



At the intersection of cultural and natural heritage: Distribution and conservation of the type localities of Italian endemic vascular plants



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ABSTRACT

We conducted a GIS spatial analysis with the aim of providing the first quantitative large-scale overview of the distribution patterns of 1536 type localities (*loci classici*) of 1216 Italian endemic vascular plants and their relationship with a set of descriptive variables. Whereas some variables were used to model the presence-absence distribution patterns of the type localities for the whole set of endemics as well as for the subset of narrow endemics, others (e.g., presence inside or outside protected areas and Italian Important Plant Areas) were considered with the purpose of assessing potential assets or risks for conservation.

The largest number of type localities was found within the Mediterranean biogeographic region (1134),

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followed by the Alpine region (306) and Continental region (96). A total of 670 locations are located on islands, whereas 866 are located on the Italian mainland (139 and 124 in the case of narrow endemics, respectively). A large number of type localities are located in mountainous areas and along the coastline, which can be seen as a potential risk for conservation. On the contrary, we detected a positive correlation with the distance from roads, which might be considered to be an asset. Importantly, 1030 type localities fall inside protected areas, whereas 506 localities fall outside protected areas, with 259 of these unprotected localities on islands.

We propose considering the results of the analysis of the distribution of type localities of Italian endemics to be a strategic tool for conservation planning and resource management. Application of plant micro-reserves and integration of diverse legislation tools are suggested to strengthen efforts and increase conservation success.

1. Introduction

It is generally agreed that among the most pressing issues challenging the global conservation community is how to identify biodiversity-rich areas and distribute limited resources between regions identified as priorities for biodiversity conservation (e.g., Cañadas et al., 2014; Wilson et al., 2006). However, biodiversity is a complex multifaceted concept that includes scales in space and time, and areas of high priority for conservation may be defined on the basis of habitat and species richness, endemism, genetic or phylogenetic diversity, the probability of species' extinctions or other indices (Ferreira and Boldrini, 2011; Li et al., 2015; Myers et al., 2000; Orme et al., 2005; Pavoine and Bonsall, 2011; Pouget et al., 2016; Schmeller et al., 2014). For example, Bonner (1984) discussed the criteria that were used to decide whether sites should be awarded the status of "Special Protected Areas" in Antarctica. Five criteria were used, including type localities. Importantly, since Moreau et al. (1945), it has been remarked that, in systematic zoology, particularly that dealing with land vertebrates, the accurate definition of the geographical position of the localities from which taxa have been described by authors is no less essential than a clear definition of the characters of the animals themselves.

The collection and analysis of biological data required for these assessments are always time consuming and expensive, particularly for rare species (Ahrends et al., 2011). Despite its importance for conservation, such work is chronically underfunded (Balmford and Gaston, 1999; Platts et al., 2014), many information gaps exist (Meyer et al., 2015) and biodiversity loss is arguably proceeding more rapidly than the documentation of species distributions and genetic diversity (Cardinale et al., 2012; Kier et al., 2009).

As a contribution to the assessment of the national floristic biodiversity, during 2012–2014, a group of botanists of the *Società Botanica Italiana* (Italian Botanical Society) published the first inventory of the type localities (*loci classici*) of 1400 Italian endemic vascular plants (Peruzzi et al., 2015). Type localities are the geographical locations documented by the valid publication of plant basionyms, accepted names and homotypic synonyms.

Type localities are point data and, as such, cannot be considered a robust proxy for the distribution, abundance and conservation status of the populations of the Italian endemics. However, in the case of the very narrow Italian endemics, we can expect to acquire useful ecological information from analysing the distribution pattern of their type localities because these locations are adequately representative of the whole ecological niche of these species and are particularly worthy of being protected. When species are known only from their type locality, the use of type locality is generally assumed as a criterion closely related to the criterion of endemism (Bonner, 1984).

Furthermore, type populations are of fundamental importance in theoretical and applied taxonomy and biodiversity conservation (e.g., Hernandez-Kantun et al., 2015; Larridon et al., 2014). Many taxonomic conclusions can be drawn directly from the study of type specimens (the specimens to which scientific names are attached, usually *exsiccata*, i.e., dried plant specimens), but this is often not satisfactory. For many types of biosystematics studies, living specimens and samples from living populations are required (e.g., Cieślak et al., 2006; Flanagan et al.,

2006; Hong and Zhou, 2003). These studies require the collection of germplasm or specimens in type localities, i.e., those localities from where the nomenclatural types were originally collected. Only this procedure will ensure that the results obtained (e.g., the chromosome number, DNA sequences, a diaspore collection for ex situ conservation purposes, and species trait analysis) will certainly apply to a certain taxon and will be taxonomically sound. Accordingly, the knowledge and conservation of these peculiar type populations and of the related sites are of crucial importance in comparative biology. In addition, these localities represent a very important cultural and historical heritage, being places that are visited, studied or described by relevant personalities in the history of botany and plant biology in general.

Species distribution models can help scientists and conservation planners estimate centres of biodiversity (Barthlott et al., 2005; Brotons et al., 2004) and identify priority areas for conservation (Elith and Leathwick, 2009) as well as patterns of major threats across the landscape, such as habitat loss, fragmentation and other anthropogenic pressures (e.g., Aben et al., 2016; Ibáñez et al., 2009; Newbold et al., 2016). In contrast, one dilemma with mapping concerns which species should be evaluated because it is impossible to map them all (Miller and Allen, 1994; Mittermeier et al., 2004; Trisurata et al., 2012). Species confined to very small distribution areas, so-called narrow endemic species (Andersen et al., 1997; Kruckeberg and Rabinowitz, 1985; Williams et al., 1996), pose very important conservation issues due to their great vulnerability to extinction (Raedig et al., 2010) and could be considered as a priority for action, including modelling and mapping efforts. A second dilemma with mapping concerns the fact that revealing geographical locations in publications can guide unscrupulous collectors from the international trade to the species, which could lead to a rapid decline in population size and even extinction (Stuart et al., 2006).

