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A comparison of three methods to survey saproxylic beetles in hollow oaks

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Abstract. One of the most endangered assemblages of species in Europe is insects associated with old trees. For that reason there is a need of developing methods to survey this fauna. This study aims at comparing three methods — window trapping, pitfall trapping and wood mould sampling — to assess species richness and composition of the saproxylic beetle fauna in living, hollow oaks. We have used these methods at the same site, and to a large extent in the same trees. Useful information was obtained from all methods, but they partially target different assemblages of species. Window trapping collected the highest number of species. Pitfall trapping collected beetles associated with tree hollows which rarely are collected by window traps and therefore it is profitable to combine these two methods. As wood mould sampling is the cheapest method to use, indicator species should preferrably be chosen among species which are efficiently collected with this method.

Key words: pitfall traps, saproxylic beetles, trapping efficiency, tree hollows, window traps

INTRODUCTION

In Europe, many invertebrates associated with old trees are threatened, as this habitat has decreased severely (Harding and Rose 1986; Speight 1989). However, information on the distribution and abundance of such species is lacking and, therefore, it is difficult to make well-founded decisions in nature conservation and management. Reliable assessments of species richness and composition are useful when identifying the most valuable sites for nature conservation and monitoring changes of the fauna over time. Therefore, in practical conservation there is a need of methods to assess presence/absence of saproxylic invertebrate species and to better understand the potential sources of error of these assessments.

In Sweden, large oaks (*Quercus robur*) sustain the most diverse fauna of beetles associated with old trees (Palm 1959). When oaks age, hollows with wood mould often form in the trunks. Wood mould is loose wood colonized by fungi, often with remains from animal nests and insect fragments. Trunk hollows with wood mould harbour a specialized fauna mainly consisting of beetles and flies

(Dajoz 1980). The beetle fauna in tree hollows has received entomologists' interest for a long time, but only recently it has been studied with quantitative methods. We have carried out surveys with use of three different methods: window trapping, pitfall trapping and wood mould sampling. Different kinds of window traps have been used in several studies on saproxylic beetles (e.g. Hammond 1997; Jansson and Lundberg 2000; Jonsell and Nordlander 1995; Kaila 1993; Martikainen et al. 2000; Økland 1996; Ranius and Jansson 2000). Pitfall traps have been widely used in studies of arthropods active on the ground (e.g. Baars 1979; Greenslade 1964; Spence and Niemelä 1994), but it seems that they have been used in quantitative assessments in tree hollows only recently (e.g. Ranius and Jansson 2000; Ranius 2001). Wood mould sampling implies that a certain amount of wood mould from each tree is examined. From a wood mould sample beetles could be extracted by a lamp (Dajoz 1980; Nilsson and Baranowski 1997) or collected by searching through the material when it is spread out on a sheet (Ranius 2000).

This paper compares the results from three methods to sample saproxylic beetles associated with living old oaks. A number of questions are addressed: Which collection method yields the largest number of beetle species? Do the different sampling methods capture different groups of species living in certain microhabitats? Are there differences in the sampling efficiency between traps in trees which are sun-exposed in comparison to trees in more shaded situations? How many samples should be taken in a stand to capture a representative fraction of the fauna present?

METHODS

Study area and tree characteristics

A 12 x 16 km wide area with Bjärka-Säby as its centre (province of Östergötland, Sweden, 58°16´N, 15°46´E) was studied. This area contains almost 2,500 hollow trees and among these, oak is the dominating tree species (Ranius et al. 2001). All trees studied were old, hollow oaks potentially sustaining a species-rich fauna. Trunk hollows begin to develop in oaks when they are 150-200 years old (Sven G. Nilsson, pers. comm.). The age of the examined trees is not known, but the oldest trees in this study might be 400 years old or more.

The same 90 oaks were surveyed with pitfall traps and window traps. Wood mould were sampled from 53 trees, including 21 which were surveyed also with the trapping methods. The diameter of the trunk and the height of the entrance hole did not differ between oaks sampled with traps and those which wood mould were sampled from (Mean diameter, trees with traps: 1.11 m; trees with wood mould sampled: 1.21 m, $p = 0.194$ (t-test); Fraction of trunks with holes > 2 m from the ground, trees with traps: 77%, trees with wood mould sampled: 64%, $p = 0.133$ (Pearson chi-square)).

