (numbers of native, endemic, threatened, extinct, alien species) and their cross-taxon species diversity congruency.

Native species numbers, and particularly, endemic species numbers are highest in large south European countries (Spain, Italy, Greece). The highest numbers of species being currently nationally threatened are located in industrialized Central European countries, whereas the highest numbers of nationally extinct species are found in Israel, Luxembourg, and Belgium. Established alien species numbers are highest in large western and (south)western European countries (United Kingdom, Spain, Italy, France).

Across all taxonomic groups, the average proportion of endemic species of total native species numbers is 3%, of threatened species it is 27%, of extinct species it is 2%, whereas established alien species make up on average 11% of native species numbers. Highest proportions of endemic species were found in fish, grasshoppers, and reptiles, of threatened species in reptiles, amphibians and dragonflies, of extinct species in fish, dragonflies and grasshoppers, and of established alien species in fish, mammals and amphibians. Pairwise cross-taxon correlations of species diversity were pronounced for native species and endemic species, whereas correlations are much weaker for threatened, extinct and alien species numbers. Species-area relationships were significant but relatively weak for numbers of native and established alien species, whereas not significant for the other diversity subsets.

This study provides an important baseline assessment for a better understanding of European species diversity patterns. Future research avenues should aim at identifying causal relationships, and test for the effects of scale, life history and ecology of different taxa. Such an extended causal analysis should include historical effects, i.e. regional differences in rates of speciation, dispersal and extinction but also short-term fluctuations in human impact on species diversity, which are notoriously difficult to quantify, but frequently shape current diversity patterns.

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1. Introduction

Species ranges vary widely from near global to regional and local distributions (Gaston, 1994; Rosenzweig, 1995). The distribution patterns often reflect differences in their evolutionary and

biogeographic history, dispersal capacity and current environmental and socio-economic factors (Hewitt, 2000; Gaston, 2003; Jansson, 2003; Sandel et al., 2011; Jetz and Fine, 2012), albeit these different drivers appear to operate at different scales (Pearson and Carroll, 1999; Field et al., 2009; Qian and Kissling, 2010). At a coarse scale (e.g. across latitudinal gradients) and across a wide range of taxa there is strong evidence that native species diversity is primarily driven by energy availability, i.e. climatic variables (e.g. Currie, 1991; Currie et al., 2004; Wolters et al., 2006; Field

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et al., 2009; Kier et al., 2009; Qian and Kissling, 2010). However, environmental and biogeographic history (Svenning et al., 2010; Wiens et al., 2011; Jetz and Fine, 2012) as well as environmental heterogeneity (Fløjgaard et al., 2011) modify this general pattern. Evidence is further accumulating that at coarse scales diversity patterns of wide-spread and range-restricted species differ substantially (Myers et al., 2000; Jansson, 2003; Jetz and Rahbek, 2003; Orme et al., 2005; Lamoureux et al., 2006; Wolters et al., 2006; Reyjol et al., 2007; Kier et al., 2009; Svenning et al., 2010; Fløjgaard et al., 2011).

Human activities increasingly alter the distribution of biota at an unprecedented scale and pace. Native species' ranges are reduced, isolated and fragmented until species might eventually be driven to regional or global extinction (Sodhi et al., 2008; Kuussaari et al., 2009; Butchart et al., 2004, 2010; Barnosky et al., 2011), whereas, at the same time alien species invasions are rapidly increasing in many parts of the world (Winter et al., 2010; Essl et al., 2011a; Ellis et al., 2012). These complementary losses and gains of local and regional floras and faunas are predominantly driven by human activities (Davies et al., 2006; Pyšek et al., 2010; Strassburg et al., 2012). Hence, the resulting alien and threatened species diversity might differ substantially from those of native and endemic species which more closely reflect evolutionary history (Lamoureux et al., 2006; Kier et al., 2009; Kreft and Jetz, 2007; Winter et al., 2009; Ellis et al., 2012; Jetz and Fine, 2012). Although Ellis et al. (2012) have recently suggested that vascular species losses and gains (by invasions) do correlate at a global scale, this is not necessarily true at finer resolutions and for other taxonomic groups as native species decline and alien species establishment are not necessarily driven by the same processes. Besides homogenization (Winter et al., 2010), the counter-acting processes of native species extinctions and alien species invasions might also cause considerable shifts in spatial biodiversity patterns.

