

# ***Robinia pseudoacacia* as a surrogate for native tree species for saproxylic beetles inhabiting the riparian mixed forests of northern Italy**

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- Abstract**
- 1 The felling and leaving of non-native trees comprise management strategies designed to increase dead wood for saproxylic fauna in forests without affecting native tree species. In northern Italy, the most widespread exotic tree in alluvial forests is the North American *Robinia pseudoacacia*.
  - 2 We quantified the difference in species composition and abundance among saproxylic beetles of two European broad-leaved trees, *Populus alba* and *Quercus robur*, and the exotic broad-leaved tree *Robinia pseudoacacia*.
  - 3 We collected beetles emerging from 29 fallen trunks with a diameter of between 29 and 31 cm and belonging to the second decomposition stage.
  - 4 We identified 249 individuals from 25 saproxylic beetle species. Species richness and composition did not differ among tree species. Although permutational multivariate analysis of variance highlighted significant differences in species composition, linear mixed effect models showed that differences depend exclusively on spatial distances between logs and not on the host tree species. The Morisita-Horn index and principal coordinate analysis confirmed this pattern.
  - 5 Thus, we found that saproxylic beetles use all dead trees available in the forest, without distinguishing between exotic or native trees but only occupying the nearest ones. From a forest management point of view, this supports the practice of leaving dead wood of exotic trees at restorations for saproxylic beetles.

**Keywords** Dead wood management, exotic tree species, riparian mixed forests, *Robinia pseudoacacia*, saproxylic beetles.

## **Introduction**

Forests are complex and dynamic ecosystems where wood accounts for the majority of standing biomass and provides, alive, decaying or dead, the medium for a highly diversified biocoenosis (Audisio *et al.*, 2014). Currently, the presence of dead wood in a forest is increasingly being used as an indicator for assessing the good health and naturalness of forest ecosystems (Cavalli & Mason, 2003; Jonsson *et al.*, 2005). The presence of fallen and standing dead trees, logs and rotting root systems significantly contributes to the survival of saproxylic species (Marchetti & Lombardi, 2006; Müller & Bussler, 2008; Müller & Bütler, 2010; Della Rocca *et al.*, 2014), which represent approximately 20–30% of the invertebrate fauna of the

European broad-leaved forests (Wermelinger *et al.*, 2002; Val-lauri *et al.*, 2005) and constitute a major part of biodiversity in woodlands (Speight, 1989). Today, many European saproxylic species are threatened (Seibold *et al.*, 2014). In Italy, the surface of some types of forests, such as lowland, riparian and hygrophilous forests, has been greatly reduced in recent historical times; in most remaining forests, the dead wood is almost completely absent as a result of management practices; in these habitats, saproxylic species are at risk (Blasi *et al.*, 2010; Audisio *et al.*, 2014). The estimate for the amount of deadwood in Italian forests produced by the Italian National Inventory of Forests and Forests Carbon Sinks (INFC) is 8.8 m<sup>3</sup>/ha (Pignatti *et al.*, 2009), which is half of the lower limit proposed in many recent studies (Müller & Bütler, 2010; Della Rocca *et al.*, 2014).

Various management strategies have been designed to increase the amount of dead wood (Hutto, 2006; Hyvärinen *et al.*, 2006). These include the conservation of old trees, maintenance of

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dead wood and decaying trees for a balanced tree dynamic in time and space, and accelerating the decay of mature trees (pre-senescence; Ranius & Jansson, 2000). In the first two cases, a certain availability of dead wood already present in the forest is necessary. In the latter case, the process of the formation of dead wood may take many decades because the natural tree mortality in the medium-aged stands typical of production forests is low (Holzwarth *et al.*, 2013; Sebek *et al.*, 2013). Therefore, the fastest way of overcoming the lack of dead wood in a forest consists of cutting live plants or placing dead wood from other locations in the forest. In light of the recent colonization of invasive species as a result of the increased introduction of exotic species and climate change conditions (Burgiel & Muir, 2010), these interventions can be made on exotic plants such as pines, eucalyptus, maples, exotic oaks, chestnuts, etc., without affecting the native tree species. Although native deadwood is assumed to provide more valuable habitats than non-native deadwood and should be retained wherever possible, there is good evidence to suggest that retaining large-diameter timber from non-native species can provide important habitats, particularly in cool and wet conditions (Humphrey & Bailey, 2012).

In this way, non-native live trees are gradually eliminated and turned into dead wood and 'microhabitats' for saproxylic fauna (Cavalli & Mason, 2003; Campanaro *et al.*, 2011).

In northern Italy, the most widespread invasive exotic tree species in relict alluvial forests are the black locust (*Robinia pseudoacacia*), the tree of heaven (*Ailanthus altissima*) and the late cherry (*Prunus serotina*) (Annighöfer *et al.*, 2015).

