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National oak monitoring: testing traps and sampling strategies

Ryan C. Burner
Anne Sverdrup-Thygeson
Tone Birkemoe

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COVER PICTURE
Window traps with and without water draining device. Photo: Ryan C. Burner

NØKKELORD
DNA strekkoding, hule eiker, insektovervåking, vindusfeller, utvalgt naturtype, ARKO-prosjektet

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Ryan C. Burner, Anne Sverdrup-Thygeson (anne.sverdrup-thygeson@nmbu.no) & Tone Birkemoe: Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, Ås, Norway.

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Forord

Arbeidet med hule eiker startet som en del av Nasjonalt program for kartlegging og overvåking av biologisk mangfold. Dette prosjektet gikk fra 2003 til 2015, og målet var å stedfeste og verdiklassifisere viktige områder for biologisk mangfold, undersøke endringer i biologisk mangfold over tid og årsakene til endringene, samt komme med forslag til tiltak og oppfølging av disse. Programmet skulle både kvalitetssikre eksisterende data, etablere aktiviteter for å tette kunnskapshull og videreutvikle kartleggings- og overvåkingsaktiviteter.

Delprosjektet som ble kalt ARKO (Arealer for Rødlistearter - Kartlegging og Overvåking) var en del av Nasjonalt program i hele prosjektperioden. ARKO ble ledet fra NINA, men med en rekke samarbeidende institusjoner. Formålet med delprosjektet var tredelt; øke kunnskapen om rødlistearter, identifisere viktige forvaltningsarealer for rødlistearter og utvikle metoder for overvåking av rødlistearter. ARKO så spesielt på sjeldne, velavgrensete naturtyper med ansamlinger av truete og nær truete arter, gjerne også med mange habitatspesifikke arter, såkalte hotspot-habitater. All publisering finnes på prosjektets hjemmeside www.nina.no/Overvåking/ARKO.aspx .

Et av hotspot-habitatene i ARKO var hule eiker, som har vært fulgt opp fra starten i 2004. I 2013, mot slutten av ARKO-prosjektet, utarbeidet prosjektgruppen et forslag til en metodikk for en nasjonal overvåking av hule eiker.

Eikene har blitt fulgt opp i forlengelse av ARKO-prosjektet. I årene 2012-2016 gjennomførte vi det første omløpet av en nasjonal overvåking, i henhold til metodikken som var utarbeidet. Dette arbeidet ble ledet fra NMBU/MINA med NINA og UiO/NHM som samarbeidspartnere. Det første omløpet er rapportert i MINA fagrapport 50 (2018).

Andre omløp av nasjonal overvåking av hule eiker ble gjennomført i 2019, og resultatene er oppsummert i MINA fagrapport 62 (2019). Der gis en oppdatering av tilstanden til de 656 overvåkingseikene som ble registrert i første omløp, det gjøres en vurdering av om fjernmåling kan bidra til å forenkle overvåkingen av eikene, og det foreslås en oppfølging for både eikeovervåking og oppstart av insektovervåking.

I 2020 utløste Miljødirektoratet en opsjon, 'Pilot for overvåking av insekter knyttet til hule eiker' (jf. kontrakt inngått i 2019 og NMBU MINA fagrapport 62, 2019). Det ble besluttet å gjennomføre et pilotprosjekt for å teste ut ulike metoder for fellefangst (ulike design av feller) og artsidentifisering (DNA strekkoding versus visuell ID) av insekter. Prosjektet har samarbeidet tett med Den nasjonale insektovervåkingen. Hensikten har vært å undersøke hvordan vi (på tvers av disse to prosjektene) best kan få oversikt over insektmangfoldet på en lokalitet på en måte som er så repeterbar som mulig, samtidig som innsamlingskostnader holdes nede.

Prosjektet har vært gjennomført ved NMBU, ledet av Anne Sverdrup-Thygeson med Tone Birkemoe og Ryan Burner (feltansvarlig og rapportansvarlig) som medlemmer i prosjektgruppen. Arbeidet er gjennomført i tett kontakt med Jens Åström (NINA) og andre i det nasjonale insektovervåkingsprosjektet. Marianne Evju (NINA) har bidratt med et overordnede perspektiver på overvåking. Det er Miljødirektoratet som har finansiert arbeidet.

Ås, mars 2021

(sign.)

Anne Sverdrup-Thygeson, MINA/NMBU

Sammendrag

Nasjonal overvåking av hule eiker-prosjektet har identifisert og overvåket over 650 hule eiker (*Quercus* sp.) over hele eikeutbredelsesområdet i Norge. Disse uvanlige, men langlivede trærne gir viktige levesteder for en rekke insektarter, inkludert biller, som igjen bidrar med ulike økosystemtjenester.

Som en naturlig forlengelse av prosjektet for overvåking av eik, har vi testet metoder for å overvåke insektsamfunnene (eller bare biller) direkte, i et utvalg av disse overvåkingstrærne. Vårt forslag, beskrevet i en tidligere rapport, var å inkludere insektovervåking i en større eikeovervåking med et 6-årig omløp, men detaljene her er avhengig av budsjetter og oppdragsspesifikasjoner og er p.t. ikke avklart.

Som forberedelse til denne insektovervåkingen gjennomførte vi, etter samtaler med Miljødirektoratet, en pilotstudie i 2020. Vi utplasserte 80 vindusfeller som var forskjellige i design og tømmefrekvens for å optimalisere fangstmetoder for fremtidig overvåking. Noen feller var utstyrt med en regnvann-dreneringsmodul, designet for å forhindre regnvann i å fortynne væsken i oppsamlingsflaskene. Fellene ble tømt hver fjerde, åtte eller tolvte uke. Vi sammenlignet også visuelle (morfologi-baserte) og molekylære (DNA-baserte) metoder når det gjaldt å identifisere billeartene vi fanget. Totalt fanget disse fellene 4.699 individer som representerer 307 billetaxa, hvorav 301 ble identifisert til artsnivå (ved hjelp av morfologiske metoder).

Vi fant ut at felleutforming var viktig; vår avledningsanordning for regnvann hjalp til med å holde regnvann ute over en 4-ukers periode (men ikke lenger), men det reduserte også insektfangsten (muligens ga den insekter en sjanse til å fly ut før de falt i oppsamlingsflaskene). Tilstedeværelsen av regnvann påvirket ikke antall biller som ble funnet i en felle. Felttømmefrekvens påvirket heller ikke antall arter som ble oppdaget, men lengre perioder mellom tømmingene vil sannsynligvis resultere i nedbrytning av det DNA'et som trengs for molekylær artsidentifisering, siden vi fant at regnvann kom inn i oppsamlingsflaskene også når avledningsanordning var montert, dersom felleperioden mellom tømminger overstiger fire uker.

Som svar på disse funnene endrer vi nå felleutformingen for den kommende feltsesongen; vi justerer avledningsanordningene for vann, og legger til et større tak i fellene som ytterligere vil forhindre at regnvann kommer inn. Vi planlegger å tømme fellene hver fjerde uke til vi har bekreftet at de modifiserte fellene er effektive mht. å utelukke regnvann.

Når det gjelder sammenligningen av identifikasjonsmetoder, var det stort overlapp mellom artene som ble identifisert ved hjelp av morfologiske og molekylære metoder, men - som forventet - også noen forskjeller. Mange av disse forskjellene kan forklares med sannsynlige identifiseringsfeil i begge metoder. DNA-identifikasjonsmetoder er bare i sin spede begynnelse for norske biller og metodene vil bli forbedret i årene som kommer. Det er ønskelig å bruke begge metodene (gitt tilstrekkelig finansiering) til de har konvergert tilstrekkelig. Dersom DNA-metoder etter hvert kan gi et klart bilde av billesamfunnene, sammenlignbart med det vi får ved morfologiske metoder, kan slike metoder etter hvert benyttes alene.

Oppsummert har denne pilotstudien gitt viktig informasjon som gjør det mulig å optimalisere en langsiktig overvåkingsplan for eikelevende insekter i fremtiden. Studien har også gitt viktige innspill til metodologiske spørsmål som er relevante for det nasjonale overvåkingsprogrammet for insekter.

Summary

The National Program for Hollow Oak Monitoring (*Nasjonal overvåking av hule eiker*) has identified and monitored more than 650 hollow oaks (*Quercus sp*.) across Norway. These rare but long-lived trees provide important habitat for many insect species, including beetles, which in turn support diverse food webs and ecosystem services.

As a natural extension of the oak monitoring project, we are preparing to directly monitor the insect communities (or just beetles) within a subset of these trees. Our suggestion, described in a previous report, was to include insect monitoring in a larger oak monitoring rotation, but the details of this rotation are subject to budget issues and not yet clear.

In preparation for this effort, we conducted a pilot study in 2020 in which we deployed 80 flight intercept traps that differed in their design and emptying frequency to optimize capture methods for future monitoring. Some traps were equipped with a device designed to prevent rainwater from diluting the insect preservation liquid to test these devices, and traps were emptied every four, eight, or twelve weeks. We also compared visual (morphology-based) and molecular (DNA-based) methods for identifying the beetle species that we captured. In total these traps captured 4,699 individuals representing 307 beetle taxa, 301 of which were identified to the species level (using morphological methods).