Sampling methods

One trap of each type was set in each of the 90 oaks. Window traps consisted of a 30 x 40 cm wide transparent plastic plate with a tray underneath (Jansson and Lundberg 2000). They were placed near the trunk (≤ 1 m), beside or in front of a hole entrance. Their position were 1.5–7 m from the ground, dependent on where the hole entrance were situated on the studied trees. Pitfall traps were plastic cups with a top diameter of 65 mm, placed with the opening at level at the wood mould surface of the tree hollows. Both types of traps were partially (about 1/2 of the volume) filled with ethylene glycol and water (50 : 50 v/v). Dishwashing detergent was added to reduce surface tension. The traps were placed in the trees between 6–13 May and removed between 8–16 August in 1994 and were emptied every third week. Thus, there was a small difference in length of the period the traps were used. However, the activity of saproxylic beetles is low in the middle of May and August, so for that reason this has a very small influence on the capture.

From each tree one sample of 8 litres of wood mould was taken. If only 2–8 litres of wood mould was available in a tree (which was the case in seven trees out of 53) all was taken as a sample. The wood mould was sieved and spread out on a white sheet in the field. Larvae, imagines and fragments of imagines were carefully collected. Afterwards the wood mould was returned to the trunk hollow. All wood mould samples were taken in August 2000. Thus, this sampling was carried out six year later than the trapping, but as fragments can accumulate over several years and the fluctuations of beetle populations in tree hollows may be low (see Discussion), this would have a minor influence on the results.

Sampling efficiency of living beetles could be influenced by that the insects' activity depends

on microclimate. This may create a bias when comparing trapping results from sun-exposed and more shaded trees. To test this assumption we divided the oaks into three groups with different vertical coverage of the canopy in the surrounding (Free-standing: 10–30% (n = 21); Half-open: 30–70% (n = 30); Shaded: 70–90% (n =39)) and compared the number of individuals and species of beetles captured by pitfall traps and window traps between these groups.

Analyses

Identification was done by Nicklas Jansson, except *Ampedus* spp. and Cryptophagidae and all beetles from the wood mould sampling, which was identified by Rickard Andersson (formerly Baranowski). The specimens collected by pitfall traps and window traps were counted, except two genera containing the largest number of individuals—*Ptinus* spp. and *Dorcatoma* spp. Due to limited time available, we left out the following taxa which are difficult to identify or regarded as being of low interest for our studies as large oaks constitute the main habitat for none or a very few of the species, in spite of that they include some saproxylic species: Anaspidae, Dasytinae, Euglenidae, Corticariidae, Nitudulidae, Ptiliidae, Salpingidae, Scolytidae, Staphylinidae (except Staphylininae and Omaliinae) and Throscidae. The beetles were divided into groups according to their microhabitat in trees (Table 1) (as in Ranius and Jansson 2000). Only saproxylic species which normally develop in old oaks were considered. Species which not are associated with trees or which we know are associated with other trees species than oaks were excluded from the analyses.

The species richness per tree for the three different sampling methods was compared by a one-way ANOVA. The correlation between species richness obtained by each method per tree were analysed by Pearson correlation coefficient. The similarity in species composition between the methods was estimated with use of Sørensen's index of similarity (Krebs 1989). In the two latter analyses only species belonging to microhabitat groups captured by all methods (*i.e.* group ROT, HOLLOW and NEST) were considered.

In order to estimate how the number of species captured changes when the number of samples is changed, we used 20 samples taken with use of each method from trees in the core (within a radius of 700 m) of the Bjärka-Säby area. In this analysis, it was not the same 20 trees used for wood-mould

sampling as for the trapping. Instead, we chose 20 trees standing as concentrated as possible, in order to simulate a situation when one single stand is sampled with a varying number of traps or wood mould samples. We divided the samples into groups with a particular number of samples each time. When we for instance formed groups with three samples, 18 samples were used to form six groups, and the remaining two samples were not used.

The differences between sun-exposed and shaded trunks were analysed by comparing the number of species and individuals captured. If samples are taken from a given site, the number of individuals captured would be proportional with the sampling effort, whereas the quotient between number of species and sampling effort decreases with the sampling effort. Therefore, the quotient between number of individuals and number of species would increase if the sampling effort is increased in a constant community. We used this relation when we analysed differences between sun-exposed and shaded trunks: if the differences in collected beetle species only are due to sampling efficiency, the quotient between individual number and species number would be higher in samples where the species number is higher. Other patterns suggest that there are real differences in the communities between sun-exposed and shaded trunks.