*Robinia pseudoacacia* is recognized as one of the most problematic invaders in Europe (Kleinbauer *et al.*, 2010), including Italy (Celesti-Grappo *et al.*, 2009) and it is probably the most abundant non-native plant in the whole Italian territory (Başnou, 2006). Its rapid growth rate and the production of a large quantity of propagules (Sabo, 2000) allow black-locust to outcompete native trees in dry and nutrient-poor sites and lowlands (Motta *et al.*, 2009) where it may alter ecosystem structures and the dynamics of native oak and chestnut forests (Tani *et al.*, 2012). *Robinia pseudoacacia* was imported from North America at the beginning of the 17th Century, and its spread was favoured indirectly by repeated coppicing. At present, *R. pseudoacacia* represents a naturalized species that is difficult to eradicate from many areas (Brusa & Castrovinci, 2007).

Although the idea of a 're-use' of the non-native woody plants as a resource for saproxylic fauna is widely accepted (Cavalli & Mason, 2003), to date, there are no studies that have demonstrated its effectiveness on saproxylic beetles. Currently, only few studies have compared saproxylic communities of coniferous forests with those of broadleaves and, in some cases, examined the preferences of saproxylic beetles for many native tree species (Dahlberg & Stokland, 2004; Lindhe & Lindhelöw, 2004; Lindhe *et al.*, 2005; Wu *et al.*, 2008; Stokland *et al.*, 2012; Milberg *et al.*, 2014; Müller *et al.*, 2015), although no research has compared the saproxylic communities inhabiting native and exotic trees in temperate forests. Therefore, in the present study, we aimed to evaluate and quantify the use of non-native tree species by saproxylic beetles. Specifically, we investigated: (i) whether there is a difference in species composition and abundance among saproxylic beetle communities that use the dead wood of native plants and those of the non-native plant

*R. pseudoacacia* and (ii) would *R. pseudoacacia*, the non-native tree species now naturalized in our territory, be a surrogate for native tree species if it was necessary to increase the dead wood biomass in a forest biotope?