We found that trap design was important; our rainwater diversion device did help to keep rainwater out over a four-week period (but not longer), but it also reduced capture rates (perhaps because it gave insects a chance to escape prior to falling into the collection bottles). Presence of rainwater did not affect the number of beetles that were detected in a trap. Trap emptying frequency also did not affect the number of species detected. But, longer emptying periods would likely result in degradation of the DNA that is needed for species identification using molecular methods, given that rainwater is able to enter traps even with our rainwater diversion devices when trap emptying periods exceed four weeks.

In response to these findings we are currently modifying our trap design for the upcoming field season; we are adjusting the water diversion devices and adding a larger roof to the traps that will further prevent rainwater from entering. We plan to empty the traps every four weeks until we have confirmed that the modified traps are effective at excluding rainwater.

Regarding the comparison of identification methods, there was much overlap between the species identified using morphological and molecular methods, but – as expected – also some differences. Many of these differences can be accounted for by likely identification errors (by both methods). DNA identification methods are in their infancy for Norwegian beetles and will likely continue to improve. In the meantime, we plan to use both methods in the first year of our monitoring program (given sufficient financing) and continue with these complimentary approaches until they have converged sufficiently such that DNA methods can give a clear picture of the beetle communities that is comparable to that provided by morphological methods.

In summary, this pilot study has provided us with important information that has allowed us to optimize our long-term monitoring plan. This study has also provided important input to methodological questions relevant for the National Monitoring Program for Insects, with which we have cooperated closely.

1. Introduction and background

Hollow oaks (*Quercus sp*.) provide important habitat for wood-living beetles and other taxa (Burner et al. 2021; Pilskog et al. 2020; Sverdrup-Thygeson et al. 2010), and the National Program for Hollow Oak Monitoring (*Nasjonal overvåking av hule eiker*; Fig. 1) has allowed us to estimate the total number of such trees in Norway (Sverdrup-Thygeson et al. 2013) and monitor their status through time (Hatlevoll et al. 2019). With this information now available, the plan is to initiate a formal, long-term monitoring of the insect communities themselves in a subset of these hollow oaks, as part of the National Program for Hollow Oak Monitoring. Insects have been shown to be in decline in many ecosystems (Didham et al. 2020; Sánchez-Bayo and Wyckhuys 2019), and it is important that we both establish a current baseline for Norwegian hollow oak communities and continue to monitor for changes in the future.

As part of this long-term monitoring plan, we have described a protocol for monitoring the hollow oaks and their insect communities on a four-year cycle (Hatlevoll et al. 2019). Briefly, we will select two groups of fifty trees, and the insect communities in each group will be monitored every fourth year (years two and three of the four-year cycle). In the remaining years we will monitor the 656 oak trees enrolled in the monitoring system (in subsets) to determine if they are still standing, and if their status or values have changed (Hatlevoll et al. 2019), and complete analyses and reports.

The goal of this monitoring is that we will have the ability to detect changes in insect populations and distributions. Yet monitoring insect populations in a way that is replicable, representative, and nonbiased can be challenging (Montgomery et al. 2020). One challenge is to know how much sampling effort is required, and during what period, to capture most of the species that occur in a site. Unless most of the species that occur in a tree are detected in a given season it is hard to detect changes through time. Weather poses challenges too – rainwater in particular can infiltrate traps and dilute the preservation fluid that holds the insects. Additionally, trapping protocols must be optimized to minimize labor and the associated expenses. Finally, there is the question of how to identify large numbers of specimens quickly and accurately.

In order to address these challenges and make an optimized sampling protocol for monitoring insect communities in the hollow oaks in the coming years, we conducted a controlled experiment during the summer of 2020. We conducted intensive beetle sampling (80 traps), using traps with and without a rainwater diversion device, and emptied these traps at varying intervals (4, 8, and 12 weeks) to determine how to best allocate resources. We also compared standard morphological identification of specimens with molecular (DNA-based) methods that are still in development.

In this report, we present results from this 2020 pilot study, in which we asked:

i. Do traps using a new rainwater excluding device outperform standard traps?
ii. How frequently should traps be emptied, and how long should traps be deployed each season?
iii. How do morphological and molecular methods of beetle identification compare?

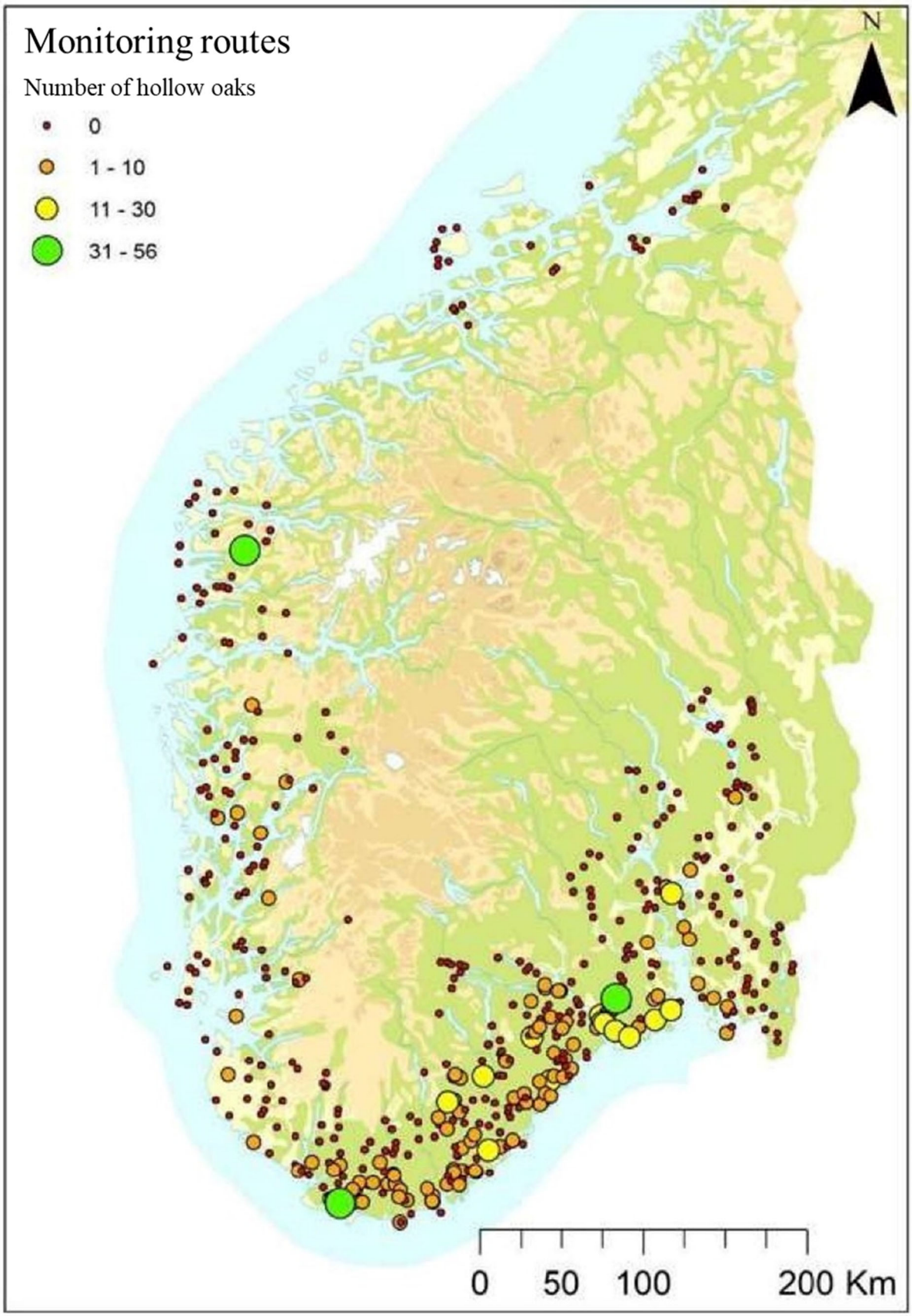

Figure 1. Hollow oak plots sampled as part of The National Program for Hollow Oak Monitoring (*Nasjonal overvåking av hule eiker*) in Norway. Red dots show plots surveyed for hollow oaks, and larger colored dots indicate presence of one or more hollow oaks within the plots. Figure modified from Hatlevoll et al. (2019).

2. Methods

2.1. Study site

We chose to conduct this pilot study in a 3.8 ha patch of mixed forest near Ås in southeastern Norway (Fig. 2) in summer 2020. This patch of forest has many large-diameter deciduous trees and was easily accessible even with COVID restrictions in place. Many large European beech (*Fagus sylvatica*) and aspen (*Populus tremula*) occur there, as well as some oaks (*Quercus spp*.). The landscape around the site is a mix of agricultural and woodlands, and it is adjacent to a grazing area for cattle and a small road. In these ways it is analogous to the habitats in which many of our hollow oaks occur.

2.2. Trap types and treatments

We developed and tested two types of flight intercept traps (Fig. 3). The traps consisted of upper and lower funnels, joined by two crossed plexiglass panes (20 x 40 cm). Flying beetles that collided with the glass panes could either fall into the funnel below, and its associated collection bottle, or climb into the container above. Both collection containers were filled with a 70:30 mixture of propylene glycol and 95% ethanol, and covered with aluminum foil to prevent UV degradation of specimens. The two trap types differed in the presence or absence of a rainwater diversion device covered with a wire mesh screen (1 mm grid). These devices help to keep rainwater from diluting the preservation fluid, but can also influence capture rates (Burner et al. 2020). We wanted to compare the effectiveness of the two trap types. The traps were painted green to blend into their surroundings.