RESULTS

A total of 125 species of saproxylic beetles were found (Table 1), including 51 on the Swedish red list (Gärdenfors 2000). Ninety window traps collected 98 species, 90 pitfall traps collected 88 species and in 53 wood mould samples 55 species were collected.

The number of species sampled differed significantly between methods ($p = 0.022$) and was highest for window traps (Table 2). Window traps caught all groups of saproxylic beetles, whereas pitfall traps and wood mould sampling mainly caught beetles associated with tree hollows and animal nests (Table 2). There were however several species associated with tree hollows (*Ampedus cardinalis*, *Cryptophagus quercinus*, *Elater ferrugineus*, *Osmoderma eremita*, *Plegaderus caesus*, *Tenebrio molitor*, *T. opacus*, *Trox scaber*) which hardly ever were captured by window traps (Table 1). Twenty-

eight species were only sampled by window traps, 15 species were only sampled by pitfall traps and six species were only sampled by wood mould sampling.

A comparison between sampling methods showed that the number of saproxylic beetle species collected per tree with each method were positively correlated (Table 3). Thus, if species richness is to be compared between individual trees similar results are to be expected independent on the sampling method chosen. Sørensen's coefficient of similarity was between 0.68 and 0.71 for all pairs of methods which were compared with each other.

We used 20 samples to estimate how the number of species captured changes when the number of samples is changed. Overall, the number of captured species increased with increasing number of samples included with similar rates in all methods (Table 4), but there were differences between microhabitat groups. With wood mould sampling, beetles associated with tree hollows were efficiently sampled with relatively small sample sizes, whereas other groups required larger sample sizes (Table 1 & 4). Also with pitfall traps, a larger fraction of species were captured with a few traps in Group HOLLOW in comparison with other groups, whereas with window traps the patterns in Group ROT, HOLLOW and NEST were similar in this respect. Among the species in Group FUNGI, DRY and BRANCH only one was frequently found with pitfall traps and wood mould sampling: *Xestobium rufovillosum*. In several inventories we have used four pitfall traps and four window traps in each area and with this effort about a half of the species were collected in comparison with a sample of 20 traps of each type (Table 4).

It tended to be more species and more individuals captured in free-standing oaks. However, the quotient between number of individuals and number of species captured per species was independent on canopy cover (Table 5).

DISCUSSION

Comparison of methods

There is no method which gives a complete and unbiased picture of the occurrence of saproxylic

beetles; even with about ten samples taken from a site, there are many saproxylic beetle species present which have still not been found. Therefore data on species richness or abundance of individual species must always include survey parameters, such as the techniques employed and the sampling effort, in order to make inventories repeatable and comparable.

If the aim of an inventory is to find as many saproxylic beetle species as possible, mainly window traps should be used. As many species are captured in low frequencies with this method, it is profitable to use many window traps in the same area. Several threatened species associated with tree hollows are hardly ever captured by window traps and therefore window trapping may be combined pitfall trapping or wood mould sampling. Beetles living in dead branches and twigs on living trees seem to be poorly inventoried by window traps, as the number of species and their frequencies of presence were low (Table 1). Special traps set on branches have been developed (Koponen et al. 1997) and these might be more efficient for a few species.

Wood mould sampling is the fastest and cheapest inventory method. A problem when assessing body parts in wood mould samples is that the smallest species (e.g. *Atomaria* spp., *Cryptophagus* spp., *Hypebaeus flavipes*, *Plegaderus caesus*, *Ptinus* spp. and *Scraptia fuscula*) are underestimated (Table 1). This is owing to difficulties to find the beetles and to identify the fragments. To improve the outcome the living adults could be extracted by using a lamp over the material (in a Tullgren funnel), however this demands much more work.

As it is expensive to carry out such extensive inventories that the majority of the species are collected, it would be useful to identify indicator species which are easy to inventory with a cheap method and whose presence are positively correlated with a high species richness or with a community with a high number of threatened species. In Sweden, several lists of saproxylic beetles possible useful as indicator species have been compiled, but it has never been clearly stated on which criteria these species have been selected (Antonsson and Wadstein 1991; Rundlöf and Nilsson 1995; Nilsson et al. 2001). To be useful as an indicator the species must be easy to survey with some technique, preferrably with wood mould sampling as this is a cheap method. However, it does not seem that this has been taken into consideration in the compiling of indicator species lists so far.