## Materials and methods

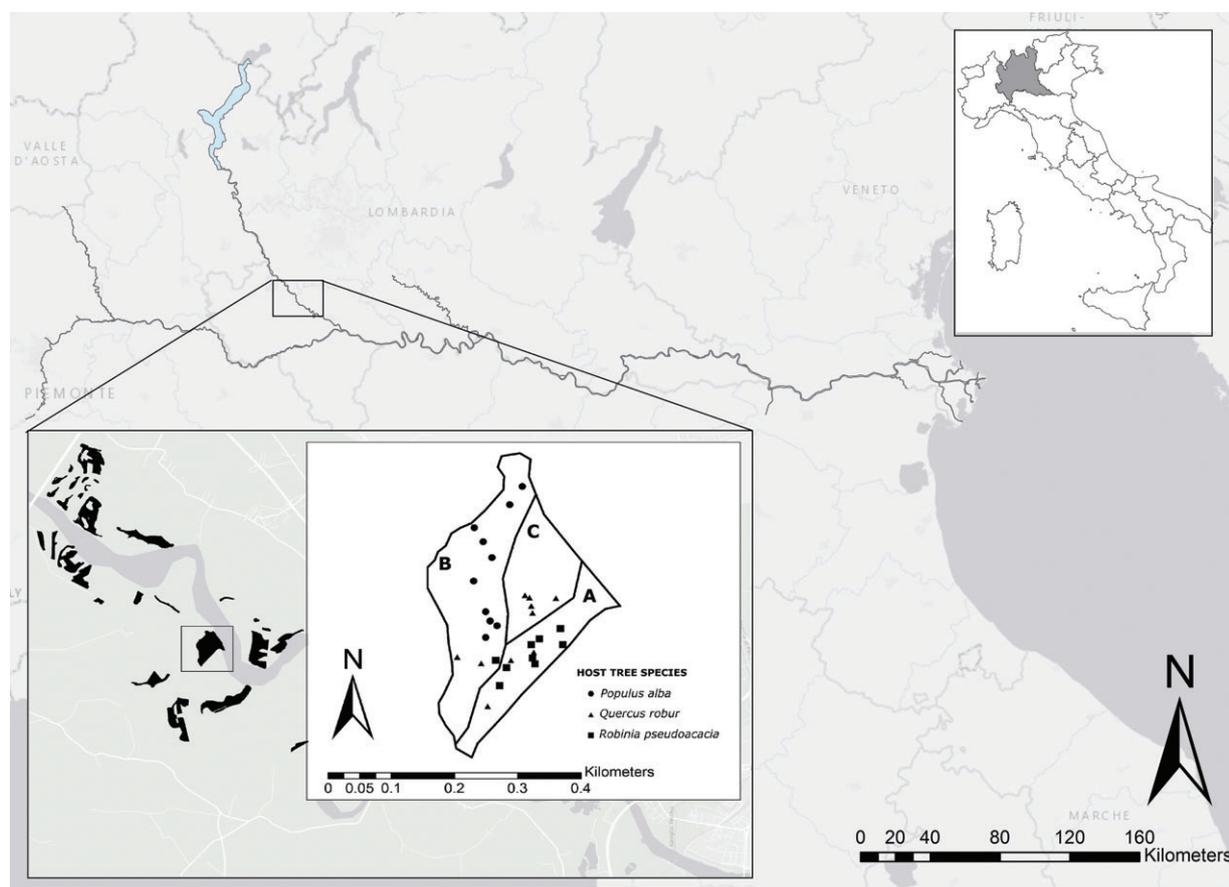
### Study area

The present study was conducted in the 'Bosco Siro Negri' natural reserve, a small forest area of approximately 20 ha located inside the Ticino Valley Regional Park (Fig. 1). Bosco Siro Negri reserve was established in 1973 and is the best-preserved forest of the Park (Sartori, 1984). It represents a small but precious relict of lowland riparian mixed forests consisting of oaks, elms and poplars, which covered the entire Po Valley until Roman colonization (1st Century BC; Tomaselli & Gentile, 1971). The area was already covered by forests in the years 1722 to 1723 subsequent to the 'Mailänder Kataster' and was no longer under silvicultural management practices after the end of the Second World War. Together with all other alluvial and mixed forests of the Ticino Valley, the area is a rare example of lowland forest vegetation with characteristics of high naturalness, a large amount of deadwood (113 m<sup>3</sup>/ha) (Sutti, 2010; Della Rocca *et al.*, 2011, 2014) and very low human disturbance (Gobbi *et al.*, 2007).

The dominant forest type is the 91F0 – Riparian mixed forests of oak (*Quercus robur*), elm (*Ulmus laevis* and *Ulmus minor*) and ash (*Fraxinus excelsior* or *Fraxinus angustifolia*) along the great rivers listed in Annex 1 of the EU Habitat directive (Falco *et al.*, 2008). The dominant native tree species is *Q. robur*, followed by *Populus alba*, whereas, among the non-native species, *R. pseudoacacia* is widespread. A previous study conducted in the southern part of the Ticino Valley Regional Park found a total of 87 saproxylic beetle species (Stefanelli *et al.*, 2014).

### Study design and beetle collection

We investigated a total of 29 fallen dead trees belonging to three different species: *Q. robur*, *P. alba* and *R. pseudoacacia*. We selected trees with a diameter between 22 and 37 cm according to Della Rocca *et al.* (2014) who found the highest number of saproxylic species in this range. Specifically, we selected: 10 *Q. robur* with a diameter (mean ± SD) of 30.4 ± 3.38 cm; 10 *P. alba* with a diameter of 31.0 ± 2.52 cm and nine *R. pseudoacacia* with a diameter of 29.8 ± 2.74 cm. To reduce experimental bias, we selected the same decomposition stage for all the trunks. We chose the second decomposition stage (Cindolo & Petriccione, 2007) because it hosts a greater number of species compared with the earlier stage of decay where only saproxylic species strictly confined to a single host-tree genus are present (Grove, 2002; Wu *et al.*, 2008; Stokland *et al.*, 2012) or the later decomposition stage where most of the broadleaf heartwood-decay beetles could be more linked to fungal colonization and therefore more host-specific (Saint-Germain *et al.*, 2007). All logs were georeferenced in the UTM WGS84 32N coordinates system using ARCGIS, version 10.1 (ESRI, Redlands, California : <http://www.esri.com/software/arcgis>) and then we also calculated the spatial distances between pairs of logs as straight line



**Figure 1** Location of the 'Bosco Siro Negri' Natural reserve. Sampling sites and forest areas are shown.

Euclidean distances. Moreover, we divided the forest into three different areas (here after 'Forest areas') on the basis of the vegetation composition and sun exposure. We thus identified the area 'A' as a marginal area with little tree cover and high brightness bordering an open field subjected to reforestation. Here, the dominant tree is *R. pseudoacacia*. The area 'B' is a marginal area too with a dominance of *P. alba* and *Populus nigra*, bordering a river oxbow. The 'C' area is the one that best represents the characteristics typical of riparian mixed forests with a dominance of oaks, and it is completely surrounded by the other areas (Fig. 1).

To collect saproxylic beetles, each fallen tree was enclosed with an eclector trap (Albrecht, 1990; Schmitt, 1992; Alinvi *et al.*, 2007) of a 1-m wide black polypropylene fabric weed barrier. A hole was made in the cloth and a lid for a translucent plastic bottle filled with a 70% ethanol solution was fastened on it. Beetles emerging from the trap were caught inside the bottle screwed into this lid (Johansson *et al.*, 2006; Della Rocca *et al.*, 2014). All traps were checked every 2 weeks from May to October 2013 to cover the seasonal activity of all the species. Beetles were separated from other insects and identified to species level by taxonomic specialists. We considered only those species that depend on dead wood in at least part of their lifecycle (Gibb *et al.*, 2006) and called them 'obligate saproxylic beetles'. Beetles from families with no obligate saproxylic members or with limited auto-ecological information were not taken into account.