To test the effect of the rainwater diversion devices, and determine how often traps should be emptied, we used 80 traps in our study site. These were divided into four treatments ('T1'-'T4'; Table 1). All traps were deployed through the entire sampling period (26 May to 27 August 2020). Eighty of these traps were 'Type-A' traps, with the water diversion device, and 20 were 'Type-B' traps, without the device. We emptied 20 (of 60 total) Type-A traps, as well as all 20 of the Type-B traps, every four weeks. This is because we knew from previous experience that traps without a rainwater diversion device would almost certainly fill with water, risking decay of the insects, if left longer than this. These 40 traps allowed us to determine the effects of the water diversion device on insect capture rates. For the remaining 40 Type-A traps, we emptied 20 after the first eight weeks, and again after an additional four weeks (for 12 weeks total). For the final 20 Type-A traps, we emptied them only once, after twelve weeks. Traps were placed throughout the study area in 20 clusters of four traps each (one for each treatment; see Fig. 2). Traps were spaced 2-5 m apart within a cluster, and the distance between clusters was 2 – 25 m.

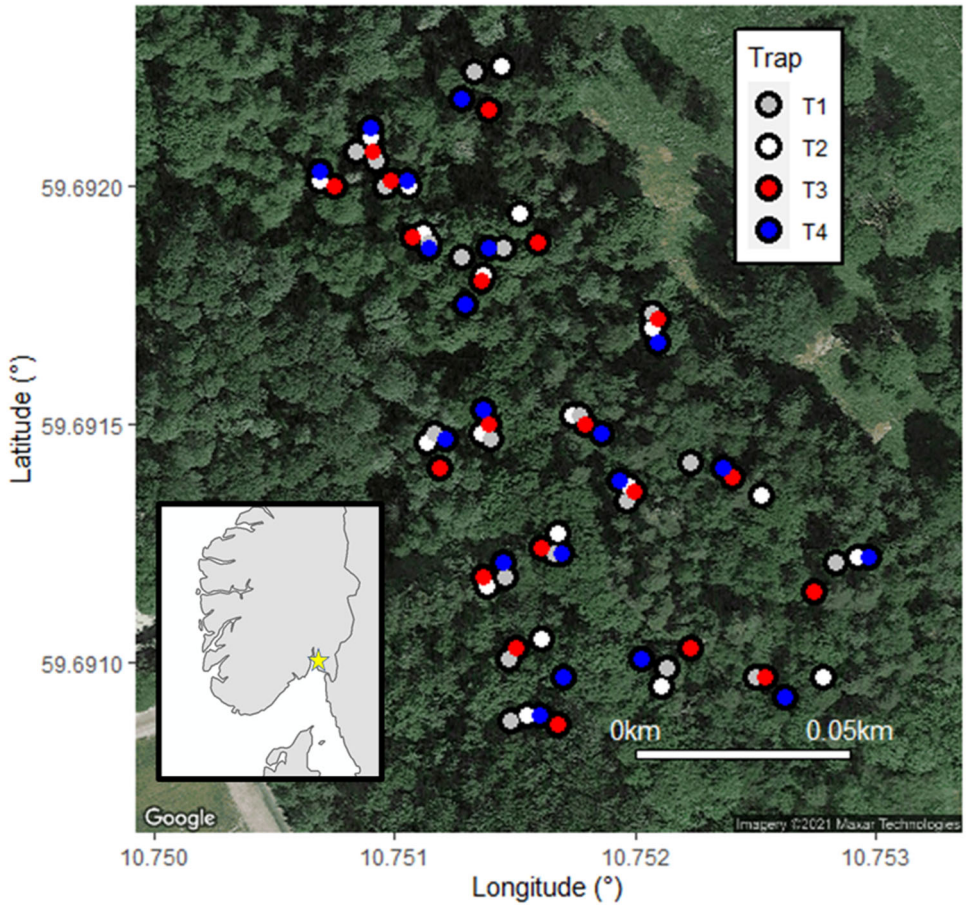

Figure 2. Map of beetle sampling locations. Inset shows location near Ås in southeastern Norway. The color of the points signifies trap treatment (see Table 1 for details).

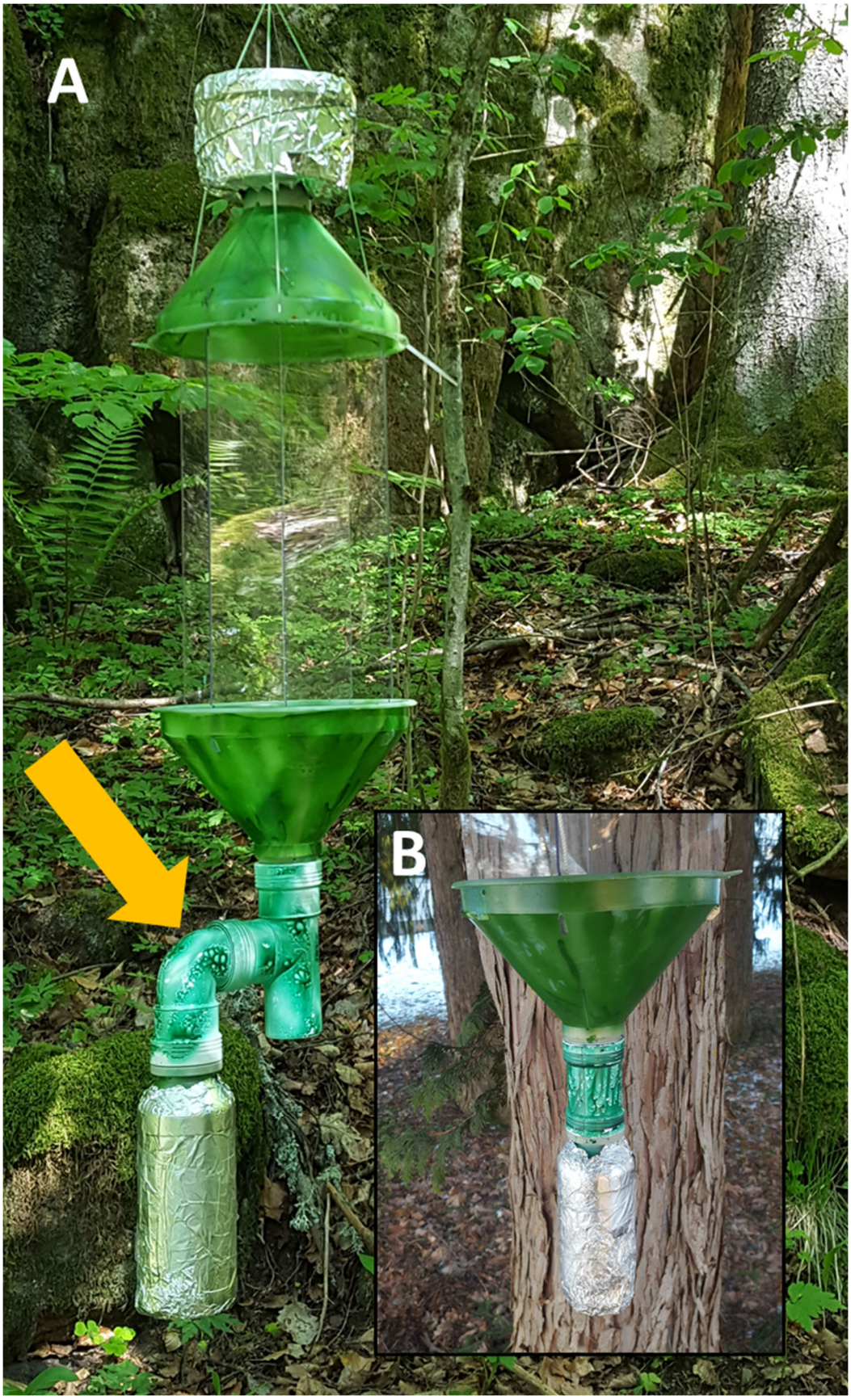

Figure 3. Trap types tested for beetle sampling in hollow oaks. Traps vary in the presence ('Type-A', left) or absence ('Type-B', inset) of a device (orange arrow) with an internal mesh screen meant to divert rainwater from the collection bottle.

Table 1. Trap treatments for a test of insect trap effectiveness in mixed forest in southeastern Norway

Treatment	Trap type	Rainwater-diversion device?	Empty interval (weeks)	Total traps (n)	Traps used for DNA identification (n)
T1	Type-A	Yes	4	20	11
T2	Type-B	No	4	20	-
T3	Type-A	Yes	8	20	-
T4	Type-A	Yes	12	20	-

2.3. Identification of beetles

All beetles were identified by an expert taxonomist (Sindre Ligaard) using morphological characteristics. Because morphological identification methods were used for all traps (as opposed to DNA methods, which were used in a small subset) the results we report from all the traps below are based on these morphological identifications. Additionally, eleven of our 20 'T1' traps (Type-A traps, emptied every 4 weeks) also had their contents identified (by NINA-Trondheim) using DNA barcoding methods. The DNA barcoding technique is known to be successful for many types or organisms (Piper et al. 2019) but is in relatively early stages of development in Norway. We used both morphological (visual) and molecular (DNA) methods on the same traps in order to compare both methods.