In window trapping, all beetles captured have obviously not been hatched in the tree of study,

as a large fraction of the insects captured were non-saproxylics (and thus not presented in this paper). Pitfall traps are much more selective, as an insect has to live in the hollow or actively move to the hollow to be trapped.

Practical considerations

Only about 30–50% of all trees with large hollows were possible to sample. To be suitable for pitfall trapping and wood-mould sampling the hollow had to be wide enough, not too far from the ground in relation to the length of the ladder, and the wood mould surface not too far from the entrance of the hollow. There are also trees where sampling has to be avoided as the hollow harbours breeding birds or wasp nests.

To reach the trunk hollows we used ladders which were 5 or 7 m. Many saproxylic beetle species associated with trunk hollows are more frequent in hollows at higher heights (Ranius, in press). Therefore, the results would differ between surveys with a ladder used and surveys solely performed near the ground.

Window traps necessitate the use of some kind of killing agent. As we used ethylene glycol, which is toxic to vertebrates, we had to place the window traps >2 m from the ground, so they could not be reached by humans, cattle or wildlife. Pitfall traps could be used either with or without a killing agent. The main advantage with using glycol is that the field work becomes more efficient, as the traps do not have to be emptied so often. We emptied both kinds of traps every third week, and only at some occasions the window traps were dried or the pitfall traps filled with wood mould.

In this study we have taken samples of wood mould, but not other types of rotten wood. Our sampling does probably not disturb the habitat and its inhabiting fauna, as we return the wood mould immediately. Quantitative assessments of the fauna have also been made in certain volumes of rotten wood (Dajoz 1980) and areas of bark peeled from dead logs (Biström and Väisänen 1988; Siitonen and Saaristo 2000). These methods destroy the habitat at least to some extent and are therefore generally not applicable on oak trunks in pasture woodlands and old-growth oak forests in Europe.

Variability in efficiency over space and time

In some surveys, the quotient between number of individuals and number of species captured with window traps has differed widely between sites (e.g. Martikainen 2001), which suggest that there are differences in the population densities or that the trap efficiency is related to some characteristic of the sites. In our study site more species have been collected in trees with less surrounding canopy cover and we have suggested this is because a warmer microclimate increases species richness (Ranius and Jansson 2000). However, an alternative explanation would be that the species richness is equal, but the catchability is higher in the more sun-exposed trees. This study gives no support for this latter view; the number of individuals per species would increase if the trap efficiency increased, but in this study the number of individuals captured per species was not related with the surrounding canopy cover (Table 5).

The higher frequency in wood mould sampling of some species indicates that fragments are accumulated over several years and that they do not ascertain presence of living adults at the particular year of study. It is not known for how long the fragments persist, but there are circumstancial evidence that they are eaten up by insect larvae and for that reason most of them disappear perhaps within a few years (Ranius and Nilsson 1997). However, in a dry environment in trees where these insects larvae are absent we can not exclude the possibility that the fragments may persist for a much longer time. The durability of fragments means that they are not reliable when assessing changes in the fauna which may have occurred over the last few years.

There are two reasons to believe that window traps and pitfall traps may yield results which differ between years: the population sizes fluctuate between years and the catchability may differ owing to for instance the weather. However, a five year study on *Osmoderma eremita*, whose larvae have a developing time of three years, shows that the population variability over time was much smaller than the variability between trees, and thus in surveys of this species it is much more important which trees that are chosen than at which year the inventory is carried out (Ranius 2001).

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Table 1. Frequency of saproxylic beetles investigated with three different methods in Bjärka-Säby. A) Species name according to Lundberg (1995). B) Microhabitat groups: Rotten wood in any part of the trunks, even on the outside (ROT), rotten wood in the trunks, exclusively from the inside, in hollows (HOLLOW), animal nests in tree hollows (NEST), fruiting bodies of saproxylic fungi (FUNGI), dead, dry wood in trunks (DRY), branches of old oaks (BRANCH). C) Red-listed (R) or not according to Gärdenfors (2000). D) Fraction of window traps with the species present and number of individuals per window trap (zeroes excluded) ± S.D. *n* = 90. E) Fraction of pitfall traps with the species present and number of individuals per pitfall trap (zeroes excluded) ± S.D. *n* = 90. F) Fraction of wood mould samples with the species present. *n* = 53. Window traps and pitfall traps were set in exactly the same trees, whereas the wood mould samples were partly taken in other trees, however within the same area. Number of specimens was not estimated for *Ptinus* spp. and *Dorcatoma* spp.