Point data, such as museum and herbarium specimen data (Rivers et al., 2011), have proven useful for the generation of species ranges (Raedig et al., 2010, and references cited therein). However, there also exist some inherent drawbacks, such as the heterogeneous sampling of space and taxa because of varying accessibility of areas, limited resources, varying attractiveness of taxa to collectors and systematic or geographical inaccuracy, for example due to efforts associated more with political and administrative rather than ecological boundaries (Cadenasso et al., 2003; Ferreira and Boldrini, 2011; Knapp, 2002; Meyer et al., 2015; Raedig et al., 2010).

To better explore the geographical distribution pattern of the whole group of type localities, on the basis of the Italian national inventory, we conducted a GIS-assisted spatial analysis specifically aiming to provide the first quantitative overview of the distribution patterns and to assess the relationship between the actual distribution of type localities and a set of descriptive variables.

To the best of our knowledge, this is the first time that this type of analysis has been applied to such a large data-set of type localities at a country level in Europe or anywhere else in the world.

2. Methods

2.1. The geographical database of Italian type localities

The type locality database described by Passalacqua et al. (2014) was used as a basis for the present analysis. It stores information on the nation-wide inventory made by Peruzzi et al. (2015) on 1400 Italian endemic vascular plant species (Peruzzi et al., 2014a, continuously updated). As described by Domina et al. (2012) and by Peruzzi et al. (2014a, 2014b, 2015) and for the purpose of the present study, Italian endemics were defined as the specific and sub-specific plant taxa occurring only in Italy, only in Italy and in Corsica (France), or in Italy and Malta.

The geographic locations were retrieved from the text of the protologues, as well as from the holotypes (or the syntypes) or after the typification process (Art. 9.11 of the ICBN: McNeill et al., 2012) as in the case of most taxa described before the 1st of January 1958 (Art. 40.1 of the ICBN). The geographical accuracy of the location stored in the national database therefore varies, and there is a clear trend between the date of the description of the type locality and the geographical accuracy, with the more recent type localities being located with greater accuracy, e.g., using Global Positioning System devices (t value 21.58, $p (> |t|) < 2 \cdot 10^{-16}$). One field in the database, based upon expert opinion, provides metadata-type information on the geographical accuracy, using a ranked scale from 1 to 5 (see also Bedini et al., 2016). Within this scale, an accuracy level equal to 5 implies that the geographical coordinates are expected to be very accurate and located within a circular area of expected error with a diameter of < 1000 m (669 type localities). Accordingly, level 4 implies 1–10 km (867 type localities), level 3 implies 10–50 km (230 type localities), level 2 implies > 50 km (42 type localities) and level 1 implies a very low accuracy. Therefore, all the type localities with low geographic accuracy (classes 1, 2, 3: 271 records) were discarded in our analysis. In addition, we did not consider all those type localities located outside the Italian territory, e.g., in Corsica and in Malta (120 type localities), and the endemic species lacking a precise type locality (32 records). Moreover, given the controversial taxonomic status of the subspecies within the genus *Hieracium* Linnaeus (1753: 799) (*Asteraceae*; approximately 220 subspecies described as potentially endemic to Italy), all these subspecies were deliberately excluded from the analysis, as in Peruzzi et al. (2015).

Therefore, in the present analysis, we considered a total number of 1536 type localities for 1216 Italian endemic species or subspecies (hereafter called species or taxon). In fact, 98 of the endemic species considered have more than one original *locus classicus* (average value 1.18 location species⁻¹, standard deviation 0.92). Among these, we marked 263 *loci classici* belonging to 247 narrow endemic species (in this subset, only 7 species have more than one location, with an average of 1.06 location species⁻¹, s.d. 0.46). Among the 263 records for narrow endemics, 86 fall in the geographic accuracy class 4, and 177 fall in class 5. Narrow endemics were delimited and identified according to all the available literature (e.g., Catoni and Gratani, 2013; Foggi et al., 2015; Mattana et al., 2010; Rossi et al., 2016), which was reviewed by expert opinion for the purposes of the present analysis. In the case of multiple locations for the same narrow endemic taxon, we verified that the difference in latitude and longitude was on average below 0.10×0.10 degrees and therefore approximately within a maximum distance of 10 km to be consistent with the operational definition used in the present analysis. However, in most cases, the maximum distance was < 1 km.

2.2. Pseudo-absences for type localities distribution pattern

Type localities are marked point data (with associated meta-data on accuracy of coordinates), and as such they cannot be considered as a proxy for modelling the distribution of all the populations of Italian

endemic species. Nevertheless, we assumed that it was feasible to perform a spatial analysis of the general distribution pattern of the whole set (considered as a single macro-unit), particularly for the subset of the loci of the narrow endemics, using the same tools and methods available to generate habitat suitability maps for species and spatially analyze marked point patterns. It is generally expected that model performance for ecologically and geographically narrow-ranged species is significantly better compared to widespread species found in a wider range of habitats (van Proosdij et al., 2016). Royle et al. (2012) discussed methods for estimating species occurrence probabilities from presence-only data. Although many interesting aspects of the species' distribution can be learned from such data (presence-only), one cannot learn the overall species occurrence probability, or prevalence, without making unjustified simplifying assumptions (Hastie and Fithian, 2013). A commonly used group of methods includes general and generalised linear models (GLMs), and generalised additive models (GAMs). These methods require good quality presence/absence data to generate statistical functions or discriminative rules that allow habitat suitability to be ranked according to the distributions of the presence and absence of species (Brotons et al., 2004; Dormann et al., 2007). Considering that our geographical database holds the presence data for 1216 endemic taxa over the total 1400 Italian endemics, we assumed that it was feasible to generate simple random pseudo-absence locations within the national borders (including all the islands) using the random-point generator engine of the GIS FLOSS software QGIS (<http://www.qgis.org/en/>). This method involves creating pseudo-absence points at random. No prior information about the presence and background data was incorporated into the creation procedure of the 1536 pseudo-absence locations that were used for the present analysis. Using the random-point generator engine of QGIS, 214 absence records were located on the islands, and 1322 pseudo-absence records were located on the mainland.