2.4. Analyses

To determine the relative performance of each trap and treatment type, we compared the total number of species captured in each trap type. This comparison allowed us to determine how trap type (presence vs. absence of the rainwater diversion device) and treatment (frequency of emptying) affected trap performance. Beetles captured during each of the emptying periods for each trap were merged for these analyses to estimate overall trap performance for the entire season.

To determine how long traps should be deployed each season we plotted species accumulation curves, which show the rate at which new species are detected as additional traps are added. For this we included all traps that were emptied every four weeks. This allowed us to consider the trap periods (June, July, and August) separately by examining how many species, and how many new/unique species, were captured in each trap period.

Finally, we compared the list of species that were identified using morphological and molecular methods. We conducted this comparison at the scale of the entire study (overall species pool), as well as at the scale of individual traps, to see how much agreement occurred between the two methods. All analyses were conducted in R (R Core Team 2020).

3. Results

3.1. Species detected

Our 80 flight intercept traps were successfully deployed throughout the 12-week trapping season. In total they captured 4,699 individuals representing 307 beetle taxa, 301 of which were identified to the species level (using morphological methods; Appendix 1). This is more than double the number we of species we typically detect at a single site, likely due to our large sampling effort. Among these species were two near threatened, two endangered, and one data deficient species, based on the Norwegian red list (Henriksen and Hilmo 2015). The upper collection containers on our window traps captured a few insects but almost no beetles, and so we exclude them from our analyses here.

3.2. Rainwater devices and emptying frequency

Our rainwater diversion devices were successful in reducing the amount of rainwater that entered traps when traps were emptied every four, but not eight or twelve, weeks ($p < 0.05$; Fig. 4). The number of species captured and identified (by morphological ID; we only did DNA metabarcoding on a subset of the traps that were emptied every 4 weeks) in a trap, however, was not related to the

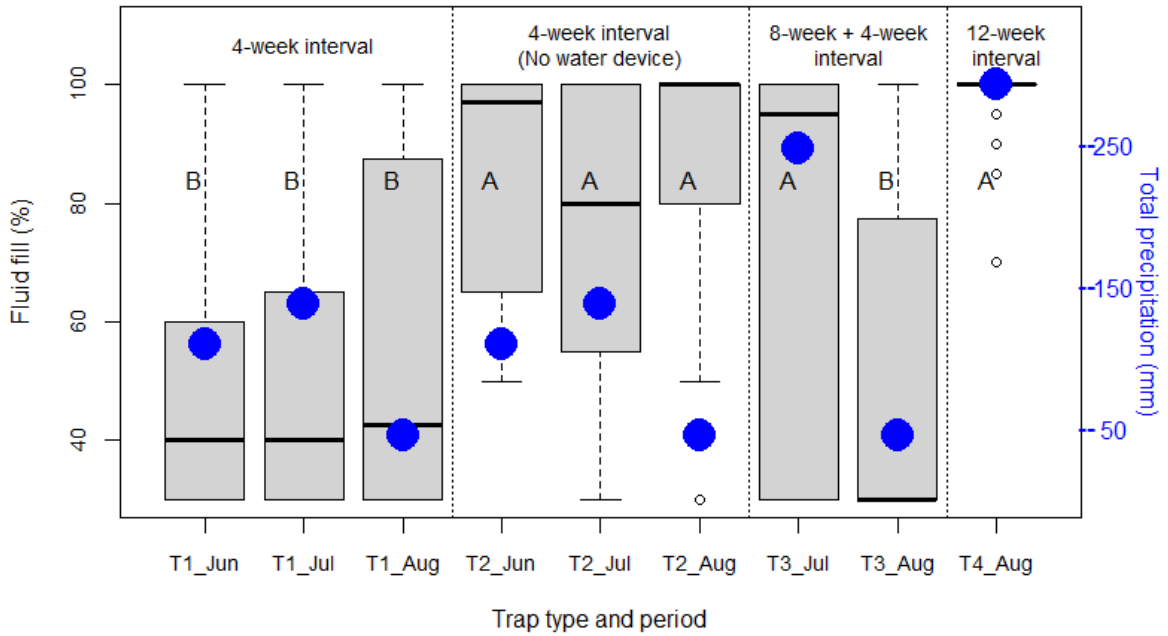

Figure 4. Capture bottle fluid % fill at time of emptying flight intercept traps. All bottles were originally filled to 30% with a mix of ethanol and propylene glycol, and additional liquid means that rainwater entered the traps. All traps were deployed for 12 weeks; text above each group of plots shows frequency of trap emptying. All treatments shown except 'T2' were equipped with a screen device meant to divert rainwater from traps. For trap treatment details see Table 1. Blue dots (scale at right) show cumulative rainfall at the study site during the trapping period for each trap; for traps deployed longer than four weeks, the precipitation values are summed monthly values for the appropriate time interval. Different letter codes (A-B) indicate statistically different fluid fill levels (based on Tukey pairwise significance test between traps, $p < 0.05$). Precipitation estimates come from the 1 km x 1 km grid cell around the trap site, based on ERA5-Land climate reanalysis (Copernicus Climate Change Service (C3S) 2017).

amount of liquid that was present (p = 0.37). The rainwater devices were effective at preventing water from entering traps when traps were emptied every four weeks, but these devices also appear to have some unintended effects of the capture rates. Traps without the device ('T2') captured more species and more individuals than any of the other trap treatments (Fig. 5). Emptying frequency (every 4, 8, or 12 weeks) did not have any effect on capture rates.

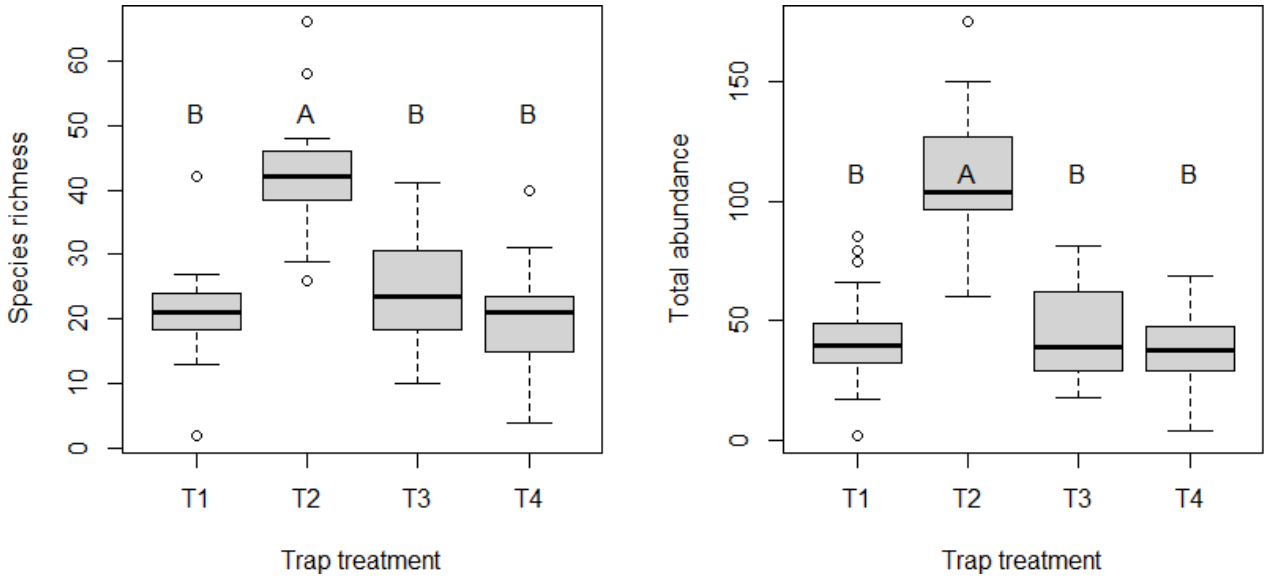

Figure 5. Species richness and total abundance of beetles captured in different trap treatments in southeastern Norway. Different letter codes (A-B) indicate statistically different capture rates (based on Tukey pairwise significance test between traps, $p < 0.01$). Trap treatment 'T2' was the only trap type that did not include a rainwater diversion device. For trap treatment details see Table 1.

3.3. Relative importance of capture periods

Traps emptied in late June (after four weeks) captured 81% of the 265 total species captured by all three of the four-week trap periods combined (T1 and T2; Fig. 6a). The July trapping period added 15% of the total species, leaving the remaining 4% of unique species to be added in August. Total numbers of species captured each month reveal a similar pattern, with a total of 1.8 and 2.9 times as many total species detected in June as in July and August, respectively (Fig. 6b).