A)	B)	C)	D)		E)		F)
Agrilus biguttatus	DRY	R	1%	1.0	0%		0%
Agrilus laticornis	BRANCH	R	2%	1.0±0.0	0%		0%
Agrilus sulcicollis	BRANCH		8%	1.1±0.4	0%		0%
Agrilus viridis	BRANCH		1%	1.0	0%		0%
Allecula morio	HOLLOW	R	30%	3.0±2.6	28%	2.8±2.5	55%
Alosterna tabacicolor	ROT		14%	1.5±0.8	11%	1.0±0.0	0%
Ampedus balteatus	ROT		8%	1.1±0.4	6%	1.2±0.4	6%
Ampedus cardinalis	HOLLOW	R	3%	1.3±0.6	17%	1.6±1.2	49%
Ampedus hjorti	HOLLOW	R	10%	1.2±0.4	13%	2.3±2.0	38%
Ampedus nigroflavus	ROT	R	1%	1.0	0%		0%
Ampedus pomorum	ROT		1%	1.0	1%	1.0	0%
Anobium nitidum	DRY		16%	1.1±0.4	0%		0%
Anobium rufipes	DRY		4%	1.0±0.0	0%		0%
Anthrenus museorum	NEST		27%	2.1±1.9	1%	1.0	0%
Anthrenus scrophulariae	NEST		8%	2.4±2.1	2%	3±2.8	0%
Athous mutilatus	HOLLOW	R	0%		0%		6%
Atomaria alpina	FUNGI	R	0%		1%	1.0	0%
Atomaria bella	FUNGI		0%		2%	1.5±0.7	0%
Atomaria morio	NEST		18%	1.3±0.4	30%	2.8±2.2	2%
Atomaria umbrina	FUNGI		0%		1%	1.0	0%
Attagenus pellio	NEST		1%	1.0	0%		8%
Batrisodes adnexus	NEST	R	0%		1%	1.0	0%
Batrisodes delaporti	NEST	R	2%	1.0±0.0	1%	1.0	0%
Batrisodes venustus	NEST		0%		0%		2%
Calambus bipustulatus	ROT	R	3%	1.0±0.0	1%	1.0	11%

Cerylon ferrugineus	ROT		8%	1.4±0.5	1%	1.0	0%
Cerylon histeroides	ROT		11%	1.4±0.5	20%	1.6±1.0	6%
Cetonia aurata	ROT		0%		0%		6%
Cis fagi	ROT		1%	1.0	0%		0%
Conopalpus testaceus	BRANCH	R	21%	2.0±1.1	0%		0%
Corticeus fasciatus	DRY	R	2%	1.0±0.0	1%	1.0	0%
Cryptophagus badius	ROT		1%	1.0	27%	2.2±1.6	2%
Cryptophagus confusus	HOLLOW	R	2%	1.0±0.0	2%	1.0	0%
Cryptophagus dentatus	FUNGI		13%	1.3±0.5	13%	1.6±0.8	0%
Cryptophagus labilis	HOLLOW	R	0%		1%	1.0	0%
Cryptophagus micaseus	NEST	R	57%	3.1±2.8	11%	1.7±0.9	0%
Cryptophagus populi	HOLLOW		4%	1.0±0.0	1%	1.0	0%
Cryptophagus quercinus	HOLLOW	R	1%	1.0	20%	3.9±7.3	2%
Cryptophagus scanicus	ROT		57%	2.2±2.0	44%	2.3±1.8	4%
Ctesias serra	ROT		72%	2.6±1.7	8%	1.7±0.8	11%
Dacne bipustulata	FUNGI		4%	1.0±0.0	0%		0%
Dendrophilus corticalis	HOLLOW		10%	3.0±4.7	39%	5.6±7.2	38%
Dermestes lardarius	NEST		2%	1.5±0.7	3%	2.3±2.3	4%
Diaperis boleti	FUNGI		27%	1.3±0.8	0%		6%
Dorcatoma chrysomelina	ROT		68%	–	39%	–	13%
Dorcatoma flavicornis	ROT	R	43%	–	17%	–	6%
Dreposcia umbrina	NEST	R	0%		0%		2%
Elater ferrugineus	HOLLOW	R	0%		9%	1.1±0.4	26%
Eledona agaricola	FUNGI		6%	1.6±0.5	6%	10.4±5.5	13%
Endomychus coccineus	FUNGI		4%	1.0±0.0	0%		0%
Euplectus bescidicus	HOLLOW		1%	1.0	1%	1.0	0%
Euplectus karsteni	HOLLOW		1%	1.0	12%	1.4±0.5	2%
Euplectus nanus	HOLLOW		1%	1.0	4%	1.3±0.5	0%
Euplectus piceus	ROT		0%		1%	1.0	0%
Euplectus punctatus	ROT		0%		1%	1.0	0%
Gastrallus immarginatus	DRY	R	30%	1.1±0.3	0%		0%
Globicornis rufitarsis	NEST	R	20%	1.2±0.5	0%		0%
Gnathoncus buyssoni/nannetensis	NEST		34%	1.8±1.7	31%	2.9±3.0	0%
Gnathoncus nidorum	NEST	R	1%	1.0	0%		0%
Gnorimus nobilis	HOLLOW	R	0%		1%	1.0	0%
Grammoptera ustulata	BRANCH	R	7%	1.0±0.0	0%		0%
Grynocharis oblonga	ROT	R	0%		6%	3.2±3.3	19%
Hadrobregmus pertinax	DRY		1%	1.0	0%		0%
Hallomenus binotatus	FUNGI		3%	1.3±0.6	0%		0%
Hapalarea pygmaea	NEST	R	11%	2.5±2.0	6%	2.2±1.6	6%
Hedobia imperalis	DRY		9%	1.1±0.4	1%	1.0	2%
Hypebaeus flavipes	ROT	R	14%	1.1±0.4	8%	1.0±0.0	0%
Hypulus quercinus	ROT	R	0%		1%	5.00	2%
Korynetes caeruleus	HOLLOW		0%		3%	2.3±2.3	4%
Leiopus nebulosus	BRANCH		7%	1.3±0.5	1%	1.0	0%
Liocola marmorata	HOLLOW	R	2%	1.0±0.0	12%	1.1±0.3	0%
Lyctus linearis	DRY	R	1%	1.0	0%		0%
Lymexylon navale	DRY	R	13%	1.3±0.7	1%	2.0±0.0	0%