2.3. GIS descriptive variables

We gathered a set of thematic GIS layers from the Italian National Cartographic web site (PCN, <http://wms.pcn.minambiente.it/>) and ISPRA (<http://www.isprambiente.gov.it/en>), from the Italian Statistical Institute web site (ISTAT, <http://www.istat.it/>), and from the European Environment Agency web data centre (EEA, <http://www.eea.europa.eu> - e.g., the CORINE Land Cover – CLC - and land cover – land use changes maps, the map of biogeographical regions, containing the official delineations used in the Habitats Directive - 92/43/EEC - and for the EMERALD Network set up under the Convention on the Conservation of European Wildlife and Natural Habitats, Bern Convention) as listed in the Supplementary material (Table 1s). It is worth noting that the CLC inventory was initiated in 1985 (reference year 1990). Updates were produced in 2000, 2006, and 2012. It consists of an inventory of land cover with 44 classes. CLC uses a Minimum Mapping Unit (MMU) of 25 ha for areal phenomena and a minimum width of 100 m for linear phenomena (Büttner et al., 2012). The Italian border (according to ISTAT) was used to derive two new explanatory variables, i.e., the binary variable “island vs. mainland” and the continuous variable “distance from the coastline”. To produce the second variable, we first converted the vector file of the Italian coastline into a raster format. Then, using the GIS software QGIS, we produced a raster proximity map, which was used to assign proximity values to each single record. A raster proximity map was also used to calculate the distance from roads and from towns. The elevation of the records was calculated online using the PCN Web Feature Services for the national elevation digital model (grid with 40×40 -m pixel size). Some records are present on very small islands, are very close to the coastline, are located on coastal vertical cliffs (*falesias*); therefore, the elevations of these potentially critically locations were cross-checked using a Keyhole Markup Language (KML) file of all the records plotted on the Google Earth online mapping system (2015 GE imagery data).

For the evaluation of the density of the type localities in the Italian territory, we used the Universal Transverse Mercator (UTM) 1×1 km grid available at the web site of the European Environmental Agency based on the European Terrestrial Reference System (ETRS89) Lambert Azimuthal Equal Area projection and composed of 309,787 quadrats. All the thematic layers were converted into EPSG4326 (geographical coordinates according to the WGS84 system) using QGIS before performing the spatial and statistical analyses.

2.4. Statistical analysis of the distribution pattern of type localities

The presence-absence of the *loci classici* was considered as a binary dependent variable within a logistic regression model (family binomial, link logit) formulated using the R statistical environment (R Core Team, 2016). The R function “step” (stepwise model selection function based on AIC) was used to perform variable selection in the full model, which included all the descriptive variables reported in the Supplementary material (Table 1s) without interaction terms, aiming to evaluate the large-scale distribution pattern of all the records of type localities and of the subset of narrow endemics.

A second model formula evaluated the presence/absence of type localities in relation to the degree of protection (number of overlapping protected areas), the 312 Important Plant Areas (IPAs) that have been identified in Italy (Blasi et al., 2011) and the CORINE Land Cover Class at Level II. Each term in the models was tested with the ANOVA function, particularly with a Chi-square test statistic. The analysis was performed both for the whole set of endemics and for the subset of narrow endemics.