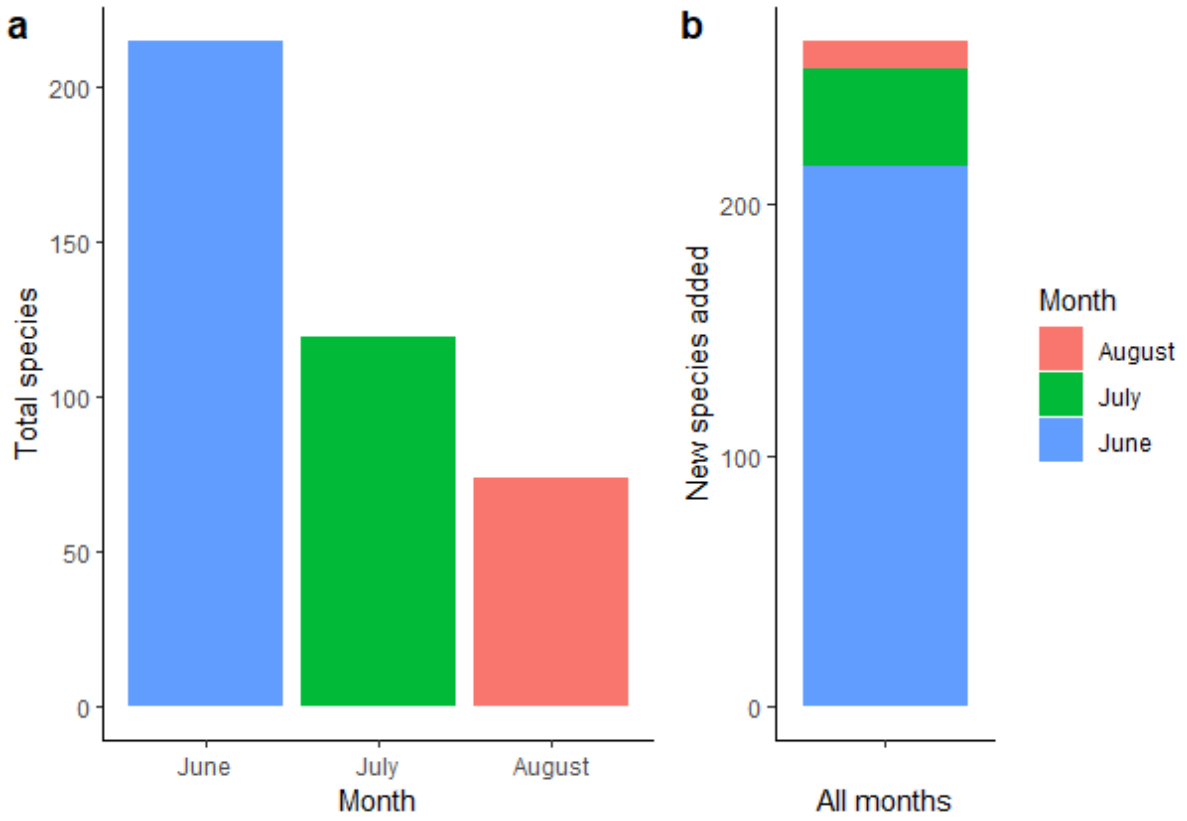

Figure 6. Number of beetle species captured by month in southeastern Norway. Forty flight intercept traps were emptied every four weeks from late May to late August. The left plot (A) show the total number of species detected in each month. The plot on the right (B) shows the number of new species added from traps emptied in June, then July, and finally August, indicating the number of new species added with each additional month.

3.4. Comparing DNA and morphological identifications

DNA identification methods detected 652 insect taxa in total (Table 2) in the 11 traps for which it was used. When considering only beetles, the only insect group that could also be identified morphologically by our taxonomist for comparison, 123 beetle species (along with about 15 additional higher-level Coleoptera taxa) were identified using DNA analyses (Appendix 2). Of these DNA-identified beetles, 77 (63%) were also detected by morphological methods in this same group of traps (Fig. 7). Of the remaining 46 species detected by DNA methods, 13 (28%) of them were detected in other traps in the study area through morphological methods (but not in the DNA traps), as were 74 (96%) of the species identified using both methods. Of 111 total beetle species identified morphologically in these same traps, DNA analyses detected 77 of them (69%) in the subset of traps used for DNA identifications.

Table 2. Insect taxa identified using molecular (DNA) methods, grouped by order.

Order	Taxa
Diptera	209
Coleoptera	138
Lepidoptera	73

Hymenoptera	50
Hemiptera	35
Orthoptera	6
Psocoptera	6
Thysanoptera	3
Trichoptera	3
Dermaptera	2
Neuroptera	2
Blattodea	1
(unknown)	124
Total	**652**

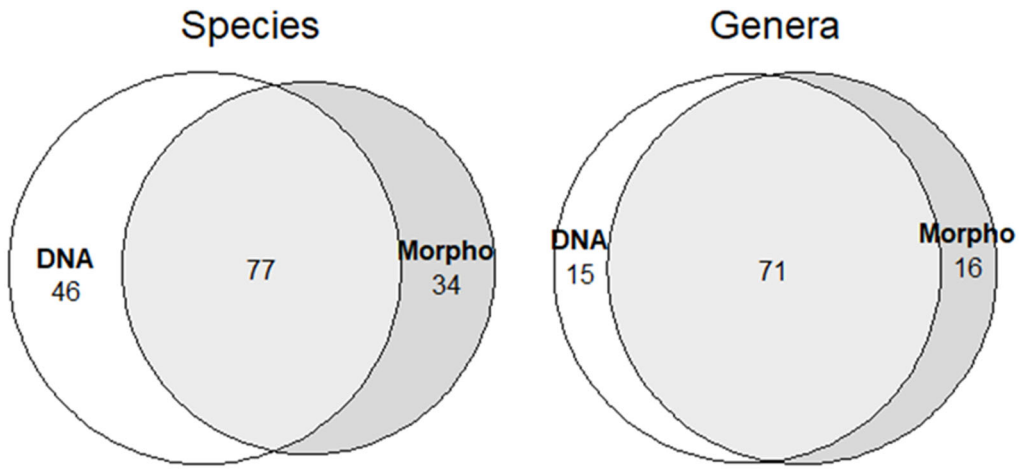

Figure 7. Overlap in beetle species (left) and genera (right) identified using DNA ('DNA') and morphological ('Morpho') methods, including the number of taxa in common between the methods. All traps (n=11) were placed in a single mixed forest stand in southeastern Norway for twelve weeks in summer 2020, and were emptied every four weeks.

If we compare on a trap by trap basis (with records from each trap split into the three trap periods), there were 416 cases of a given species being detected in a given trap by one or both methods. Of these, in 179 cases (43%) a species was detected in the same trap by both methods. In 138 cases (33%), a species was detected in a trap only by the DNA identification. In slightly fewer cases (99; 24%), a species was detected in a trap only by morphological identification.

A number of taxa were identified by DNA analyses only to the level of genus; this was true for the morphological identifications of several taxa as well. Even when DNA or morphological examinations did results in a species-level identification, there can still be uncertainty because closely related species often resemble each other, variation in taxonomy can result in unrecognized synonyms in the datasets, and DNA reference databases may at time have misidentified sequences. For this reason, it is informative to also compare all taxa at the genus level as well.

When considering genus-level identifications pooled from all the traps, 86 beetle genera were identified using DNA analyses. Of these, 71 (83%) were also detected by morphological methods in this same group of traps (Fig. 8). Of the remaining 15 genera detected by DNA methods, 9 (60%)

were detected in other traps in the study area through morphological methods (but not in the DNA traps), as were 66 (93%) of the genera identified using both methods. Of 87 genera identified morphologically in the DNA traps, DNA analyses detected 71 (82%) of them in the DNA traps.

Comparing on a trap by trap basis (again, with records split by month for each trap), we find that there were 381 cases of a given genus being detected in a given trap by one or both methods. Of these, in 192 cases (50%) a genus was detected in the same trap by both methods. In 105 cases (28%), a genus was detected in a trap only by the DNA identification. In slightly fewer cases (84; 22%), a genus was detected in a trap only by morphological identification.

4. Discussion and future plans

This pilot study gave an important information about the function of traps that may lead to a successful and consistent monitoring program of insects in hollow oaks. We found that our water diversion devices have a negative impact on capture rates, in spite of the fact that they do reduce the amount of water entering traps during a 4-week (but not 8 or 12-week) interval. This may be because insects are somehow able to land in the diversion device without falling immediately into the capture bottle, giving them an opportunity to fly out. This effect appears to be strongest for small-bodied species, which is the opposite of what we expected given that another type of flight intercept trap with a water exclusion device performs better with small species than with large ones (Burner et al. 2020). We are now adjusting the trap design to hopefully account for these challenges.

We also found that the interval at which traps are emptied does not have a large effect when using morphological identification methods. However, we know from other studies (Åström et al. 2020) that DNA can degrade when insects are left in traps for more than four weeks if the preservation liquid is diluted by rainwater. Given the negative impacts of rainwater, we are currently redesigning the rainwater devices to make it easier for insects to enter the collection bottles. We will remove the top capture containers (which caught very few insects, and almost no beetles, in this pilot study) and replace them with larger-diameter flat roofs that allow rainwater to drain outside of the trap. This should allow beetles to be captured effectively, while also preventing rainwater from entering the traps. The plan for the monitoring program is to empty traps every four weeks, but if we find that this new trap design is effective at keeping out rainwater the interval between emptying traps could be extended, saving time and effort.

Our comparison of morphological and molecular identification methods reveals both the potential of DNA-based methods as well as their current limitations. Both methods were in general agreement on the number of taxa that they detected, and there was roughly 50% overlap in the species lists from both methods. With regards to the other half of the species that each detected, however, they still produce rather different results. Most discrepancies are likely due to a few causes: misidentification of very similar species by one or both methods, identification errors of sequences in DNA barcoding databases and difficulties of identifying some species that have changed coloration as a result of the DNA extraction process. As we move into the future in which these powerful molecular methods will become more prominent, it will be important to use consistent methods from year to year. Because of this, our advice is to continue both morphological and molecular identification methods in the first years of the oak monitoring protocols, until such time as the two methods converge sufficiently to be comparable. We will also continue to contribute beetle specimens to DNA identification reference databases to facilitate method improvement.