### Statistical analysis

We used the pooled sample of 29 traps in the analysis. As a measure of species richness, we plotted the number of species versus the number of specimens in a size-based rarefaction curve (Chao & Jost, 2012; Müller *et al.*, 2013) using INEXT (interpolation/extrapolation) (<http://chao.stat.nthu.edu.tw/inext>). We used the size-based rarefaction curve to graphically compare species richness among the host tree species; we used the chi-squared test to verify significant differences. To compare species richness among the host tree species, we also computed coverage-based rarefaction curves (Chao & Jost, 2012; Müller *et al.*, 2013) for each community. With the coverage-based rarefaction analysis, we estimated the coverage deficit of our sampling effort as the probability that the next sampled individual belongs to a new species not previously collected (Olszewski, 2004). This approach goes a step further than the traditional rarefaction technique because it compares samples of equal completeness instead of equal size satisfying a replication principle that is an essential property for characterizing diversity (Jost, 2010; Chao & Jost, 2012). Differences in species richness among the three host species were also evaluated with the permutational multivariate analysis of variance (PERMANOVA) using PRIMER, version 6 with PERMANOVA+ (Anderson *et al.*, 2006; Clarke & Gorley, 2006). PERMANOVA is a semi-parametric test analogous to multivariate analysis of variance but with pseudo *F*-ratios and *P*-values

**Table 1** List of the saproxylic species collected

Beetle family	Beetle species	Tree species			Total
		<i>Populus alba</i>	<i>Robinia pseudoacacia</i>	<i>Quercus robur</i>	
Anobiidae	<i>Priobium carpini</i>	0	0	1	1
Anthribidae	<i>Phaenotherion fasciculatum</i>	1	1	0	2 (2)
Cerambycidae	<i>Aegosoma scabricorne</i>	1	2 (1)	0	3 (2)
Cerambycidae	<i>Leptura aurulenta</i>	4 (2)	0	0	4 (2)
Cerylonidae	<i>Cerylon ferrugineum</i>	5 (5)	2 (2)	8 (4)	15 (11)
Cetoniidae	<i>Cetonia aurata</i>	3 (3)	3 (2)	4 (3)	10 (8)
Cetoniidae	<i>Valgus hemipterus</i>	0	5 (2)	1	6 (3)
Dryophthoridae	<i>Dryophthorus corticalis</i>	5 (1)	29 (2)	10 (5)	44 (8)
Elateridae	<i>Ampedus pomorum</i>	0	2 (1)	1	3 (2)
Elateridae	<i>Lacon punctatus</i>	1	1	1	3 (3)
Elateridae	<i>Melanotus villosus</i>	1	1	1	3 (3)
Erotylidae	<i>Dacne bipustulata</i>	0	0	2 (2)	2 (2)
Histeridae	<i>Paromalus flavicornis</i>	2 (2)	4 (2)	10 (2)	16 (6)
Latritiidae	<i>Enicmus rugosus</i>	0	1	3 (2)	4 (3)
Latritiidae	<i>Latridius hirtus</i>	0	0	1	1
Lucanidae	<i>Dorcus parallelepipedus</i>	20 (7)	3 (2)	13 (5)	36 (14)
Monotomidae	<i>Rhizophagus bipustulatus</i>	3 (3)	14 (6)	40 (5)	57 (14)
Staphylinidae	<i>Scaphidium quadrimaculatum</i>	1	0	8 (1)	9 (2)
Tenebrionidae	<i>Hypophloeus fasciatus</i>	0	0	2 (1)	2 (1)
Tenebrionidae	<i>Mycetochara linearis</i>	0	0	1	1
Tenebrionidae	<i>Prionychus</i> sp.	0	1	1	2 (2)
Tenebrionidae	<i>Scaphidema metallicum</i>	0	0	1	1
Tenebrionidae	<i>Uloma culinaris</i>	0	0	1	1
Zopheridae	<i>Pycnomerus terebrans</i>	0	15 (2)	4 (4)	19 (6)
Zopheridae	<i>Rhopalocerus rondanii</i>	1	1	2 (2)	4 (4)
<b>Total</b>		48	85	116	249

The number of individuals collected in each tree species is shown. The number of logs is shown within brackets.

generated by 9999 permutations; thus, it is less sensitive to assumptions of parametric tests that are frequently violated by ecological data sets (Anderson, 2001; Anderson *et al.*, 2008). We performed PERMANOVA to also determine whether species composition of saproxylic beetles assemblage differs among host tree species and forest areas. In this case, we nested the dataset into the factors 'Tree species' and 'Forest areas' (see above) and performed PERMANOVA on the basis of Bray–Curtis similarity matrix using standardized and square root transformed abundance data. Pairwise post-hoc comparisons were performed under 9999 permutations whenever significant differences were found; for further details, see Anderson (2005).

We also used the Bray–Curtis similarity matrix in a principal coordinates analysis (PCO) (Gower, 2005) to display similarities in species composition among all samples. PCO is an unconstrained metric multidimensional scaling ordination that extracts major variance components from the multivariate data set to reduce dimensionality of the data cloud by minimizing the residual variation in the space of any chosen resemblance measure.