Malachius bipustulatus	ROT		2%	1.0±0.0	0%		0%
Megatoma undata	ROT		28%	1.4±0.8	1%	1.0	2%
Melanotes castanipes	ROT		8%	1.0±0.0	7%	1.3±0.5	0%
Melanotes erythropus	ROT		8%	1.0±0.0	6%	1.6±0.5	2%
Mycetaea subterranea	ROT		0%		2%	1.0±0.0	2%
Mycetina cruciata	FUNGI	R	0%		1%	1.0	0%
Mycetochara axillaris	HOLLOW	R	3%	1.0±0.0	0%		6%
Mycetochara flavipes	ROT		1%	1.0	0%		0%
Mycetochara humeralis	HOLLOW	R	24%	1.8±1.1	4%	1.3±0.5	8%
Mycetochara linearis	ROT		31%	2.4±1.7	4%	1.3±0.5	4%
Mycetophagus piceus	ROT	R	60%	3.1±3.6	10%	1.0±0.0	2%
Mycetophagus populi	HOLLOW	R	2%	1.0±0.0	2%	1.0±0.0	0%
Mycetophagus quadriguttatus	FUNGI	R	0%		1%	1.0	0%
Nemadus colonoides	NEST	R	3%	1.0±0.0	8%	1.9±0.7	6%
Orchesia micans	FUNGI		7%	1.0±0.0	0%		0%
Orchesia undulata	FUNGI		2%	1.0±0.0	0%		0%
Osmoderma eremita	HOLLOW	R	1%	1.0	30%	3.2±4.4	64%
Palorus depressus	NEST		1%	1.0	0%		0%
Paromalus flavicornis	ROT		3%	1.0±0.0	3%	1.3±0.6	0%
Pentaphyllus testaceus	HOLLOW	R	4%	2.5±1.9	1%	1.0	2%
Phymatodes testaceum	DRY		20%	1.7±0.9	1%	1.0	4%
Plectophloeus nitidus	HOLLOW	R	0%		2%	1.0±0.0	0%
Plegaderus caesus	HOLLOW	R	0%		9%	1.9±1.1	0%
Prionychus ater	HOLLOW		20%	1.3±0.6	38%	1.9±2.0	40%
Procraerus tibialis	HOLLOW	R	6%	1.0±0.0	10%	1.2±0.4	43%
Pseudocistela ceramboides	HOLLOW		18%	1.6±1.3	22%	1.5±0.8	15%
Ptinus fur	HOLLOW		16%	–	79%	–	13%
Ptinus rufipes	ROT		54%	–	11%	–	0%
Ptinus subpilosus	HOLLOW		83%	–	68%	–	4%
Quedius brevicornis	NEST		1%	1.0	12%	1.4±0.7	4%
Quedius cruentus	NEST		11%	1.1±0.3	1%	1.0	0%
Quedius microps	NEST		0%		0%		6%
Quedius scitus	NEST		2%	1.0±0.0	9%	1.5±0.8	0%
Rhizophagus cribratus	ROT		0%		3%	1.3±0.6	0%
Rhyncolus ater	ROT		0%		9%	1.3±0.7	0%
Rhyncolus sculpturatus	ROT		2%	1.0±0.0	0%		0%
Scraptia fuscula	NEST	R	43%	2.4±1.9	21%	1.8±1.5	0%
Scydmaenus hellwigi	NEST		0%		1%	2.00	0%
Sinodendron cylindricum	ROT		3%	1.3±0.6	2%	2.0±0.0	9%
Stenichnus godarti	HOLLOW		0%		4%	1.0±0.0	2%
Tenebrio molitor	NEST		2%	1.0±0.0	20%	5.6±6.9	55%
Tenebrio opacus	HOLLOW	R	0%		13%	3.1±4.8	36%
Tillus elongatus	ROT		9%	1.1±0.4	1%	2.00	0%
Trichocoeble memnonia/floralis	ROT	R	46%	1.6±0.8	1%	1.0	0%
Triplax aenea	FUNGI		2%	1.0±0.0	0%		0%
Triplax russica	FUNGI		2%	1.0±0.0	0%		0%
Trox scaber	NEST		2%	1.0±0.0	28%	2.7±2.8	8%
Uloma culinaris	ROT	R	1%	1.0	0%		4%