In summary, this pilot study has provided us with important information that has allowed us to optimize a long-term monitoring plan. This study has also provided important input to methodological questions relevant for the National Monitoring Program for Insects, with which we have cooperated closely.

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Appendices

Appendix 1. List of beetle taxa detected in flight intercept traps in southeastern Norway. Species were identified by an expert taxonomist using morphological methods.

Family	Species	Red list status*	Traps occupied**	Total abundance	Present in 11 traps used for DNA ID?†	Also detected by DNA ID?
Anthribidae	*Anthribus nebulosus*	LC	1	1	-	-
Apionidae	*Betulapion simile*	LC	1	1	-	Y
Apionidae	*Protapion fulvipes*	LC	1	1	-	-
Byturidae	*Byturus ochraceus*	LC	1	1	-	-
Cantharidae	*Ancistronycha tigurina*	LC	1	1	-	-
Cantharidae	*Cantharis nigricans*	LC	2	2	-	-
Cantharidae	*Cantharis pellucida*	LC	1	1	-	-
Cantharidae	*Malthinus flaveolus*	LC	2	2	-	-
Cantharidae	*Malthodes brevicollis*	LC	1	1	-	-
Cantharidae	*Malthodes crassicornis*	LC	2	2	-	-
Cantharidae	*Malthodes fibulatus*	LC	1	1	-	Y
Cantharidae	*Malthodes flavoguttatus*	LC	2	2	Y	-
Cantharidae	*Malthodes guttifer*	LC	1	1	-	-
Cantharidae	*Malthodes minimus*	LC	2	2	-	-
Cantharidae	*Malthodes sp. hunner*	-	15	17	Y	-
Cantharidae	*Malthodes sphatifer*	LC	2	2	-	-
Cantharidae	*Podabrus alpinus*	LC	1	1	-	-
Cantharidae	*Rhagonycha lignosa*	LC	14	14	Y	Y
Cantharidae	*Rhagonycha limbata*	LC	1	1	-	-
Carabidae	*Amara familiaris*	LC	4	4	Y	-
Carabidae	*Amara similata*	LC	2	2	-	-
Carabidae	*Bembidion deletum*	LC	2	2	Y	Y
Carabidae	*Dromius fenestratus*	LC	2	2	Y	Y
Carabidae	*Elaphrus cupreus*	LC	1	1	-	-
Carabidae	*Harpalus laevipes*	LC	3	3	Y	Y
Carabidae	*Platynus assimilis*	LC	1	1	Y	-
Cerambycidae	*Alosterna tabacicolor*	LC	1	1	-	-
Cerambycidae	*Leiopus nebulosus*	LC	1	1	-	-
Cerambycidae	*Molorchus minor*	LC	14	18	Y	Y
Cerambycidae	*Oxymirus cursor*	LC	2	2	-	-
Cerambycidae	*Rhagium mordax*	LC	4	4	-	-
Cerambycidae	*Stictoleptura maculicornis*	LC	2	2	Y	Y
Cerambycidae	*Tetropium castaneum*	LC	2	2	-	-
Cerylonidae	*Cerylon fagi*	LC	9	9	Y	-
Cerylonidae	*Cerylon ferrugineum*	LC	22	30	Y	-
Cerylonidae	*Cerylon histeroides*	LC	4	4	Y	-
Chrysomelidae	*Crepidodera nitidula*	LC	4	5	-	-
Chrysomelidae	*Donacia versicolorea*	LC	1	1	-	-
Chrysomelidae	*Gonioctena quinquepunctata*	LC	1	1	-	-

Ciidae	*Cis boleti*	LC	2	2	-	-
Ciidae	*Cis dentatus*	LC	1	1	-	-
Ciidae	*Cis festivus*	LC	3	3	-	-
Ciidae	*Cis micans*	LC	3	3	-	-
Ciidae	*Cis punctulatus*	LC	3	3	-	-
Ciidae	*Ennearthron cornutum*	LC	1	1	-	-
Ciidae	*Orthocis alni*	LC	6	6	-	-
Coccinellidae	*Propylea quatuordecimpunctata*	LC	3	3	-	-
Corylophidae	*Orthoperus atomus*	LC	9	9	-	-
Corylophidae	*Sericoderus lateralis*	LC	1	1	-	-
Cryptophagidae	*Antherophagus pallens*	LC	2	2	-	-
Cryptophagidae	*Atomaria alpina*	LC	1	2	-	-
Cryptophagidae	*Atomaria atrata*	LC	2	2	-	-
Cryptophagidae	*Atomaria atricapilla*	LC	2	2	-	-
Cryptophagidae	*Atomaria fuscata*	LC	6	6	-	-
Cryptophagidae	*Atomaria longicornis*	LC	1	1	-	-
Cryptophagidae	*Atomaria nigrirostris*	LC	1	2	-	-
Cryptophagidae	*Atomaria ruficornis*	LC	4	4	-	-
Cryptophagidae	*Atomaria sp.*	-	1	2	Y	-
Cryptophagidae	*Atomaria turgida*	LC	9	9	Y	-
Cryptophagidae	*Atomaria vespertina*	LC	2	2	-	-
Cryptophagidae	*Cryptophagus dorsalis*	LC	1	1	-	-
Cryptophagidae	*Cryptophagus micaceus*	LC	27	32	Y	-
Cryptophagidae	*Cryptophagus populi*	LC	1	1	-	-
Cryptophagidae	*Cryptophagus scanicus*	LC	10	12	Y	Y
Cryptophagidae	*Cryptophagus sp.*	-	124	391	Y	-
Cryptophagidae	*Micrambe abietis*	LC	8	8	Y	Y
Cryptophagidae	*Pteryngium crenatum*	LC	2	2	-	-
Curculionidae	*Anisandrus dispar*	LC	60	173	Y	Y
Curculionidae	*Ceutorhynchus typhae*	LC	3	3	Y	-
Curculionidae	*Cryphalus abietis*	LC	6	7	Y	Y
Curculionidae	*Crypturgus cinereus*	LC	4	4	Y	Y
Curculionidae	*Crypturgus hispidulus*	LC	4	4	-	-
Curculionidae	*Dorytomus dejeanis*	LC	1	1	-	-
Curculionidae	*Dorytomus tremulae*	LC	1	1	-	-
Curculionidae	*Dryocoetes alni*	LC	3	3	-	-
Curculionidae	*Dryocoetes autographus*	LC	14	19	Y	-
Curculionidae	*Hylastes brunneus*	LC	1	1	-	-
Curculionidae	*Hylastes cunicularius*	LC	24	28	Y	Y
Curculionidae	*Hylesinus crenatus*	LC	1	1	-	-
Curculionidae	*Hylesinus varius*	LC	1	1	-	-
Curculionidae	*Hylobius excavatus*	LC	1	1	Y	Y
Curculionidae	*Ips duplicatus*	LC	1	1	-	-
Curculionidae	*Ips typographus*	LC	3	3	-	-
Curculionidae	*Magdalis duplicata*	LC	1	1	-	-
Curculionidae	*Orchestes fagi*	LC	2	2	-	-
Curculionidae	*Orchestes quercus*	LC	1	1	-	-

Curculionidae	*Otiorhynchus scaber*	LC	2	3	-	-
Curculionidae	*Otiorhynchus singularis*	LC	5	5	-	-
Curculionidae	*Phloeotribus spinulosus*	LC	1	1	-	-
Curculionidae	*Phyllobius argentatus*	LC	5	5	-	Y
Curculionidae	*Pityogenes chalcographus*	LC	3	4	-	-
Curculionidae	*Pityophthorus micrographus*	LC	2	2	-	-
Curculionidae	*Polydrusus tereticollis*	LC	1	1	-	-
Curculionidae	*Polygraphus poligraphus*	LC	4	4	-	-
Curculionidae	*Rhyncolus elongatus*	LC	1	1	Y	-
Curculionidae	*Sciaphilus asperatus*	LC	4	4	-	-
Curculionidae	*Strophosoma capitatum*	LC	6	6	Y	-
Curculionidae	*Trypodendron domesticum*	LC	8	8	-	-
Curculionidae	*Trypodendron lineatum*	LC	5	8	Y	-
Curculionidae	*Trypophloeus bispinulus*	LC	1	1	-	-
Curculionidae	*Xyleborinus saxensenii*	LC	5	6	Y	Y
Curculionidae	*Xyleborus cryptographus*	LC	2	2	-	-
Dasytidae	*Dasytes plumbeus*	LC	49	143	Y	Y
Dermestidae	*Ctesias serra*	LC	1	1	-	-
Dytiscidae	*Hydroporus memnonius*	LC	1	1	-	-
Elateridae	*Ampedus nigrinus*	LC	1	1	Y	Y
Elateridae	*Ampedus sanguineus*	LC	1	1	-	-
Elateridae	*Athous subfuscus*	LC	34	84	Y	Y
Elateridae	*Athous vittatus*	LC	24	64	Y	Y
Elateridae	*Dalopius marginatus*	LC	56	97	Y	Y
Elateridae	*Denticollis linearis*	LC	14	15	Y	Y
Elateridae	*Melanotus castanipes*	LC	38	60	Y	Y
Endomychidae	*Endomychus coccineus*	LC	1	1	-	-
Erotylidae	*Triplax aenea*	LC	3	3	-	-
Erotylidae	*Triplax rufipes*	LC	2	2	Y	Y
Erotylidae	*Triplax russica*	LC	3	3	Y	-
Eucnemidae	*Microrhagus pygmaeus*	LC	5	5	Y	Y
Histeridae	*Margarinotus striola*	LC	2	2	Y	-
Hydrophilidae	*Cercyon analis*	LC	1	1	Y	-
Hydrophilidae	*Cercyon imprerssus*	LC	2	2	Y	-
Hydrophilidae	*Cercyon lateralis*	LC	1	2	Y	Y
Hydrophilidae	*Cercyon melanocephalus*	LC	1	1	-	Y
Hydrophilidae	*Cryptopleurum minutum*	LC	2	2	-	-
Hydrophilidae	*Megasternum concinnum*	LC	5	5	Y	Y
Latridiidae	*Cartodere constricta*	LC	8	11	Y	-
Latridiidae	*Cartodere nodifer*	LC	13	14	Y	Y
Latridiidae	*Corticaria rubripes*	LC	1	1	-	-
Latridiidae	*Corticaria serrata*	LC	1	1	-	-
Latridiidae	*Corticarina parvula*	LC	1	1	-	-
Latridiidae	*Corticarina similata*	LC	58	250	Y	-
Latridiidae	*Cortinicara gibbosa*	LC	36	72	Y	Y
Latridiidae	*Enicmus planipennis*	LC	3	3	-	-
Latridiidae	*Enicmus rugosus*	LC	16	21	-	-
Latridiidae	*Enicmus testaceus*	LC	23	24	Y	-

