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Macrofungal taxa and human population in Italy's regions

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Abstract Fungi are relatively understudied, particularly in terms of biogeographical patterns. We analyse whether there is a spatial correlation between macrofungi (Basidiomycota) and human population (both in terms of size and rate of change) in Italy's regions. Although current fungal taxonomic richness increases with increasing number of inhabitants (censused in 1986 and 2006 and predicted for 2026) and with their density, these relationships are not significant when controlling for variations in area amongst regions. This result, along with other recent independent studies, suggests that the large-scale spatial correlation of people and species can be often explained by both variables correlating with a third factor such as area, habitat heterogeneity or energy availability. Macrofungal richness significantly increases with percentage of forest cover, but not with percentage of protected area, suggesting that the conservation of Italian fungi needs to be addressed also outside the current network of national and regional nature reserves. The absence of any significant association of the estimate of macrofungal taxa with human population change observed in the last and predicted for the next two decades implies that there is no current clear trend towards a change of the ratio between macrofungal taxa and human presence at this scale of analysis. Further work at a higher resolution is needed to assess the consequences for Italy's fungal biodiversity of the abandonment of marginal land and the expansion of urbanized areas in regions of high environmental productivity.

Keywords Biogeography \cdot Fungal checklist \cdot Human disturbance \cdot Land use patterns \cdot Macroecology \cdot Population density \cdot Reserve selection \cdot Spatial autocorrelation \cdot Species—area relationship \cdot Study grain

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Introduction

Recent analyses have shown that, at large scales of observation, there is a substantial spatial co-occurrence of high number of species and of human beings. This at first sight counterintuitive coincidence of species diversity and of human presence has been documented in a number of regions for plants and animals and has obvious implications for conservation (e.g., Balmford et al. 2001; Araújo 2003; Burgess et al. 2007). A plausible explanation of this correlation is that both biodiversity and human population positively correlate with environmental factors such as primary productivity and habitat heterogeneity (e.g., Luck 2007b; Hugo and van Rensburg 2008). If areas of high biodiversity and of preferential human settlement overlap, then conservation biologists should enable the coexistence of people and nature, rather than trying to keep people away from wilderness areas (e.g., Deguise and Kerr 2006; Ceballos 2007; Virkkala and Rajasarkka 2007).

However, the conservation biology of fungi is largely based on studies carried out in habitats with low human disturbance, given that many red-listed fungal species are dependent on old-growth forests (e.g., Berg et al. 2002; Juutinen et al. 2006; Junninen et al. 2007). Fungi are a hyper-diverse kingdom, but, relatively to plants and vertebrates, they are rarely investigated (e.g., Strobel et al. 1996; Hawksworth and Rossman 1997; Lonsdale et al. 2008). Scientists are beginning to examine regional and large-scale patterns of fungal biodiversity (e.g., Rydin et al. 1997; Küffer and Senn-Irlet 2005; Peay et al. 2007; Schmit and Müller 2007), and there are some local studies on the impact of urbanization on fungal communities (e.g., Pouyat et al. 1994; Baxter et al. 1999; Cousins et al. 2003; Tarvainen et al. 2003; Ochimaru and Fukuda 2007), but, to the best of our knowledge, no attention has been addressed to the issue of the large-scale species-people correlation for fungi.

The aim of this paper is to investigate the hypothesis that the estimated number of macrofungal taxa in Italy's regions correlates with human presence. This hypothesis is based on the observation of such a positive, regional species-people correlation for other taxa (e.g., Luck 2007b), and on the often reported coincidence in the geographic patterns of biodiversity for different taxa (e.g., Jetz et al. 2008). Italy is part of the Mediterranean hotspot of plant diversity (e.g., Caldecott et al. 1996; Cowling et al. 1996; Malcolm et al. 2006). Given that fungal species richness is often positively related to the number of plant species (Chiarucci et al. 2005; Schmit et al. 2005; Gabel and Gabel 2007), Italy is likely to be an important region also from a mycological point of view, although this can only be the subject of speculation at the present stage given the paucity of macrofungal checklists for different countries (Schmit and Müller 2007). The Italian regional checklist of fungal species (Onofri et al. 2005), on which this analysis is based, estimates at roughly 4,000 the total number of macrofungal species present in Italy. Of these, ca. 30 are assessed as endemic species and nearly 300 are rare species (Ripa et al. 2003).