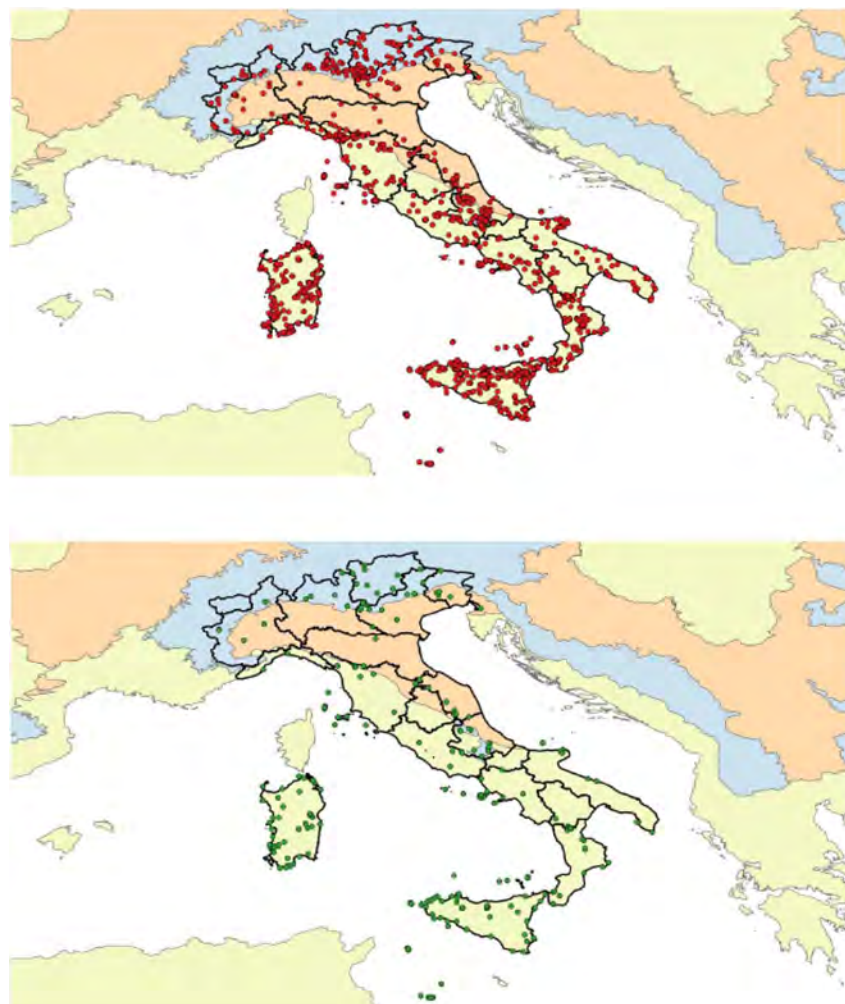


Fig. 1. Distribution of the 1536 type localities of the Italian endemic taxa across the three biogeographical regions (Mediterranean, Continental, Alpine – Map from the European Environment Agency web data centre, available at <http://www.eea.europa.eu/> - EEA, 2016). Below, the distribution of the 263 type localities of the narrow endemic taxa. Country border and borders of the 20 Italian administrative regions are shown in black.

We used additional logistic models, as described in the results, case by case, to test single distribution patterns, e.g., across the different biogeographic regions.

In addition, considering the bimodal distribution of the type localities with altitude and distance from coast, these two predictors were also separately modelled using GAM (Faraway, 2006). The comparison of AIC values highlighted that the GAM was more effective in predicting the distribution of the presence of type localities in relation to altitude and distance from the coast when compared to a logistic model.

3. Results

3.1. Distribution patterns of type localities of endemic and narrow endemic taxa

The large-scale distribution pattern of the 1536 type localities was first disentangled according to the EEA biogeographical map of Europe (Fig. 1). The largest number of locations was found within the Mediterranean biogeographic region (1134), followed by the Alpine (306) and the Continental region (96). When considering only the narrow endemics, the distribution is as follows: Mediterranean (197), Alpine (41) and Continental (25). Fitting a simple logistic model on the presence-absence in relation to the distribution in the 3 biogeographical regions, we conducted our tests using ANOVA and found that the differences between these 3 biogeographical regions were highly significant ($Pr > Chi$, $2.2 \cdot 10^{-16}$ for all endemics and $Pr > Chi$, $1.522 \cdot 10^{-12}$ for the subset of narrow endemics).

At the scale of the 20 Italian administrative regions (Supplementary

material, Table 2s), the largest number of type localities was found in the insular region of Sicily (437 *loci classici* belonging to 307 species), followed by Sardinia (193/186) and Tuscany (154/108), whereas the 2 equally lowest values (4/4) resulted in Valle d'Aosta and Molise. The average number of *loci classici* per region was 76.80 (but with a considerably high value of s.d., 100.55).

The highest number of type localities of narrow endemics was present in Sicily (75/72), followed by Sardinia (43/43) and Tuscany (26/22), whereas the lowest number was in Umbria (1/1) (Valle d'Aosta and Molise had no type localities of narrow endemics). Fitting a simple logistic model on the presence-absence in relation to the regional distribution, we conducted our tests by using ANOVA and found that the differences between regions were highly significant in both cases ($Pr > \chi^2$, $2.2 \cdot 10^{-16}$). The correlation matrix (Supplementary material, Fig. 1s, Tables 2s and 3s) clearly shows that the regional richness of type localities for all endemics and for narrow endemics is positively correlated with the number of Italian endemic species recorded in each region by Peruzzi et al. (2014a, 2014b).

A total of 670 records over 1536 were located on islands, whereas the other portion (866) was located on the Italian mainland (139 and 124, respectively, in the case of narrow endemics). Therefore, we detected a higher probability of finding a type locality on an island than on the mainland (contingency tables, $\chi^2 = 330.3$, $df = 1$, p -value = $8.451 \cdot 10^{-74}$ for all *loci classici*, and $\chi^2 = 89.82$, $df = 1$, p -value = $2.604 \cdot 10^{-21}$ for narrow endemics) and rejected the null hypothesis of independence between these two factors.

An uneven and non-random distribution of the 1536 locations of the type localities was further supported taking into account the national UTM grid. Importantly, we found that the 1536 locations were clustered in 1261 of the total $309,787 \times 1 \text{ km}$ UTM grid quadrats covering the Italian territory (including all the islands), with the range of density varying from 1 to 9 *loci classici* km^{-2} (the two highest values were found both in the Abruzzo region, one in the protected area "Parco Nazionale del Gran Sasso e Monti della Laga" and one in the protected area "Parco Nazionale della Maiella"). The second highest value, i.e., 7 *loci classici* km^{-2} , is in Sicily, inside the protected area "Parco delle Madonie". The 263 locations of the narrow endemics type localities were clustered in 248 UTM grid quadrats, with the range of density varying from 1 to 3 *loci classici* km^{-2} , with 1 *loci classici* km^{-2} in 240 quadrats, 2 *loci classici* km^{-2} in 10 quadrats, and 3 *loci classici* km^{-2} in 1 UTM quadrat. A higher density was detected in the island of Sicily (Site of Community Importance "Monte S. Giuliano").

According to the GLM analysis, the density of type localities (number- km^{-2}) was highly significantly correlated with the average elevation of the UTM quadrat in which they are included (estimate = $2.715 \cdot 10^{-3}$, standard error = $2.150 \cdot 10^{-4}$, t value = 12.63, $Pr > |t| < 2.00 \cdot 10^{-16}$ for all the records and with estimate = $7.530 \cdot 10^{-4}$, standard error = $7.317 \cdot 10^{-5}$, t value = 10.290, $Pr > |t| < 2.00 \cdot 10^{-16}$ for the subset of narrow endemics).