Latridiidae	*Enicmus transversus*	LC	3	3	Y	Y
Latridiidae	*Latridius consimilis*	LC	10	13	Y	Y
Latridiidae	*Latridius hirtus*	LC	5	5	-	-
Latridiidae	*Latridius minutus*	LC	4	4	-	Y
Latridiidae	*Stephostethus alternans*	NT	1	1	-	-
Latridiidae	*Stephostethus pandellei*	LC	78	235	Y	Y
Latridiidae	*Stephostethus rugicollis*	LC	7	7	-	-
Leiodidae	*Agathidium badium*	LC	20	34	Y	Y
Leiodidae	*Agathidium confusum*	LC	5	5	Y	-
Leiodidae	*Agathidium nigripenne*	LC	42	66	Y	Y
Leiodidae	*Agathidium seminulum*	LC	10	11	Y	Y
Leiodidae	*Agathidium varians*	LC	2	2	-	-
Leiodidae	*Anisotoma humeralis*	LC	1	1	Y	Y
Leiodidae	*Anisotoma orbicularis*	LC	2	2	Y	-
Leiodidae	*Catops coracinus*	LC	1	1	-	-
Leiodidae	*Catops picipes*	LC	1	1	-	-
Lycidae	*Dictyoptera aurora*	LC	3	3	-	-
Lymexilidae	*Elateroides dermestoides*	LC	19	20	Y	Y
Melandryidae	*Abdera flexuosa*	LC	1	1	-	-
Melandryidae	*Orchesia minor*	LC	3	3	-	-
Melandryidae	*Orchesia undulata*	LC	14	14	Y	Y
Melandryidae	*Serropalpus barbatus*	LC	2	2	Y	Y
Monotomidae	*Rhizophagus bipustulatus*	LC	27	32	Y	Y
Monotomidae	*Rhizophagus cribratus*	LC	1	1	-	-
Monotomidae	*Rhizophagus fenestralis*	LC	9	10	-	-
Monotomidae	*Rhizophagus ferrugineus*	LC	1	1	-	-
Monotomidae	*Rhizophagus parallelocollis*	LC	2	2	-	-
Mycetophagidae	*Litargus connexus*	LC	4	4	-	-
Mycetophagidae	*Mycetophagus atomarius*	LC	3	4	Y	Y
Nitidulidae	*Cychramus luteus*	LC	21	27	Y	Y
Nitidulidae	*Cychramus variegatus*	LC	19	21	Y	-
Nitidulidae	*Epuraea aestiva*	LC	1	1	-	-
Nitidulidae	*Epuraea marseuli*	LC	4	4	-	-
Nitidulidae	*Epuraea melina*	LC	1	1	-	-
Nitidulidae	*Epuraea neglecta*	LC	1	1	-	-
Nitidulidae	*Epuraea placida*	LC	1	1	Y	-
Nitidulidae	*Epuraea pygmaea*	LC	23	33	Y	Y
Nitidulidae	*Epuraea rufomarginata*	LC	4	4	-	-
Nitidulidae	*Epuraea unicolor*	LC	1	1	-	-
Nitidulidae	*Glischrochilus hortensis*	LC	16	18	Y	-
Nitidulidae	*Glischrochilus quadripunctatus*	LC	11	12	Y	Y
Nitidulidae	*Ipidia quadriplagiata*	LC	6	6	Y	Y
Nitidulidae	*Meligethes aeneus*	LC	4	4	-	-
Nitidulidae	*Meligethes brunnicornis*	LC	1	1	-	-
Nitidulidae	*Meligethes nigrescens*	DD	2	2	-	-
Nitidulidae	*Meligethes ochropus*	LC	1	1	-	-
Nitidulidae	*Omosita discoidea*	LC	1	1	-	-

Nitidulidae	*Pityophagus ferrugineus*	LC	4	4	Y	-
Nitidulidae	*Pocadius ferrugineus*	LC	3	3	-	-
Nitidulidae	*Soronia grisea*	LC	3	3	-	-
Orsodacnidae	*Orsodacne cerasi*	LC	4	4	Y	Y
Ptiliidae	*Acrotrichis sp.*	-	46	103	Y	-
Ptiliidae	*Ptenidium myrmecophilum*	LC	1	1	-	-
Ptiliidae	*Ptenidium nitidum*	LC	2	2	-	Y
Ptinidae	*Anobium nitidum*	LC	3	3	-	-
Ptinidae	*Anobium rufipes*	LC	3	3	-	-
Ptinidae	*Ernobius abietinus*	LC	1	1	-	-
Ptinidae	*Ernobius mollis*	LC	1	1	-	-
Ptinidae	*Microbregma emarginatum*	EN	2	3	-	-
Ptinidae	*Ptinus subpilosus*	LC	4	4	Y	Y
Pyrochroidae	*Schizotus pectinicornis*	LC	1	1	-	-
Salpingidae	*Rabocerus foveolatus*	LC	4	4	-	-
Salpingidae	*Salpingus planirostris*	LC	94	158	Y	Y
Salpingidae	*Salpingus ruficollis*	LC	23	29	-	Y
Scarabaeidae	*Anoplotrupes stercorosus*	LC	1	1	-	-
Scarabaeidae	*Aphodius ater*	LC	17	23	Y	Y
Scarabaeidae	*Aphodius depressus*	LC	31	35	Y	Y
Scarabaeidae	*Aphodius equestris*	LC	2	2	Y	Y
Scarabaeidae	*Aphodius foetens*	LC	1	1	Y	-
Scarabaeidae	*Aphodius prodromus*	LC	1	1	-	-
Scarabaeidae	*Aphodius rufipes*	LC	51	99	Y	Y
Scarabaeidae	*Aphodius rufus*	LC	25	29	Y	Y
Scarabaeidae	*Aphodius sticticus*	EN	10	10	-	-
Scarabaeidae	*Protaetia metallica*	LC	1	1	-	-
Scarabaeidae	*Serica brunnea*	LC	35	52	Y	Y
Scirtidae	*Cyphon coarctatus*	LC	5	5	-	-
Scirtidae	*Cyphon padi*	LC	1	1	-	-
Scirtidae	*Cyphon variabilis*	LC	1	1	-	-
Scirtidae	*Elodes minuta*	LC	10	13	Y	Y
Scraptiidae	*Anaspis frontalis*	LC	1	1	-	-
Scraptiidae	*Anaspis marginicollis*	LC	1	1	-	-
Scraptiidae	*Anaspis rufilabris*	LC	12	12	Y	Y
Scraptiidae	*Anaspis thoracica*	LC	4	4	-	-
Silphidae	*Nicrophorus vespilloides*	LC	2	3	Y	Y
Silphidae	*Oiceoptoma thoracicum*	LC	2	2	-	-
Silvanidae	*Silvanoprus fagi*	LC	6	7	Y	-
Silvanidae	*Silvanus bidentatus*	LC	2	2	-	-
Sphindidae	*Aspidiphorus orbiculatus*	LC	2	2	-	-
Sphindidae	*Sphindus dubius*	LC	1	1	-	-
Staphylinidae	*Acrotona fungi*	LC	9	9	-	-
Staphylinidae	*Aleochara brevipennis*	LC	1	1	-	-
Staphylinidae	*Aleochara lanuginosa*	LC	1	1	-	-
Staphylinidae	*Aleochara sparsa*	LC	1	1	-	-
Staphylinidae	*Aleochara stichai*	LC	2	2	Y	-
Staphylinidae	*Amischa analis*	LC	7	7	Y	Y