Italy is also a country of relatively high human population density (e.g., Pautasso and Weisberg 2008), with a long history of civilization and related landscape modifications (e.g., Grapow and Blasi 1998; Schulze 2002; Canova 2006), even if the current proportions of protected (19%) and forest (23%) area are relatively high. Although Italy's fertility rate has now declined to one of the lowest in the world (e.g., Livi-Bacci 2001; Kohler et al. 2002), this is currently still compensated by migration (e.g., Sardon 2004, but see Feld 2000). The impact of human beings on Italian biodiversity can have been heightened or lessened by recent regional increases and decreases in human population (e.g., Tasser and Tappeiner 2002; Gondard et al. 2006; Falcucci et al. 2007). If regions with higher biodiversity are those where human population has increased and is predicted not to decline, there is the potential for a conservation conflict (e.g., Araújo and Rahbek 2007;



Luck 2007a). We thus test whether the current estimate of macrofungal taxonomic richness of Italy's regions is associated with variations in human population observed during the last twenty years and predicted for the next two decades.

Materials and methods

Data of the estimated current macrofungal taxonomic richness for the 20 administrative regions of Italy were obtained from Onofri et al. (2005). This check-list includes only Hymenomycetes (Basidiomycota). It contains more than twenty thousand records and is based on the work of nearly two hundred local mycologists and mycological groups and associations (from roughly 1970 to 2000, although the sampling period may vary slightly from region to region). The checklist is a revision of a previous list (Ripa et al. 2003) and results presented here are confirmed using data from that previous work, which for most regions has a higher number of taxa reported than the new checklist due to the presence of synonyms. Geographical coordinates and climatic data of the administrative center, human population, total, protected (2003) and forest (2005) area of the Italian regions were obtained from ISTAT (http://www.istat.it/). Human population data refer to 1986, 2006 and (average predicted value) 2026.

The correlation of macrofungal taxonomic richness with human presence (both in terms of population size and density) was analysed in SAS 9.1. Number of fungal taxa, mean annual temperature and precipitation, human population, density and area of regions were log-transformed to conform to the assumptions of statistical tests. We studied log-transformed macrofungal taxonomic richness as a function of log-transformed human population size/density using a linear model, as a quadratic term was not significant and did not improve the proportion of variance explained. Spatial autocorrelation was controlled for using mixed models with exponential co-variance structure (as e.g., in Pautasso and Chiarucci 2008). Results from spatial and non-spatial models are consistent, but we present only the more robust results which take into account a potential spatial non-independence of data. There may be spatial autocorrelation amongst regions in survey intensity, climate, and taxonomic presence due to easier spore dispersal at closer distance.

Results

Current observed macrofungal taxonomic richness varied amongst Italy's regions from 198 (Molise) to 2,186 (Emilia Romagna) (Table 1). Mean taxonomic richness was 1,095, median 1,183, and the standard deviation was 668. Human population varied in 2006 between c. 124,000 (Valle d'Aosta) and c. 9,500,000 (Lombardy). Mean population was c. 2,940,000, median c. 1,830,000, and the standard deviation was c. 2,400,000. The smallest region (3,266 km²) was also the least populated, but the largest (Sicily, 25,701 km²) was not the most populated. Mean area of Italy's regions was 7,418 km², median 14,341 km², and the standard deviation was 15,059 km². Population density ranged in 2006 between 38 (Valle d'Aosta) and 426 inhabitants per km² (Campania). Italy's population density was in 2006 slightly lower than 200 inhabitants per km². The proportion of protected area varied between 1% (Molise) and 28% (Abruzzi). The proportion of forest area ranged from 6% (Puglia) to 53% (Liguria).