A general explanation for the large-scale distribution pattern of type localities was provided by two logistic models evaluating the presence-absence of type localities both for all endemics and for narrow endemics in relation to insularity (presence-absence on islands), elevation (m a.s.l.), distance from the coast, distance from roads and distance from towns, both for all the endemics and for the narrow endemics. Table 1 reports the results of the two logistic models, highlighting that the distribution of type localities, both for all endemics and for the subset of narrow endemics, is significantly dependent on insularity (positive coefficient, z value = 13.932, probability ($> |z|$) $< 2 \cdot 10^{-16}$, and z value = 8.809, with probability ($> |z|$) $< 2 \cdot 10^{-16}$ in the case of narrow endemics), from elevation (positive coefficient), and distance from roads (positive coefficient). The analysis of deviance for the two logistic models (Table 2) further supports the significance of the descriptive variables explaining the Italian large-scale distribution of type localities (insularity, elevation, distance from the coast, longitude, distance from roads and distance from towns). 1-(residual deviance/

null deviance) was a good indicator of overall model fit.

A large number of type localities is located in mountain areas, with 475 localities between 1000 and 2000 m a.s.l., 121 localities between 2000 and 3000 m (63 type localities for narrow endemics are located between 1000 and 2000 m, and 11 localities are between 2000 and 3000 m) and no localities above 3000 m.

However, the distribution of the type localities showed a bimodal trend, both with the elevation gradient and with the distance from the coast. For this reason, these two predictors were also separately modelled using GAM. The comparison of AICs values highlighted that the GAM was more effective for predicting the distribution of the presence of type localities in relationship to elevation and the distance from the coast in comparison to a logistic model (3456.488 vs. 3707.788 for all endemics and 589.9133 vs. 703.53721 for narrow endemics).

3.2. Protection level and potential assets and threats for the conservation of type localities

The second analysis of the large-scale distribution pattern of type localities was performed using a different model formula in the logistic model, i.e., evaluating the presence-absence of type localities for all the endemics and for the narrow endemics in relation to the level of protection (number of overlapping protected areas), the CORINE Land Cover Class (II Level of the classification system) and the Italian Important Plant Areas.

The distribution of type localities of Italian endemic plant species was found to be positively correlated with the protection level. All the type localities and the subset of type localities for the narrow endemics showed a similar trend. A large number of type localities were inside a protected area (494) or even inside two overlapping protected areas (534) (Table 3). The largest number of type localities (319, including 65 for narrow endemics, Table 4) was found inside Sites of Community Importance (SCIs, Council Directive 92/43/EEC of 21 May 1992), followed by National Parks (297) and Regional/Provincial Nature Parks (240). Similarly, the largest clusters of type localities were located inside protected areas, as in the case of the "Parco Naturale Regionale delle Madonie" (73 type localities), "Parco Naturale delle Alpi Apuane" (50), "Parco Nazionale del Gran Sasso e Monti della Laga" (47), "Parco Nazionale del Golfo di Orosei e del Gennargentu" (38), "Parco Nazionale del Pollino" (28).

Importantly, 506 type localities (which are representative of 418 species and include 73 type localities belonging to 71 narrow endemic species) were outside any protected area, and 259 of these unprotected locations were located on islands (Table 3). However, insularity and the

Table 1

Results of the GLM analysis (logistic regression) of the large-scale distribution pattern of type localities of Italian endemic species and narrow endemic species. Deviance residuals of the first model are as follows: Min -2.73766, 1Q -0.91477, Median -0.04064, 3Q -0.04064, Max 2.29155. Deviance residuals of the second model are: Min -2.1699, 1Q -0.9104, Median -0.6338, 3Q 0.8894, Max 1.8589. Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.'.

Coefficients	Estimate	Std. error	z value	Pr(> z)
Intercept	-1.372e + 00	2.646e - 01	-5.186	2.15e - 07***
Island (Y/N)	1.566e + 00	1.124e - 01	13.932	< 2e - 16***
Elevation	1.300e - 03	7.964e - 05	16.327	< 2e - 16***
Dist. from coast.	-9.983e - 01	1.031e - 01	-9.679	< 2e - 16***
Longitude	6.181e - 02	1.773e - 02	3.487	0.000488***
Dist. from roads	6.468e + 00	1.969e + 00	3.285	0.001019**
Dist. from towns	-9.802e - 01	1.818e - 01	-5.391	7.01e - 08***
Narrow LC				
Intercept	-2.6759049	0.5263065	-5.084	3.69e - 07***
Island (Y/N)	2.1676160	0.2460616	8.809	< 2e - 16***
Elevation	0.0005756	0.0001633	3.524	0.000426***
Longitude	0.1248712	0.0380154	3.285	0.001021**
Dist. from roads	5.0608474	3.8472715	1.315	0.188363

Table 2

Analysis of deviance for the GLMs (logistic regression of presence-absence for type localities of all endemics and narrow endemics). Terms added sequentially (first to last). Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.'. The difference between the NULL deviance and the residual deviance (Resid. Df) shows how these 2 models are doing against the null model (i.e., the model with only the intercept). There is a clear drop-in deviance when adding each predictor variable one at a time. The small *p*-values indicate that all variables are needed to explain the presence-absence model for type localities of all endemics.

All LC	Df	Deviance	Resid. Df	Resid. Dev	Pr (> Chi)
NULL			3071	4258.7	
Island (Y/N)	1	342.69	3070	3916.0	< 2.2e – 16***
Elevation	1	248.99	3069	3667.0	< 2.2e – 16***
Dist. from coast.	1	172.55	3068	3494.5	< 2.2e – 16***
Longitude	1	12.13	3067	3482.3	0.0004961***
Dist. from roads	1	5.23	3066	3477.1	0.0221510*
Dist. from towns	1	26.94	3065	3447.5	5.206e – 08***
Narrow LC					
NULL			535	742.87	
Island (Y/N)	1	93.75	534	649.11	< 2.2e – 16***
Elevation	1	13.32	533	635.80	0.0002632***
Longitude	1	11.23	532	624.57	0.0008035***
Dist. from roads	1	2.10	531	622.46	0.1470813

Table 3

Number of protected areas overlapping the location of the Italian *loci classici* and for all the investigated taxa and for the subset of narrow endemics. For the first two rows, Pearson's Chi-squared test with simulated *p*-value (based on 10,000 replicates) equals to 2.8371, with *df* = NA, *p*-value = 0.4619; 1.1545, *df* = NA, *p*-value = 0.5689.