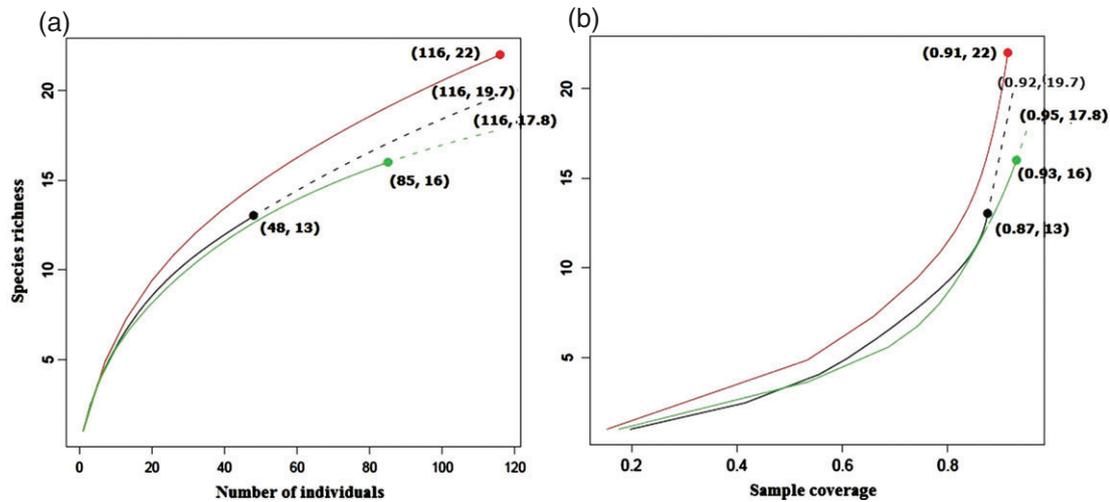
To test for differences in saproxylic community structure among host tree species, we also used the Morisita–Horn abundance-based similarity index between pairs of assemblages (Magurran, 2004) available in R statistical software (<http://cran.r-project.org>). This index, which is considered as the best overall measure of similarity (Magurran, 2004), is based on the probability that two individuals taken from each of two communities belong to the same shared species (Chao *et al.*,

2005, 2006). Its values range from 0 (no similarity) to 1 (total similarity).

Finally, we examined how much of the similarity in saproxylic species composition was explained by spatial distance also taking into account the effect of Tree species. Thus, we tested the relationship between similarities in species composition (Bray–Curtis similarity matrix), spatial distance between pairs of logs and tree species by using linear mixed effect models (NLME package in R; Pinheiro *et al.*, 2014). In our case, the Bray–Curtis similarity matrix was the response variable, spatial distances and tree species were considered as fixed factors, and, because pairwise distance estimates do not provide independent data, a Toeplitz covariance matrix was taken into account as a random effect (Selkoe *et al.*, 2010). We evaluated the effect of predictors with respect to explaining similarity in species compositions based on standardized regression coefficients,  $\beta$  (Van Strien *et al.*, 2012). The higher a standardized  $\beta$ -value, the higher (in absolute value) is its presumed effect on the response variable (i.e. similarity in species composition). We used 10 000 permutations to assess significance using the PGIRMESS package in R (Giraudeau, 2015).

## Results

We found a total of 249 individuals from 25 obligate saproxylic beetle species in the whole study area (Table 1). Species richness



**Figure 2** Comparison of saproxylic species richness among the host tree species: *Populus alba* (black), *Quercus robur* (red) and *Robinia pseudoacacia* (green). (a) Size-based rarefaction curves (solid lines) of the three host species and extrapolation (dashed lines) up to 116 individuals (sampling effort of *Q. robur*) for *P. alba* and *R. pseudoacacia*. (b) Coverage-based rarefaction curves (solid lines) of the three host species and extrapolation curves (dashed lines) of *P. alba* and *R. pseudoacacia*. The sample coverage reaches the 0.91, 0.92 and 0.95 in *Q. robur*, *P. alba* and *R. pseudoacacia*. Reference samples are indicated by solid black dots.

did not differ among the host tree species (PERMANOVA test: pseudo- $F = 0.128$ ,  $P = 0.162$ ). However, size-based rarefaction curves show that *Q. robur* hosts the highest number of species and individuals, with 22 species and 116 specimens, followed by *R. pseudoacacia*, with 85 specimens belonging to 16 species, and *P. alba* hosting the poorest community, with 48 individuals belonging to 13 saproxylic species (Fig. 2a). The absence of difference in species richness is also confirmed by the chi-squared test ( $\chi^2 = 2.471$ ,  $P = 0.30$ ). The size-based rarefaction curve also shows that an extrapolated estimate of species richness at the sampling effort of *Q. robur* (116 individuals) would lead to an increase of seven species for *P. alba* and two species for *R. pseudoacacia* (Fig. 2b). We can see that our sampling efforts reach 91% of sample completeness for *Q. robur*, 87% for *P. alba* and 93% for *R. pseudoacacia*. Extrapolating the estimate of species richness at the sampling effort of *Q. robur* (116 individuals) would lead to an increase of sample completeness of 5% more for *P. alba* and 2% more for *R. pseudoacacia*. PERMANOVA analysis shows that saproxylic assemblage differed significantly among host tree species (Table 2) but not among forest areas. Moreover, the interaction between the two factors 'Forest areas' and 'Tree species' does not show a significant effect. A post-hoc analysis of saproxylic beetle composition between pairs of host tree species showed no difference between *Q. robur* and *R. pseudoacacia*. Conversely, *P. alba* appears to be significantly different from both *Q. robur* and *R. pseudoacacia* (Table 3).