There was a significant positive relationship between the current estimated number of macrofungal taxa and the number of inhabitants in 2006 (n = 20, $r^2 = 0.53$,



Table 1 Estimated number of macrofungal taxa, human inhabitants (Pop, in thousands, for 1986, 2006 and (predicted) 2026), their percent variation (Δ^1 from 1986 to 2006 and Δ^2 from 2006 to 2026), area (km²), human density (D, in n km⁻², for 1986, 2006 and 2026), and proportion of protected (%p, 2003) and forested (%f, 2005) area for Italy's regions

| Region | Taxa | Pop ₈₆ | Δ^1 | Pop ₀₆ | Δ^2 | Pop ₂₆ | Area | D_{86} | D_{06} | D_{26} | %p | %f |
|---------------|-------|-------------------|------------|-------------------|------------|-------------------|---------|----------|----------|----------|----|----|
| V. d'Aosta | 198 | 112 | 10.1 | 124 | 0.7 | 125 | 3,266 | 34 | 38 | 38 | 13 | 24 |
| Molise | 225 | 329 | -2.6 | 321 | -3.9 | 308 | 4,438 | 74 | 72 | 69 | 1 | 16 |
| Liguria | 1,351 | 1,747 | -7.9 | 1,610 | -12.8 | 1,404 | 5,421 | 322 | 297 | 259 | 5 | 53 |
| Friuli V.G. | 584 | 1,214 | -0.5 | 1,208 | -5.1 | 1,147 | 7,712 | 157 | 157 | 149 | 7 | 24 |
| Umbria | 305 | 808 | 7.4 | 868 | -1.2 | 858 | 8,454 | 96 | 103 | 101 | 7 | 31 |
| Marche | 254 | 1,416 | 8.0 | 1,529 | -0.2 | 1,526 | 9,695 | 146 | 158 | 157 | 9 | 17 |
| Basilicata | 398 | 611 | -2.8 | 594 | -4.9 | 565 | 9,992 | 61 | 59 | 57 | 13 | 19 |
| Abruzzi | 880 | 1,231 | 6.1 | 1,305 | -0.3 | 1,301 | 10,793 | 114 | 121 | 121 | 28 | 21 |
| Campania | 643 | 5,549 | 4.4 | 5,791 | -0.3 | 5,775 | 13,592 | 408 | 426 | 425 | 24 | 21 |
| Trentino A.A. | 2,091 | 876 | 12.5 | 985 | 4.2 | 1,026 | 13,599 | 64 | 72 | 75 | 21 | 46 |
| Calabria | 1,169 | 2,083 | -3.8 | 2,004 | -3.9 | 1,926 | 15,083 | 138 | 133 | 128 | 17 | 32 |
| Lazio | 1,238 | 5,064 | 4.7 | 5,305 | 2.0 | 5,409 | 17,210 | 294 | 308 | 314 | 12 | 22 |
| Veneto | 1,724 | 4,349 | 8.9 | 4,738 | -0.5 | 4,715 | 18,390 | 237 | 258 | 256 | 5 | 15 |
| Puglia | 800 | 3,957 | 2.9 | 4,071 | -2.4 | 3,972 | 19,364 | 204 | 210 | 205 | 7 | 6 |
| E. Romagna | 2,186 | 3,919 | 6.9 | 4,187 | -1.7 | 4,115 | 22,122 | 177 | 189 | 186 | 4 | 18 |
| Toscana | 2,090 | 3,555 | 1.8 | 3,620 | -4.3 | 3,466 | 22,990 | 155 | 157 | 151 | 7 | 39 |
| Lombardia | 1,952 | 8,829 | 7.3 | 9,475 | -1.3 | 9,353 | 23,861 | 370 | 397 | 392 | 5 | 21 |
| Sardegna | 1,198 | 1,621 | 2.2 | 1,656 | -7.1 | 1,538 | 24,090 | 67 | 69 | 64 | 4 | 22 |
| Piemonte | 1,408 | 4,377 | -0.8 | 4,342 | -5.3 | 4,110 | 25,398 | 172 | 171 | 162 | 7 | 26 |
| Sicilia | 1,197 | 4,949 | 1.4 | 5,017 | -2.7 | 4,881 | 25,701 | 193 | 195 | 190 | 11 | 9 |
| Italy | 4,198 | 56,598 | 3.8 | 58,752 | -2.1 | 57,522 | 301,171 | 188 | 195 | 191 | 19 | 23 |