	0	1	2	3
All	506	494	534	2
Narrow	73	94	96	0
On islands (ALL)	224	211	233	2
On islands (Narrow)	35	50	54	0

level of protection are independent factors for all endemics (Chisq = 2.8371, *df* = 3, *p*-value = 0.4174) and for the narrow endemics (Chisq = 1.1545, *df* = 2, *p*-value = 0.5614).

A total number of 874 type localities are inside the borders of 143 Italian Important Plant Areas, whereas 146 type localities for narrow endemics are included in 66 IPAs, so there is a significantly larger number of type localities inside the IPAs (Chi = 29.26, *df* = 1, *p*-value = 6.328e – 08 for all type localities and Chi = 3.1977, *df* = 1, *p*-value = 0.07374 for narrow endemics). There are also IPAs holding very large clusters of type localities, as in the case of three IPAs located in the island of Sicily (13 “Madonie”, 10 “Capo Gallo, Rilievi di Palermo e F. Oreto”, 11 “Boschi Ficuzza e Cappelliere e Rocca Busambra”), with 74, 35 and 26 type localities, respectively. Three other IPAs, in Tuscany (“Alpi Apuane”, 54 type localities), Abruzzo (“Maiella”, 49) and Sardinia (“Golfo di Orosei e Gennargentu”, 47) are among the richest

Table 4

Distribution of type localities for all the Italian endemic species (ALL) and for the subset of narrow endemics (Narrow) in the main types of protected areas, according to the classification made by WDPA. The second and fourth column indicate, respectively, the number of endemic species to whom the type localities belong.

WDPA categories	Loci ALL	Species ALL	Loci Narrow	Species Narrow
Sites of Community Importance (Habitats Directive)	319	295	65	62
National Parks	297	253	52	48
Regional/Provincial Nature Parks	240	183	24	23
Regional/Provincial Nature Reserves	110	102	26	24
Special Protection Areas (Birds Directive)	23	23	10	10
State Nature Reserve	14	14	3	3
World Heritage Site	11	9	2	2
Natural Marine Reserves & Natural Protected Marine Areas	8	7	5	4
Other Protected Natural Regional Areas	5	5	2	2
International significance Natural Marine Areas	3	3	1	1
UNESCO-MAB Biosphere Reserve	0	0	0	0
None (outside protected areas)	506	418	73	71

areas. In contrast, 164 IPAs of the 312 located in Italy have no type localities inside their borders.

We detected negative relationships between the presence of type localities and those CORINE Land Cover classes, which can be considered as proxies for constant human disturbance (Supplementary material, Table 4s, e.g., 2.1 Arable land, *z* value = – 8.18, probability (> |*z*|) ≤ 2e – 16) or represent strongly modified land uses (e.g., 1.1 Urban fabric, *z* value = – 4.045, probability (> |*z*|) = 5.23 0.011 e – 05). It is worth noting that both for all type localities and for the subset of narrow endemics, we found that the largest numbers were located in land cover classes 3.2 (shrub and/or herbaceous vegetation associations: 488 type localities, with 81 for narrow endemics), 3.1 (forests: 379/51) and 3.3 (open spaces with little or no vegetation: 188/31). Although many type localities were found within class 3.1 (forest), this class resulted in a significantly negative relationship in the logistic model (Supplementary material, Table 4s). In the CORINE legend, this class is defined as “areas occupied by forests and woodlands with a vegetation pattern composed of native or exotic coniferous and/or deciduous trees and which can be used for the production of timber or other forest products”.

The availability of the CLC-Change maps provided the possibility to detect that 109 type localities (6 for narrow endemics) were located in areas where a change of land use had occurred between 2000 and 2006. Considering that the 1536 locations of the type localities are clustered in 1261 of the total 309,787 1 × 1 km UTM grid quadrats, we observed that 141 of these 1261 quadrats were affected by land-use changes in the period of 2000–2006. Another group of 152 quadrats (populated by type localities) was affected in the following period of 2006–2012.

4. Discussion

Type localities are point data and, as such, they cannot be considered as a proxy for the distribution of Italian endemic plants. Although a study on the distribution of the populations of all of the Italian endemics has never been performed, we can very likely assume that no uniform trend will be detected. The habitat requirements of endemic plants are rather species specific and there might be only a few, large-scale, general trends that might be detected by GIS spatial analysis. National or regional endemism is certainly a phenomenon with a very inherent complex nature, which is influenced by a wide range of factors (e.g., Crisci et al., 2003; Tribsch, 2004; Wasof et al., 2015).

Nevertheless, our spatial analysis on the large-scale distribution of the Italian type localities provided us with valuable insight that has improved our knowledge and will hopefully help in the implementation of management and conservation strategies for these sites and species. In addition, we highlighted both similarities and differences of the large-scale distribution pattern of type localities for endemics and narrow endemics. In the latter case, it can be assumed that more

relevant information was acquired because these locations are more representative of the whole ecological niche of these narrow-range species and their type locality locations are particularly worthy of protection.