Velleius dilatatus	NEST	R	42%	2.9±2.7	2%	1.0±0.0	4%
Xestobium rufovillosum	DRY		6%	2.0±2.2	61%	3.9±2.9	21%
Xyletinus longitarsis	ROT	R	1%	1.0	0%		0%
Xyletinus pectinatus	ROT	R	3%	1.0±0.0	0%		0%

Table 2. Number of saproxylic beetle species per tree (Mean ± S.D.) captured with different methods. The beetles are divided in six groups: Rotten wood in any part of the trunks, even on the outside (ROT), rotten wood in the trunks, exclusively from the inside, in hollows (HOLLOW), animal nests in tree hollows (NEST), fruiting bodies of saproxylic fungi (FUNGI), dead, dry wood in trunks (DRY), branches of old oaks (BRANCH). *n* = 21. The difference in species number between methods was tested by One-way ANOVA. Total number of species and the number of red-listed species (Gärdenfors 2000).

	Group							
Method	ROT	HOLLOW	NEST	FUNGI	DRY	BRANCH	Total	Red-listed
Window traps	4.6±0.4	2.5±0.3	2.6±0.3	0.7±0.1	1.0±0.2	0.6±0.2	12.0±0.9	5.2±0.5
Pitfall traps	2.3±0.4	4.8±0.5	1.8±0.4	0.3±0.1	0.9±0.2	0.0	10.1±1.0	3.2±0.4
Wood-mould sampling	1.2±0.3	5.1±0.5	1.0±0.2	0.2±0.1	1.0±0.1	0.0	8.5±0.7	4.5±0.4
p	<0.001	<0.001	0.001	0.009	0.890	<0.001	0.022	0.005
Total	6.8±0.6	8.8±0.6	4.9±0.5	1.0±0.2	2.0±0.2	0.6±0.2	24.1±1.5	10.4±0.7

Table 3. Similarity of species composition between different methods measured by Sørensen's similarity coefficient (mean from 21 trees). Pearson correlation coefficient and statistical significance between species richness per tree (i.e. number of saproxylic beetle species captured in each tree of Group ROT, HOLLOW and NEST) assessed by three different methods. $n = 21$.

	Pitfall trapping	Wood mould sampling
Window trapping	Sørensen: 0.70	Sørensen: 0.68
	Pearson: 0.53	Pearson: 0.50
	$p = 0.014$	$p = 0.021$
Wood mould sampling	Sørensen: 0.71	
	Pearson: 0.40	
	$p = 0.070$	

Table 4. Number of saproxylic beetle species sampled with a differing number of traps or wood mould samples. (A) The number of species present in one sample consisting of 20 trees and (B) Fraction (and number) of species present in blocks of varying sizes in relation to the twenty-trees-sample (mean from all blocks yielded when the twenty-trees-sample is divided into as many blocks as possible) . The fraction is not given for groups with <5 species in the twenty-trees-sample.