logtaxa = 0.09 + 0.46 logpop, slope standard error (s.s.e.) = 0.09, P < 0.0001; Fig. 1a). Macrofungal taxa also increased significantly with increasing population in 1986 and with predicted population in 2026, with no significant differences in the slope and intercept of the three relationships. Whilst human population significantly increased with mean annual temperature and precipitation, there was no significant relationship of mean annual temperature and precipitation with the number of macrofungal taxa, and these factors were thus dropped from the analysis.

A significant positive relationship was present also between number of taxa and region area $(n=20,\ r^2=0.57,\ \log \tan = -0.62 + 0.86\ \log \arctan$, s.s.e. $=0.15,\ P<0.0001$). This was to be expected given the positive relationship between human population and region area (for 2006: $n=20,\ r^2=0.71,\ \log pop=0.13+1.50\ \log area$, s.s.e. $=0.22,\ P<0.0001$). There was no significant difference in slope and intercept of the increase with region area of human population in 1986, 2006 and 2026. In all these cases this relationship was more than proportional, i.e., with a slope steeper than one. This implies that there was an increase of human population density with region area (for 2006: $n=20,\ r^2=0.21,\ \log n=0.13+0.50\ \log n=0.13+0.50\ \log n=0.22,\ P=0.04$).

Macrofungal taxonomic richness increased significantly with human population density (for human data of 2006: n = 20, $r^2 = 0.25$, logtaxa = 1.65 + 0.60 logdens, s.s.e. = 0.20, P = 0.007; Fig. 1b). There were no significant differences in intercept and slope of



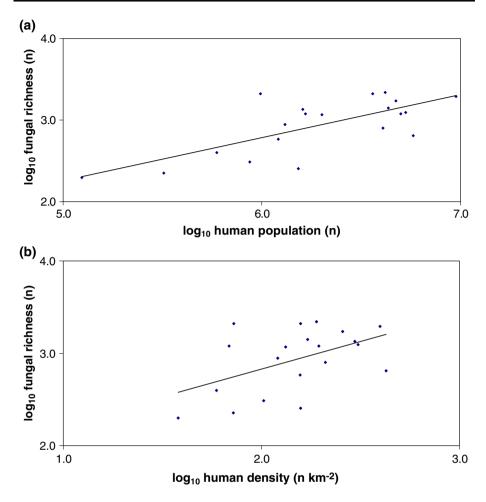


Fig. 1 The correlation between macrofungal taxonomic richness and human population **a** size, **b** density for Italy's regions. Human population data refer to 2006

the increase of fungal taxa with human population density for 1986, 2006 and 2026. However, given that human population density was not independent of region area, the latter needed to be controlled when modeling number of taxa as a function of human density. In this case, there was a significant increase of fungal taxonomic richness with region area but not with human population density (for 2006: n = 20, $r^2 = 0.60$, logtaxa = -0.53 + 0.18 logdens + 0.75 logarea, s.s.e. = 0.18, 0.19, P = 0.33, 0.001). This was the case also using human population density data for 1986 and 2026, with no significant differences in the parameter estimates of the models.