The largest number of type localities was observed within the Mediterranean biogeographic region, followed by the Alpine and Continental regions. Notoriously, the largest Mediterranean islands (Sicily, Sardinia, Corsica, Cyprus, Crete) represent single units of 10 Mediterranean hotspots, as defined by Médail and Quézel (1997, 1999) and Myers et al. (2000). Therefore, the detected high richness of type localities in the Mediterranean region and in Italian islands could have been reasonably expected and is possibly related to the high number of endemic and narrow endemic species that are present on the islands and have been described since the past. For example, in the case of Sicily, the large cluster of type localities on Madonie mountains would be expected by the presence of an overlapping Italian Important Plant Area, and its presence is in line with the study of Bonanno and Veneziano (2016). Similarly, in Sardinia, Cañadas et al. (2014) identified three micro-hotspots hosting more than the 20% of the 171 Sardinian endemic taxa, i.e., *Supramontes*, *Iglesiente* and *Gennargentu* regions. These three micro-hotspots are overlapped by a large number of type localities for endemic and narrow endemics species (Fig. 1). At the country level, our results are comparable with the distribution maps of the Italian Flora of Community Interest (protected by the Habitats Directive 92/43/EEC) elaborated by Fenu et al. (2017). These authors produced distribution maps for 103 species on a 10 × 10 km UTM grid. The largest number of vascular plants occurred in the Mediterranean bioregion. The endemism rate of Italian vascular plants of European interest was 57.29% (55 endemic species), and the distribution data showed the prevalence of plants with narrow or extremely narrow ranges; in particular, 11 plant species occurred in only 1 grid-cell and 28 occurred in the range of 2–5 grid-cells.

However, one potential limitation of the dataset investigated in our study is that the Alpine biogeographic region, which is also a renowned biodiversity hotspot, is shared by different European countries, and only the Italian endemics were recorded in the database supporting the present study (Peruzzi et al., 2014a, 2014b, 2015). Importantly, Casazza et al. (2010) studying the Maritime and Ligurian Alps, i.e., another hotspot of the Mediterranean region according to Médail and Quézel (1997, 1999), highlighted the presence of 107 endemic taxa, representing 3.4% of the local flora. Similarly, many other studies have commented on the importance of the Alpine region for the presence of both endemic and narrow endemic taxa (e.g., Lavergne et al., 2004; Merxmüller, 1952, 1953, 1954).

We detected that 1030 type localities, of the 1536 investigated, are inside protected areas. This can be seen as a good achievement for the international and national networks of protected areas. This is, of course, only a proxy for the real level of protection of type localities. Protected areas vary widely between and within countries and regions, and the varying characteristics include the institution date, conservation focus, effective level of protection, permanence of protection, constancy of protection, ecological scale of protection, type of management, management authority and reference legislation, to cite some of them. In addition, the effectiveness of the selection process and the resulting Natura 2000 network have often been questioned because each country made its designations largely independently, and the designation of sites has been criticised as depending too strongly on governmental politics, economic and cultural criteria, and interactions between society and the environment (Blicharska et al., 2016; Fenu et al., 2017; Gruber et al., 2012; Orlikowska et al., 2016; Trochet and Schmeller, 2013). In addition, in their analysis, Trochet and Schmeller (2013) demonstrated that the Natura 2000 network also covers species not listed in the annexes of the Habitats Directive, at least in the case of mammals, birds and reptiles; this might happen also for plants. Concerns also exist on the role of protected areas, in general, in providing effective biodiversity conservation (Geldmann et al., 2015; Le Saout

et al., 2013).

Land-use/land-cover change is among the most important factors causing biodiversity loss at the global level (e.g., Newbold et al., 2015, 2016). The Mediterranean region has been affected by anthropic disturbances for thousands of years, and is, today, one of the most significantly altered hotspots in the world, with Italy following this general trend (Dalla Valle et al., 2009; Niedertscheider and Erb, 2014; Pelorosso et al., 2009; Shelef et al., 2016). Concurrently, the Mediterranean hotspots, similarly to other sites of biodiversity, are characterized by high human population densities (Aben et al., 2016). In the last 40 years, a particular pattern of land-use/land-cover change has taken place in the Mediterranean basin, especially in Mediterranean Europe and Italy: plains are being increasingly used; hilly and mountain areas are being abandoned by humans and naturally reforested; and human settlements are quickly increasing along the coastline, with the resident population doubling every 30 years and tourists' presence doubling every 15 years (Falcucci et al., 2007; Lambin et al., 2001, 2003). Falcucci et al. (2007) measured an increase in forests, especially in mountains; an increase in artificial areas, especially in coastal zones; and a decrease in pastures in Italy. Intensively cultivated areas showed a limited decrease, whereas extensively cultivated ones showed a marked decrease. In our analysis, we detected that the 1536 type localities are clustered in 1261 1 × 1 km UTM grid quadrats, and we observed that 141 quadrats were affected by land-use changes in the period of 2000–2006 and 152 in the period of 2006–2012. This certainly is a very short time interval, and it gives no information about what could have happened in the past; however, it represents an alarming indicator of the rate of change at the national level.

In addition, we detected a clear negative correlation between the distribution of type localities and the distance from the coastline; that is, many locations are located in coastal habitats. Many major processes may influence the conservation and the stability of the coast profile, including land subsidence of both natural and anthropogenic origin, urbanization, pollution and the medium sea level rise caused by global climate change. We can, therefore, consider that the location on the coast, itself, is an indication of a potential risk for the conservation of type localities. On the contrary, the detected positive correlation with the distance from roads might be considered as an asset for the conservation of type localities.

A large number of type localities are located in mountain areas. This trend is comparable with the distribution of endemic species described for the Iberian Peninsula, where mountain ranges exhibit a great diversity of species, at least of the widespread type (Buirra et al., 2017). In addition to land-use changes, changes in climate, notably a warming climate, are expected to strongly impact biodiversity in mountain environments (Gottfried et al., 2012; Pauli et al., 2012; Stöcklin et al., 2009; Thuiller et al., 2014). Species are expected to migrate upward to keep pace with suitable climates, which should lead to an increase of diversity in higher altitudes in the near term (Walther et al., 2005). However, it has been demonstrated by Thuiller et al. (2014) that those studies carried out at European scales and coarse spatial resolution were not able to correctly account for mountain peculiarities, such as topographic micro-heterogeneity and meso-scale refuges, and that more recent studies have instead shown that when models are applied at high resolution, specifically over mountains, the results are less pessimistic, indicating that mountain floras can persist in some specific areas (Engler et al., 2011; Dullinger et al., 2012; Thuiller et al., 2014). However, changes in climatic conditions in the mountain areas may lead to a translocation of type populations, and this potential risk will require a dedicated study and monitoring. If the type population of one endemic species would disappear from its *locus classicus*, this certainly requires the need to identify and map its new geographical position and to reconsider protecting measures.