Different taxonomic groups might be differently correlated with environmental and anthropogenic factors which might result in divergent diversity patterns. So far, however, most studies have addressed cross-taxon relationships in species richness at small scales (e.g. Sauberer et al., 2004; Tscharnke et al., 2005; Marini et al., 2008; Toranza and Arim, 2010) for a few well-known groups only (e.g. vertebrates, vascular plants), whereas comparatively little research has been done at coarse scales (but see e.g. Qian and Ricklefs, 2008; Schuldt et al., 2009; Qian and Kissling, 2010; Jetz and Fine, 2012).

In this paper, we analyse diversity patterns at large geographical scales by using data of nine taxonomic groups from 38 European countries and Israel, and five species-diversity subsets (native, endemic, threatened, extinct, alien). Specifically, we address the following questions: (1) What are the patterns of these different subsets of species diversity across European countries? (2) Where are the hotspots of these subsets of species diversity situated in Europe? (3) How closely are species diversity patterns of these subsets correlated within and across taxonomic groups?

2. Material and methods

2.1. Species data

We included 39 countries (38 European countries and Israel) in the analyses, but excluded tiny countries and city states (<100 km²). We only screened well-known taxonomic groups to avoid problems of insufficient taxonomic, faunistic respectively floristic knowledge affect the results. Further, only taxonomic groups for which national Red lists were available for most of these countries were considered. The following nine terrestrial and aquatic taxonomic groups fulfilled our criteria and were included in the

analyses: two plant groups (vascular plants, bryophytes), five vertebrate groups (birds, mammals, reptiles, amphibians, freshwater fish), and two invertebrate groups (dragonflies, grasshoppers). For each taxonomic group, we collected the following data per country (if available) (Supplementary Online Material 1): numbers of native, endemic, established alien (sensu Richardson et al., 2000), threatened and nationally extinct species.

Species numbers were extracted from a range of data sources (Supplementary Online Material 2). Total numbers of native bryophyte and vascular plant species were derived from national checklists and standard floras, with some updates by national experts. For the purpose of this study we define a species as endemic if its range is restricted to one of the analysed countries. Numbers of total native and endemic animal species have been calculated using data from Essl et al. (2012), which are based on an updated version of the Fauna Europaea project (www.fauna-eur.org). Subnational Fauna Europaea regions have been merged to correspond to countries. Numbers of Red-listed species were taken from the most recent national Red lists, most of which have been published between 1995 and 2011. For calculating numbers of threatened and extinct species, we included species facing medium to high extinction risks (IUCN categories EN, VU, CR, IUCN 2011) and those reported to have already gone extinct in a country (IUCN categories EX, EW), respectively. Numbers of established alien species were extracted from the DAISIE project (www.europe-aliens.org, Pyšek et al., 2010), with a few updates (e.g. bryophytes, Essl et al., 2013). For dragonflies and grasshoppers, insufficient data on alien species numbers were available, and hence we did not analyse alien species patterns for these two taxa. Finally, only a few data gaps remained, which can be attributed to the absence of the corresponding national data (e.g. Red lists, checklists).

2.2. Statistical analyses

To analyse cross-taxon diversity patterns across European countries, we tested how the different diversity subsets are correlated between taxonomic groups using Pearson product moment correlations with two-sided tests. The empirical ranges (5% and 95% confidence interval) of the correlation coefficients were assessed by bootstrap calculations with 1000 iterations (Supplementary Online Material 3). To eliminate area bias because of different sized national territories, native species numbers were area corrected. The log transformed species numbers were regressed on the log area of each country by means of Gaussian family GLMs and we correlated the resulting residuals instead of species numbers. All other diversity subsets were converted into proportions of native species numbers to avoid area effects.

To calculate cross-taxon indices of the diversity subsets we combined the species numbers of all analysed taxonomic groups. We eliminated the effect of different absolute species numbers between taxonomic groups by calculating the relative proportion of species numbers in a country relative to the highest species number within this taxonomic group in any country of our data set. Subsequently, we calculated cross-taxon diversity indices per country by averaging these proportions across all taxonomic groups. We used these cross-taxon indices to test which taxonomic groups are most closely correlated with these overall species richness measures. To test for area dependency we regressed the cross-taxon indices on log transformed country size by means of Gaussian family GLMs.

As a result of the limited sample size we accept the alternative hypotheses at an α -level of 0.1 in our analyses. Statistical analyses were carried out in R, Version 2.13.1 (R Development Core Team, 2012)

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