Also human population size was not independent of region area. When controlling for the latter, there was no significant increase of fungal taxa with human population size (for 2006: n = 20, $r^2 = 0.60$, $\log \tan x = -0.53 + 0.18$ $\log x = 0.57$ $\log x = 0.18$, 0.33, P = 0.33, 0.10). In this case, number of fungal taxa did not increase significantly also with region area, and this was the case also using human data for 1986 and 2026. In these models as well as in those with population density, including the percentage of forest and



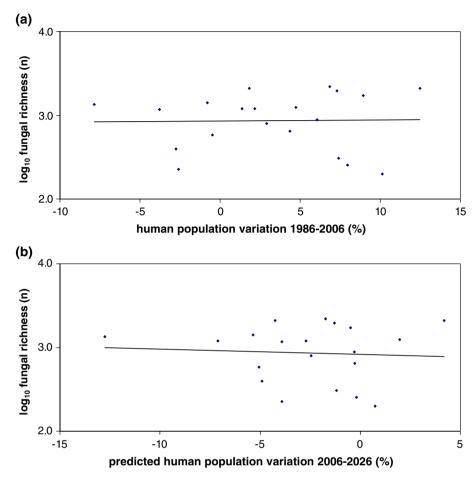


Fig. 2 The correlation between macrofungal taxonomic richness and the percent variation of human population in Italy's regions for the period **a** 1986–2006 (observed) and **b** 2006–2026 (predicted) for Italy's regions

protected area did not change results qualitatively, and quantitative changes did not alter any of the conclusions drawn. Percentage forest area was significantly positively associated with macrofungal richness, whilst percentage protected area (comprising both national and regional parks) was not significantly associated with macrofungal richness (for human density, and for 2006: n = 20, $r^2 = 0.80$, logtaxa = -1.99 + 0.20 logdens + 1.01 logarea + 0.014 for % -0.001 prot%, s.s.e. = 0.16, 0.17, 0.004, 0.005, P = 0.22, P < 0.0001, P = 0.001, 0.87, respectively).

The number of fungal taxa was not significantly associated with the percent variation of human population from 1986 to 2006 (n = 20, $r^2 = 0.00$, logtaxa = 2.95 $- 0.00 \Delta^1$, s.s.e. = 0.01, P = 0.85; Fig. 2a) and from 2006 to 2026 (n = 20, $r^2 = 0.00$, logtaxa = 2.93 $- 0.00 \Delta^2$, s.s.e. = 0.01, P = 0.89; Fig. 2b). The two variations of human population (from 1986 to 2006 and from 2006 to 2026) were significantly positively associated (n = 20, $r^2 = 0.72$, $\Delta 2 = -4.85 + 0.63 \Delta 1$, s.s.e. = 0.07, P < 0.0001) as regions which have recently declined in population are predicted to continue losing inhabitants, and vice



versa, although the relationship was less than proportional (i.e., the slope was significantly shallower than one). This is the consequence of a predicted decline in population for some regions which increased their population over the last two decades.

Discussion

We found no significant increase in the number of macrofungal taxa with increasing human population size and density of Italy's regions when controlling for variations in area. There was a significant increase of macrofungal taxonomic richness with human population size and density, but only without controlling for variations in area amongst regions. This result is in disagreement with previous studies reporting significant positive relationships between the species richness of various taxa other than fungi and human presence at broad scales (e.g., Rondinini et al. 2006; Vazquez and Gaston 2006; Moreno-Rueda and Pizarro 2007; Steck and Pautasso 2008; Schlick-Steiner et al. 2008).

However, there is evidence that also at least some of the previously observed positive correlations between biodiversity and people disappear if confounding variables are controlled for (e.g., Chown et al. 2003). Examples include a study of the species richness of butterflies, birds and mammals in Australia, which correlates with human population presence only because the latter occurs in regions of high net primary productivity (Luck 2007a). A similar argument is made as a potential explanation of the co-occurrence of human population and (1) bird diversity in parts of the Andean highlands (Fjeldså 2007), (2) anuran diversity in the Brazilian Cerrado (Diniz et al. 2006; but see Rangel et al. 2007), (3) and species richness of several animal groups in the USA (McKinney 2006). Moreover, the positive human-biodiversity correlation turns into negative when controlling for variations in productivity for birds in East Asia (Ding et al. 2006). In the present analysis, there is no evidence that the positive macrofungal taxonomic richness-people correlation is the consequence of both variables being positively related to energy availability, as only the number of people, but not the number of fungal taxa, increases with mean annual temperature and precipitation. This discrepancy might be present because, in regions of pervasive anthropogenic influences, human beings have frequently modified patterns in environmental productivity, which might thus not be related to biodiversity any longer (Koh et al. 2006).