Ordinations with PCO confirm this pattern. The first axis explains 65.9% of variance and clearly separates *P. alba* from *Q. robur* and *R. pseudoacacia* beetle communities, whereas there was no clear separation pattern between these two latter species (Fig. 3).

On the basis of the Morisita-Horn index, *Q. robur* and *R. pseudoacacia* shared the highest number of saproxylic species ( $n = 14$ ) followed by the pairs *P. alba*-*Q. robur* and *P. alba*-*R. pseudoacacia* that shared, respectively, 10 and 11 saproxylic

species (Table 4). Only nine out of 25 saproxylic species (36%) are shared by all the host tree species.

The minimum distance between *R. pseudoacacia* and *Q. robur* is 13.89 m, whereas the minimum distance between *P. alba* and the two host species *R. pseudoacacia* and *Q. robur* is 60 and 44.5 m, respectively (see Supporting information, Table S1). Similarity in species compositions between pairs of logs was significantly explained by spatial distances ( $P = 0.009$ ) but not by tree species ( $P = 0.689$ ) in linear mixed effect models. Moreover, the standardized  $\beta$ -values of spatial distances were higher (in absolute value) than those of tree species ( $-0.097$  and  $-0.017$ , respectively), highlighting that spatial distance had a negative effect on community similarity.

## Discussion

In the present study, we investigated the difference in saproxylic beetle composition and abundance among three host tree species, two native European broad-leaved trees, *Q. robur* and *P. alba*, and one North American broad-leaved tree *R. pseudoacacia*, aiming to evaluate the use of the latter as a surrogate for native tree species for increasing deadwood in a forest.

The results obtained show that saproxylic communities inhabiting the second decomposition stage of *Q. robur*, *P. alba* and *R. pseudoacacia* are basically very similar in terms of species richness and composition. The similar number of saproxylic beetle species among the tree communities was supported by size-based and coverage-based rarefaction curves that highlighted only a small difference in species evenness between *R. pseudoacacia* and the two native species *Q. robur* and *P. alba*, and a small difference in species richness between *P. alba* and the other two host trees. The similarity in species richness between *Q. robur* and the other two species is somewhat surprising because *Q. robur* has been considered to be the most species-rich tree in

**Table 2** Results from permutational multivariate analysis of variance for differences in saproxylic species composition among the factors host tree species, forest area, and their interactions (Ts × Fa = Tree species × Forest area) based on a Bray-Curtis resemblance matrix with *P*-values obtained by 9999 permutation

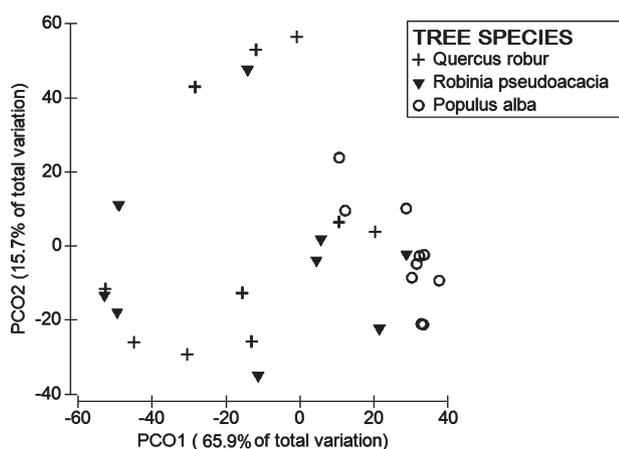
Source	d.f.	SS	MS	Pseudo- <i>F</i>	<i>P</i> (perm)	Unique permutations
Tree species	2	17349	8674.3	2.531	<b>0.001</b>	9919
Forest area	2	4888.2	2444.1	0.713	0.833	9903
Tsp × Fa	1	6122	6122	1.786	0.053	9932
Res	23	78804	3426.3	—	—	—
Total	28	1.07E+05	—	—	—	—

SS, sum of squares; MS, mean sum of squares; Pseudo-*F*, *F* value by permutation. Bold indicates statistical significance at *P* < 0.05.

**Table 3** Results from permutational multivariate analysis of variance pairwise tests for differences in saproxylic beetle composition between pairs of host tree species

Tree species	<i>t</i>	<i>P</i> (perm)	Unique permutations
<i>Quercus</i> , <i>Robinia</i>	0.564	0.949	9939
<i>Quercus</i> , <i>Populus</i>	2.062	<b>0.000</b>	9929
<i>Robinia</i> , <i>Populus</i>	1.776	<b>0.000</b>	9874

The significantly different species composition is indicated by bolded *P*-values obtained by permutation.