(A)

Twenty trees (n = 1)

	ROT	HOLLOW	NEST	FUNGI	DRY	BRANCH	Total
Window trap	22	13	14	8	9	3	69
Pitfall trap	17	21	13	3	3	0	57
Wood mould	14	16	6	2	2	0	40
Window + pitfall trap	27	24	18	9	9	3	90

(B)

One tree / sample (n = 20)

	ROT	HOLLOW	NEST	FUNGI	DRY	BRANCH	Total
Window trap	21% (4.6)	20% (2.6)	18% (2.5)	9%(0.7)	12% (1.1)	–	17% (11.7)
Pitfall trap	13% (2.2)	23% (4.8)	12% (1.6)	–	–	–	17% (9.7)
Wood mould	7% (1.0)	30% (4.8)	15% (0.9)	–	–	–	19% (7.6)
Window + pitfall trap	22% (5.9)	25% (6.0)	21% (3.8)	9% (0.8)	18% (1.6)	–	21% (18.9)

Three trees / sample (n = 6)

	ROT	HOLLOW	NEST	FUNGI	DRY	BRANCH	Total
Window trap	45% (9.9)	46% (6.0)	39% (5.5)	23% (1.8)	31% (2.8)	–	39% (26.9)
Pitfall trap	30% (5.1)	46% (9.7)	29% (3.8)	–	–	–	37% (21.1)
Wood mould	17% (2.4)	60% (9.6)	36% (2.2)	–	–	–	39% (15.6)
Window + pitfall trap	41% (11.1)	49% (11.8)	42% (7.6)	26% (2.3)	41% (3.7)	–	41% (36.9)

Five trees / sample (n = 4)

	ROT	HOLLOW	NEST	FUNGI	DRY	BRANCH	Total
Window trap	55% (12.1)	60% (7.8)	54% (7.6)	34% (2.7)	44% (4.0)	–	51% (35.2)
Pitfall trap	47% (8.0)	65% (13.7)	51% (6.6)	–	–	–	56% (31.9)

Wood mould	32% (4.5)	72% (11.5)	46% (2.8)	–	–	–	52% (20.8)
Window + pitfall trap	56% (15.1)	60% (14.4)	64% (11.5)	39% (3.5)	53% (4.8)	–	56% (50.4)

Ten trees / sample (n = 2)

	ROT	HOLLOW	NEST	FUNGI	DRY	BRANCH	Total
Window trap	77% (16.9)	81% (10.5)	75% (10.5)	69% (5.5)	72% (6.5)	–	75% (51.8)
Pitfall trap	65% (11.1)	86% (18.1)	69% (9.0)	–	–	–	75% (42.8)
Wood mould	57% (8.0)	84% (13.4)	75% (4.5)	–	–	–	71% (28.4)
Window + pitfall trap	78% (21.1)	83% (19.9)	78% (14.0)	67% (6.0)	67% (6.0)	–	77% (69.3)

Table 5. Saproxylic beetles per tree, divided into categories differing in the surrounding canopy cover. Number of individuals and species (*Dorcatoma* spp. and *Ptinus* spp. excluded, as all individuals of these species were not counted) and the quotient (number of individuals per species).

Window traps

	n	No. species±S.E.	No. individuals±S.E.	Quotient±S.E.
Free-standing (10–30%)	21	12.6±0.8	25.6±2.6	2.0±0.2
Half-open (30–70%)	30	10.3±0.9	19.4±2.1	1.8±0.2
Shaded (70–90%)	39	9.7±0.7	18.0±1.5	1.8±0.1
p (one-way ANOVA)		0.053	0.032	0.407

Pitfall traps

	n	No. species±S.E.	No. individuals±S.E.	Quotient±S.E.
Free-standing (10–30%)	21	9.6±0.9	22.6±2.9	2.4±0.3
Half-open (30–70%)	30	7.1±0.8	18.5±3.2	2.3±0.2
Shaded (70–90%)	39	7.1±0.5	18.2±2.8	2.3±0.2
p (one-way ANOVA)		0.032	0.578	0.954

n = number of hollow oaks.