Another explanation of large-scale positive biodiversity-people relationship can be that more populated regions have been more thoroughly sampled. However, sampling bias does not appear to explain the observed species-people correlation for birds in Britain and for plants in the USA (Evans et al. 2007; Pautasso and McKinney 2007). Similarly, the flora of German urban areas is believed to be naturally species-rich (Kühn et al. 2004). In the case of macrofungi in Italy's regions, the robustness to sampling bias of the results presented here is suggested by their consistency using the data of a previous checklist. Nevertheless, given that we find no significant variations in macrofungal taxa with increasing number of people when controlling for area, sampling bias does not need to be invoked to explain a relationship which is not present.

We found no significant differences in the patterns reported when using human data for 1986, 2006 and 2026. This is consistent with a study of avian biodiversity in South Africa, where both species richness and human population were sampled at two different points in time (Evans et al. 2006). Here, only an estimate for current fungal richness was available, so it was not possible to analyze whether variations in human populations accompanied variations in taxonomic presence. However, we were able to analyze currently estimated



fungal taxonomic richness as a function of (i) human population size observed now, 20 years ago and predicted in twenty years time, and (ii) human population change over the last and next two decades.

The absence of differences in the correlation between fungal taxa and human population using human data from different time points can be the consequence of the current relative stability of human population in Italy, although some regions have increased the number of inhabitants by up to 15% in the last two decades and some others are predicted to decrease their population by 5% over the next two decades (Table 1). This result also suggests that the correlation between species and people might be resilient to temporal changes in the number of people, which would argue against a causal relationship between high numbers of people and species. Other factors such as human development index, intensity of land use and environmental awareness can be better indicators of human impacts on biodiversity than numbers of inhabitants alone (e.g., Scharlemann et al. 2004; Faggi et al. 2006; Jha and Bawa 2006; Teyssedre and Couvet 2007). However, high numbers of people have been frequently shown to pose a threat to species (e.g., Kirkland and Ostfeld 1999; Thompson and Jones 1999; Cincotta et al. 2000; Scharlemann et al. 2005). Since the relation between the spatial concentration of people and presence of threatened species is likely to suffer from scaledependence and could differ amongst taxa (Pandit and Laband 2007; Pautasso 2007) there is the need for an assessment of this issue also for fungi over a range of scales.

Interestingly, we found no association of the number of fungal taxa with the observed and predicted rate of change in human population for the past and future 20 years. This means that there are regions with high estimated fungal biodiversity where human population has increased (e.g., Emilia Romagna, Lombardia, Trentino Alto Adige, Veneto) but other regions with relative high fungal richness where human population has declined (e.g., Liguria, Piemonte). Similar examples can be found for the predicted rate of change of human population for the next two decades and current estimated fungal biodiversity (Table 1).

Italian regions that stand out in the regression of macrofungal taxonomic richness against human population and area are Liguria and Trentino Alto Adige. The latter has a higher estimated number of macrofungal taxa than expected from its population and the former than expected from its area. Both regions have a high proportion of forest cover (Liguria 53%; Trentino Alto Adige:46%). Moreover, Liguria is an Italian hotspot of macrofungal species diversity (Zotti and Orsino 2001; Zotti and Zappatore 2006). Less than 3% of the Italian population live in Liguria (and this proportion is expected to decline), and this region only covers 2% of the country area, but nearly 40% of the fungal species recorded in Italy are present there. Trentino Alto Adige is a region of relatively low human density but probably a region more thoroughly sampled than others (Ripa et al. 2003). It is also one of the few Italian regions where human population is expected to increase over the next two decades.