**Figure 3** Scatter plot showing the ordination produced by principal coordinate analysis (PCO) in the Bray-Curtis distance matrix for the 29 plots belonging to *Populus alba*, *Robinia pseudoacacia* and *Quercus robur*. The first two axes explain 81.6% of the total variation, with PCO1 explaining 65.9% of total variation.

many European countries (Jonsell *et al.*, 1998; Müller & Goßner, 2007; Irmeler *et al.*, 2010), except for Sweden, where a recent study found no difference in saproxylic species richness between *Q. robur* and other native species such as *Acer platanoides*, *F. excelsior* and/or *Tilia cordata*. However, oak trees can reach large sizes and host many different microhabitats for saproxylic beetles (Larrieu & Cabanettes, 2012). It is possible that the young oaks in the present study did not have sufficient time to develop this diversity of microhabitats and, consequently, the number of saproxylic beetles is low compared with what would be expected for this species.

Our results are also in contrast to Lachat *et al.* (2006) who found significant differences in species richness between beetles inhabiting native trees and those inhabiting exotic trees in western African tropical forests. However, they studied beetle assemblages by comparing two distinct forest systems, a semi-deciduous forest with native trees and a plantation with exotic trees, and it is very likely that these two different forests can host different insect communities. Conversely, in the present study, exotic and native trees are both present in the same forest, and this is the only possible way of understanding the real difference among the communities (Lachat *et al.*, 2006).

We found a clear similarity in saproxylic species composition among the three communities. This finding is partially in agreement with those of other studies conducted on high stumps (Lindhe & Lindhelöw, 2004; Lindhe *et al.*, 2005) and on logging residues (Jonsell *et al.*, 2007) of spruce, birch, aspen and oak trees. In these studies, although the different tree species hosted different assemblages of saproxylic beetles, among the deciduous trees, there was considerable overlap, especially between birch and oak (Lindhe & Lindhelöw, 2004). Another study on logs and stumps only found small differences between the tree species beech, alder and spruce (Irmeler *et al.*, 1996).

In the present study, although PERMANOVA analysis highlighted a significant difference in saproxylic species composition between *P. alba* and the other two host species, linear mixed effect models showed that this difference depends exclusively on the spatial distance between logs and not on the host tree species. Also, the similarity among logs expressed by the Morisita-Horn index and the PCO analysis confirmed this pattern. Indeed, the most similar tree species in terms of saproxylic species composition, *Q. robur* and *R. pseudoacacia*, are also the nearest ones, whereas *P. alba* and *R. pseudoacacia*, in addition to being significantly different in terms of specific composition, are also the more spatially distant. This inverse relationship between community similarity and spatial distance has been already described in the literature as the 'distance decay of similarity' (Nekola & White, 1999), and it has been reported for a variety of organisms and at different spatial scales (Tuomisto *et al.*, 2003; Qian & Ricklefs, 2007; Soininen *et al.*, 2007). Community similarity tends to decrease with increasing spatial distance as a result of factors that include decreased environmental similarities, dispersal limitations of individuals and niche width differences (Nekola & White, 1999). In the present study, we found a clear tendency of saproxylic beetles to use all the dead trees available in the forest without distinguishing between exotic or native trees but only occupying the nearest ones. Thus, even if the present study was carried out at a finer scale than other research investigating the

**Table 4** Morisita-Horn similarity index comparing saproxylic beetle communities for pairs of tree species

Pair of tree species	Number of shared species	Percentage of shared species	Morisita-Horn similarity index		
			Estimate	Estimate S.E.	95% confidence interval
<i>Quercus/Robinia</i>	14	63.6 (Q versus R) 87.5 (R versus Q)	0.662	0.095	(0.476, 0.849)
<i>Quercus/Populus</i>	10	45.45 (Q versus P) 76.9 (P versus Q)	0.582	0.105	(0.376, 0.789)
<i>Robinia/Populus</i>	11	84.6 (P versus R) 68.7 (R versus P)	0.368	0.102	(0.167, 0.568)
<i>Quercus/Robinia/Populus</i>	9	—	0.305 <sup>a</sup>	0.080	(0.148, 0.463)

<sup>a</sup>A similarity measure of comparing three communities using all shared information.

The number and percentage of shared saproxylic species between pairs of tree species are also shown.

distance–decay effect (Nekola & White, 1999; Soininen *et al.*, 2007; Jobe, 2008), we hypothesize that spatial distance is the main factor driving the assembly of the saproxylic beetle communities of Bosco Siro Negri as a result of the low dispersal ability of these species. Indeed for saproxylic beetles, short-distance movements are more frequent than long-distance movements (Jonsell *et al.* 2003), and a study conducted in Germany reported that 46 of 81 saproxylic beetles (57%) fly distances of less than 30 m (Irmeler *et al.*, 2010) and only 16% fly farther than 80 m. However, it was not the goal of the present study to investigate the dispersion ability of saproxylic beetles. To study colonization probability, many factors should be taken into account, such as flight ability, the density of populations, the age of woods, the character of habitats between woods and the size of woods (Jonsell *et al.*, 1999). Moreover, for many species collected in the present study, dispersal ability is currently unknown. Thus, further studies should be carried out to clarify this aspect.