So far, 506 type localities are located outside protected areas. In many cases, these locations are very close to protected areas (Barni et al., 2010), as in the case of *Isoetes malinverniana* Ces. & De Not.

(Isoetaceae), which is located in close proximity to the SCI “Lame del Sesia ed Isolone di Oldenico”; thus, it would be feasible to propose a minimal modification of the boundaries of that protected area. On the contrary, the type localities of species such as *Helleborus viridis* subsp. *bocconei* (Ten.) Peruzzi (Ranunculaceae) and *Adoxa moschatellina* subsp. *cescae* Peruzzi & N.G. Passal. (Adoxaceae) are located far from the closest protected area (Parco Nazionale della Sila). However, at a global level, an emphasis on the strategic expansion of protected areas' networks might be seen as controversial. Protected areas are often understaffed, underfunded, and beleaguered in the face of external threats, and efforts to expand protected area coverage should be complemented by appropriate management of the conservation of existing protected areas (Le Saout et al., 2013).

One possible solution would be to apply to Italy the idea of Plant Micro-Reserves, originally defined by Laguna (2001a, 2001b) and Laguna et al. (2004) as small land plots (up to 20 ha) of peak value in terms of plant species' richness, endemism or rarity, given over to long-term monitoring and conservation of plant species and vegetation types. In fact, the protection of type localities was expressly mentioned among the goals proposed with the approval of some of the initial micro-reserves. On the contrary, other conservation tools and guidelines do not take into account such perspective for reserve area selection. The Convention on Biological Diversity Global Strategy for Plant Conservation (CBD, 2012) does not include any mention of type localities, nor does the recently approved IUCN initiative on Key Biodiversity Areas. This criterion is also missing from the guidelines to identify PlantLife Important Plant Areas (Anderson, 2002).

The integration of diverse international and national legislation tools might of course strengthen efforts and increase conservation success. Among the more intuitive options is to concentrate efforts in places where multiple conservation benefits can be achieved simultaneously whenever such multi-objective hotspots are ecologically appropriate and socio-economically equitable (Beger et al., 2015; Kark et al., 2009; Venter et al., 2014). Since the World Heritage Convention was adopted in 1972, the World Heritage List has continually evolved and is growing steadily. The World Bank uses a broad definition of the concept of cultural heritage: “Movable or immovable objects, sites, structures, groups of structures, and natural features and landscapes that have archaeological, paleontological, historical, architectural, religious, aesthetic, or other cultural significance”. In this framework, we observe a paved road for including the presence of the type localities of plants among the criteria to be considered for the selection of dedicated cultural heritage sites.

Across Europe and the world, accelerating rates of urbanization, changing demographic and diet patterns, technological changes, deepening market integration, and climate change are placing unprecedented demands on land. Addressing the issues raised, the European Union's 7th Environment Action Programme aims to ensure that by 2020, land is managed sustainably. In particular, this commitment requires coordinated governance and integration of environmental considerations (including agricultural and forestry policy, water management and biodiversity protection) into territorial planning decisions on land use (EEA, 2015). Land policy targets would also help in achieving this goal, and the 7th Environment Action Programme specifically suggests a target of “no net land take” by 2050. This aim is in line with the UN Rio + 20 Summit call for a land-degradation-neutral world in the context of sustainable development, a goal to which the European Union has subscribed (Dooley et al., 2015). Generally, this target is regarded as ambitious, but integrating different policies of land and nature conservation is clearly a wise solution.

We propose considering the present methodology of analysing and modelling the distribution of type localities of Italian endemic vascular plant species and using the results as a strategic tool for conservation planning and resource management. The reality of “always limited funds and resources for nature conservation” requires that criteria and spatial priorities for conservation be clearly identified and periodically

revised (e.g., Butchart et al., 2010; de Dios et al., 2017; Margules and Pressey, 2000; Platts et al., 2014) to tackle unprecedented rates of biodiversity loss at both the global and local levels. It has been widely recognized that endemic plants are, in general, not evenly distributed in space (e.g., Harrison and Noss, 2017; Hobohm, 2014; Kier et al., 2009; Kruckeberg and Rabinowitz, 1985; Mráz et al., 2016). Whereas some areas are very poor in endemics, other regions, called areas of endemism, harbour high numbers of endemic taxa. A similar pattern was found for the distribution of the Italian endemics type localities.

The populations of many endemic species are seriously threatened or affected by a degradation syndrome and are not always satisfactorily mapped within their ranges. The parties to the Convention on Biological Diversity have agreed on 20 targets to improve the state of biodiversity by 2020 (<https://www.cbd.int/sp/targets/>). Aichi Target 19 specifically mandates the development of an advanced and shared biodiversity knowledge base. Information on species distributions in space is a central aspect of biodiversity knowledge that can enable the effective management of biodiversity and associated ecosystem services in a rapidly changing world. Species distributions are critical for informing actions towards multiple Aichi targets, associated environmental indicators and the recently launched assessment work of the Intergovernmental science-policy Platform on Biodiversity and Ecosystem Services.

Knowledge of the distribution pattern and conservation of type localities itself cannot be considered to be an ultimate solution for the conservation of the population of all Italian endemic plant species. However, it has to be considered an important step towards specific action plans for biodiversity conservation.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found in the online version, at <http://dx.doi.org/10.1016/j.biocon.2017.07.024>. These data include the Google map of all the 1536 type localities of 1216 Italian endemic vascular plants described in this article.

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