Even if the correlation between number of macrofungal taxa and human population can be explained by variations in area amongst regions (larger Italian regions have more fungal taxa and are more densely populated), on a first approximation more densely populated Italian regions still have a higher number of estimated macrofungal taxa. There is thus a potential for a conservation conflict, given that the number of people and their density are a rough indicator of potential human impact on ecosystems. However, if more densely populated regions have a higher presence of fungal taxa, then there is also the opportunity for the majority of Italian people to experience a wide variety of fungal forms in their neighbourhoods (e.g., Miller 2005). Although species richness is only one argument in conservation and although this study will need to be extended for endemic and rare fungal species, the absence of correlation between macrofungal richness and percentage of



protected area implies that the conservation of fungal biodiversity needs to be made compatible with the presence of people in today's human-modified landscapes (e.g., Scott et al. 2001; Andelman and Willig 2003; Real et al. 2003; Brandon et al. 2005). This is particularly true for Italy, where civilization has influenced nature for a very long time (Hall 2000; Maiorano et al. 2006; Falcucci et al. 2007), but can also apply to other countries where the impact of urbanization and agriculture is more recent (e.g., Develice and Martin 2001; Taylor et al. 2001; Gibertoni et al. 2007).

Compared to the amount of studies in urban settings dealing with plants, insects, and vertebrates, not enough mycological attention is given to human-modified habitats (e.g., Calvino 1963; Ławrynowicz 1982; Markkola et al. 1995; Gaston et al. 2005; Lonsdale et al. 2008). Human presence appears to create new ecological niches also for fungi. Examples are macrofungal species often found in urban environments (e.g., allotments, private gardens, tree avenues) or at the outskirts of towns in areas heavily modified by human activities (e.g., relict agricultural land, roadsides, wasteland), which include in Italy *Agaricus bresadolanus* Bohus, *Agrocybe aegerita* (V. Brig.) Singer, *Amanita ovoidea* (Bull.) Link., *Coprinopsis cinerea* (Schaeff.) Redhead, Vilgalys & Moncalvo, *Tricholoma scalpturatum* (Fr.) Quél., *Xerocomus rubellus* (Krombh.) Quél. Some of these species are very adaptable and manage to thrive in spite of urbanization, other species instead are even typical of urban habitats and not normally found in other environments (e.g., *Inocybe langei* R. Heim, *I. furfurea* Kuhner, *Russula ochrospora* (Nicolay) Quadr., *R. hortensis* Sarnari.).

Further research is needed on the human-biodiversity correlation for fungi and on its implications for conservation. The relative paucity of data on fungal species occurrences and abundances over a range of human population densities needs to be overcome with systematic sampling and monitoring in a long-term perspective. However, we already know that some structural (e.g., deadwood; Travaglini et al. (2007)), functional (e.g., tree species diversity; Schmit et al. (2005)), and temporal (e.g., age; Humphrey (2005)) features of ecosystems are important for macrofungal biodiversity. Therefore some recommendations for policy-makers can already be given. The observed positive association of percentage forest cover with macrofungal taxonomic richness in Italy's region suggests that (1) substantial amounts of deadwood need to be retained, even in urbanized ecosystems, (2) semi-natural patches of vegetation in fertile plains are to be preserved and connected, and their tree species diversity maintained, and (3) fire prevention should be implemented with more success, particularly for ancient woodlands in Mediterranean coastlands. Given that studies of fungal biodiversity tend to be performed preferentially in remnants of natural vegetation (e.g., Luschka 1997; Zotti and Zappatore 2006; Nordén et al. 2007; Ortega and Lorite 2007), more work in less pristine ecosystems is needed to assess the potential impacts of marginal land abandonment and further urban sprawl for the conservation of different functional groups of macrofungi in Italy and other countries.

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