Our finding of no differences in saproxylic species composition among exotic and native trees is in contrast to those of other studies in which there emerged a clear avoidance by saproxylic beetles of exotic tree species such as *Pinus brutia* in Israel (Buse *et al.*, 2010) and *Pseudotsuga menziesii* in Germany (Müller *et al.*, 2015). However, the introduction of these exotic trees is relatively recent compared with that of *R. pseudoacacia* (approximately 400 years ago). Indeed, *P. menziesii* was introduced in Europe approximately 150 years ago, and *P. brutia* was introduced in Israel less than approximately 100 years ago. Some studies supported the hypothesis that the use of exotic plants by native insects increases with the area covered by these introduced plants (Branco *et al.*, 2015) and with the time subsequent to the exotic plant having been introduced (White *et al.*, 2006; Brändle *et al.*, 2008). Thus, considering the wide distribution of *R. pseudoacacia* and its presence for a long time in the riparian mixed forests of northern Italy, it is likely that saproxylic beetles use this exotic species similarly to other native species such as *Q. robur* and *P. alba*.

#### Study limitations

We acknowledge that the main limitation of the present study is the small sample size as a result of the trapping method used. It is known that the use of emergence traps means that large samples of dead wood are needed to produce sufficient individuals per species to make statistical analyses possible (Brin *et al.*, 2011). Because of the small size of our study area, it was impossible to

find more than 10 dead trees per species with a diameter between 22 and 37 cm and also belonging to the second decaying class. For the same reason, we could not enlarge our dataset including dead trees from other decomposition stages (thus, we could not analyze some aspects of the community, such as the succession of saproxylic species among the decaying process). However, the local species richness was within the range expected for this habitat-type based on previous studies where the same sampling technique was applied (Della Rocca *et al.*, 2014). Moreover, the completeness of sampling was higher than 85% for all the communities, indicating that most of the saproxylic species linked to the second decomposition stage of *Q. robur*, *P. alba* and *R. pseudoacacia* were collected. The good quality of our sampling is also confirmed by the fact that all 29 traps were able to catch saproxylic beetles, unlike other studies such as that by Nittérus *et al.* (2004), who found no insect emergence from 34% of their rearing devices, or by Brin *et al.* (2011), where 49% of their traps did not provide any saproxylic beetles. Despite the low number of individuals collected for two-thirds of the species (20% of species are singleton and 16% doubleton), rarefaction curves showed that the saproxylic beetle community inhabiting the three arboreal species and the second decaying class of the ‘Siro-Negri’ forest is well represented.

It has been widely demonstrated that emergence traps generally catch a lower number of saproxylic beetles compared with others kinds of traps, such as window or malaise traps (Bakke, 1999; Schiegg, 2000; Ranius & Jansson, 2002). However, this trapping method is the most appropriate for investigations on the microhabitat requirements of saproxylic insect species (Økland, 1996; Wikars *et al.*, 2005; Alinvi *et al.*, 2007) because it captures insects from a known substrate. Emergence trapping is widely used in studies such as the present one where quantitative sampling of insects emerging directly from logs is needed (Alinvi *et al.*, 2007).

We demonstrated the efficiency of emergence traps in catching saproxylic beetles at the within-site level compared with other trapping methods in a recent study carried out in the same area (Stefanelli *et al.*, 2014). In this case, we used both windows and emergence traps to evaluate differences in species richness between managed and unmanaged forests, although only insects caught by emergence traps were found to be highly correlated with deadwood present in the same area. Also, only data from emergence traps were used in another of our studies (Della Rocca *et al.*, 2014).

### Management implications

We demonstrated that the dead wood of *R. pseudoacacia*, even if it is an exotic species, hosted a wide range of saproxylic beetles shared with that of *Q. robur* and *P. alba*, the two main tree species of the Siro Negri forest, and more generally of the riparian mixed forest of north Italy.

The possibility of using the dead wood of *R. pseudoacacia* as part of forest management operations aimed at restoring habitats for saproxylic beetles has a double advantage. Indeed, the controlled cutting of exotic trees could lead to the death of an invasive tree species and, in the meantime, restore deadwood for saproxylic species without affecting the original forest structure.

In any case, we should also take into account the important conservation value of oaks for saproxylics, especially in oak-dominated landscapes. Oak trees are potentially older and larger than other tree species and provide, in proportion to the size, more wood mould per tree and over a longer time period per tree (Milberg *et al.*, 2014). Moreover, some studies suggest that oak wood is slower to decompose, creating more long-lasting wood mould (Flæte *et al.*, 2009; Milberg *et al.*, 2014). Thus, from a forest management point of view, deadwood from *R. pseudoacacia* can be used for restoring forest deadwood in combination with other trees species, in particular *Q. robur*.

### Conclusions

The present study represents the first time that saproxylic beetle communities of native and exotic tree species have been compared within a mature temperate forest. The present study highlights the advantages and cost-effectiveness of increasing deadwood through the re-use of the non-native woody plant *R. pseudoacacia*. This should be carried out in combination with the retention of native trees to obtain the best results in terms of forest conservation at the same time as minimizing the costs.

The controlled cutting of exotic tree species adds new potential habitats and opens up an opportunity to use several tree species in conservation management.

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### Supporting information

Additional Supporting information may be found in the online version of this article under the DOI reference: 10.1111/afe.12157

**Table S1.** Spatial distances between pairs of logs as straight line Euclidean distances (m).

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