Staphylinidae	*Anomognathus cuspidatus*	LC	7	16	-	-
Staphylinidae	*Anotylus rugosus*	LC	1	1	-	-
Staphylinidae	*Atheta incognita*	LC	1	1	Y	Y
Staphylinidae	*Atheta sp.*	-	1	1	Y	-
Staphylinidae	*Atheta vaga*	LC	19	20	Y	-
Staphylinidae	*Atrecus longiceps*	LC	1	1	Y	Y
Staphylinidae	*Autalia rivularis*	LC	1	1	-	-
Staphylinidae	*Bibloporus bicolor*	LC	14	16	-	-
Staphylinidae	*Bisnius fimetarius*	LC	4	4	-	-
Staphylinidae	*Coprophilus striatulus*	LC	1	1	-	-
Staphylinidae	*Dinaraea aequata*	LC	1	1	-	-
Staphylinidae	*Euplectus bescidicus*	LC	1	1	-	-
Staphylinidae	*Euplectus karstenii*	LC	1	1	-	-
Staphylinidae	*Euplectus mutator*	LC	1	1	-	-
Staphylinidae	*Euplectus nanus*	LC	3	3	-	-
Staphylinidae	*Euplectus punctulatus*	LC	8	12	-	-
Staphylinidae	*Eusphalerum luteum*	LC	21	36	Y	Y
Staphylinidae	*Gabrius splendidulus*	LC	7	7	Y	Y
Staphylinidae	*Gabrius trossulus*	LC	3	3	-	-
Staphylinidae	*Gyrohypnus punctulatus*	LC	1	1	-	-
Staphylinidae	*Hapalaraea pygmaea*	LC	1	1	-	-
Staphylinidae	*Haploglossa villosula*	LC	4	5	Y	Y
Staphylinidae	*Homalota plana*	LC	2	2	-	-
Staphylinidae	*Ischnoglossa prolixa*	LC	1	1	-	-
Staphylinidae	*Lathrobium sp.*	-	1	1	Y	-
Staphylinidae	*Leptusa fumida*	LC	2	2	-	-
Staphylinidae	*Leptusa pulchella*	LC	1	1	-	-
Staphylinidae	*Leptusa ruficollis*	LC	3	3	-	-
Staphylinidae	*Lesteva longoelytrata*	LC	3	3	Y	Y
Staphylinidae	*Lordithon lunulatus*	LC	1	1	-	-
Staphylinidae	*Nevraphes elongatulus*	LC	3	3	-	-
Staphylinidae	*Nudobius lentus*	LC	2	2	Y	Y
Staphylinidae	*Omalium rivulare*	LC	1	1	-	-
Staphylinidae	*Omalium rugatum*	LC	2	3	Y	Y
Staphylinidae	*Oxytelus laqueatus*	LC	2	2	Y	Y
Staphylinidae	*Philonthus addendus*	LC	1	1	-	-
Staphylinidae	*Philonthus cognatus*	LC	3	3	Y	Y
Staphylinidae	*Philonthus decorus*	LC	7	10	-	-
Staphylinidae	*Philonthus succicola*	LC	1	1	-	-
Staphylinidae	*Phloeonomus planus*	LC	2	2	-	-
Staphylinidae	*Phloeonomus pusillus*	LC	1	1	-	-
Staphylinidae	*Phloeopora corticalis*	LC	1	1	-	Y
Staphylinidae	*Phloeopora testacea*	LC	13	14	Y	-
Staphylinidae	*Phyllodrepa floralis*	LC	1	1	-	-
Staphylinidae	*Phyllodrepa melanocephala*	LC	8	8	-	-
Staphylinidae	*Placusa depressa*	LC	3	3	-	-
Staphylinidae	*Placusa tachyporoides*	LC	63	123	Y	Y
Staphylinidae	*Plataraea brunnea*	LC	6	7	-	-

Staphylinidae	*Quedius cruentus*	LC	24	34	Y	Y
Staphylinidae	*Quedius lucidulus*	LC	1	1	-	-
Staphylinidae	*Quedius maurus*	LC	1	1	-	Y
Staphylinidae	*Quedius mesomelinus*	LC	120	575	Y	Y
Staphylinidae	*Quedius scitus*	LC	3	3	-	-
Staphylinidae	*Quedius xanthopus*	LC	67	140	Y	Y
Staphylinidae	*Rugilus rufipes*	LC	2	2	-	-
Staphylinidae	*Scydmaenus hellwigii*	NT	1	1	-	-
Staphylinidae	*Sepedophilus littoreus*	LC	17	25	Y	Y
Staphylinidae	*Sepedophilus testaceus*	LC	2	3	Y	Y
Staphylinidae	*Stenichnus bicolor*	LC	5	5	-	-
Staphylinidae	*Stenichnus collaris*	LC	1	1	Y	-
Staphylinidae	*Stenichnus godarti*	LC	1	1	-	Y
Staphylinidae	*Stenus nanus*	LC	1	1	Y	-
Staphylinidae	*Stilicus rufipes*	LC	2	2	Y	Y
Staphylinidae	*Syntomium aeneum*	LC	1	1	-	-
Staphylinidae	*Tachinus laticollis*	LC	5	5	-	-
Staphylinidae	*Tachinus pallipes*	LC	3	3	-	-
Staphylinidae	*Tachinus rufipes*	LC	14	15	Y	Y
Staphylinidae	*Tachyporus chrysomelinus*	LC	5	5	Y	Y
Staphylinidae	*Tachyusa leucopus*	LC	1	1	-	-
Staphylinidae	*Tinotus morion*	LC	1	1	-	-
Staphylinidae	*Trimium brevicorne*	LC	5	5	-	-
Tenebrionidae	*Bolitophagus reticulatus*	LC	5	5	Y	-
Tenebrionidae	*Diaperis boleti*	LC	3	3	-	-
Tetratomidae	*Hallomenus binotatus*	LC	1	1	-	-
Throscidae	*Trixagus carinifrons*	LC	58	166	Y	Y
Throscidae	*Trixagus dermestoides*	LC	71	176	Y	Y
Trogossitidae	*Nemozoma elongatum*	LC	15	25	-	-
Trogossitidae	*Peltis ferruginea*	LC	2	2	-	-

* Red list status is taken from the Norwegian Red list (Henriksen and Hilmo 2015); codes include least concern (LC), near-threatened (NT), vulnerable (VU), endangered (EN), and data deficient (DD)
** Out of 180 trap empty events
† Based on morphological identification methods

Appendix 2. List of beetle taxa detected in eleven flight intercept traps in southeastern Norway. Species were identified using DNA barcoding methods.

Family	Species	Traps occupied*	Also detected morphologically (11 traps)?	Also detected morphologically (other 69 traps)?
Brentidae	*Betulapion simile*	1	-	Y
Cantharidae	*Malthinus punctatus*	2	-	-
Cantharidae	*Malthodes fibulatus*	1	-	Y
Cantharidae	*Malthodes mysticus*	2	-	-
Cantharidae	*Malthodes spathifer*	2	-	-
Cantharidae	*Rhagonycha fulva*	1	-	-
Cantharidae	*Rhagonycha lignosa*	3	Y	Y
Carabidae	*Bembidion deletum*	1	Y	Y
Carabidae	*Dromius fenestratus*	1	Y	Y
Carabidae	*Harpalus laevipes*	1	Y	Y
Cerambycidae	*Molorchus minor*	4	Y	Y
Cerambycidae	*Rusticoclytus rusticus*	5	-	-
Cerambycidae	*Stictoleptura maculicornis*	1	Y	Y
Chrysomelidae	*Callosobruchus sp. 1*	8	-	-
Chrysomelidae	*Crepidodera aurata*	1	-	-
Chrysomelidae	*Longitarsus jacobaeae*	2	-	-
Chrysomelidae	*Longitarsus succineus*	2	-	-
Ciidae	*Cis castaneus*	1	-	Y
Coccinellidae	*Adalia decempunctata*	2	-	-
Coccinellidae	*Halyzia sedecimguttata*	2	-	-
Corylophidae	*Orthoperus sp. 1*	1	-	-
Corylophidae	*Orthoperus punctatus*	1	-	-
Cryptophagidae	*Cryptophagus dentatus*	8	-	-
Cryptophagidae	*Cryptophagus pilosus*	2	-	-
Cryptophagidae	*Cryptophagus pubescens*	1	-	-
Cryptophagidae	*Cryptophagus scanicus*	3	Y	Y
Cryptophagidae	*Micrambe abietis*	2	Y	Y
Cryptophagidae	*Micrambe villosus*	1	-	-
Curculionidae	*Anisandrus dispar*	7	Y	Y
Curculionidae	*Cryphalus abietis*	1	Y	Y
Curculionidae	*Crypturgus cinereus*	1	Y	Y
Curculionidae	*Crypturgus subcribrosus*	1	-	-
Curculionidae	*Hylastes cunicularius*	1	Y	Y
Curculionidae	*Hylobius sp. 1*	1	-	-
Curculionidae	*Hylobius excavatus*	1	Y	Y
Curculionidae	*Phyllobius argentatus*	1	-	Y
Curculionidae	*Strophosoma fulvicorne*	4	-	-
Curculionidae	*Xyleborinus saxensenii*	2	Y	Y
Elateridae	*Ampedus sp. 1*	1	-	-
Elateridae	*Ampedus sp. 12*	1	-	-
Elateridae	*Ampedus sp. 3*	1	-	-

Elateridae	*Ampedus nigrinus*	1	Y	Y
Elateridae	*Athous subfuscus*	3	Y	Y
Elateridae	*Athous vittatus*	2	Y	Y
Elateridae	*Dalopius marginatus*	7	Y	Y
Elateridae	*Denticollis linearis*	2	Y	Y
Elateridae	*Melanotus castanipes*	7	Y	Y
Erotylidae	*Triplax rufipes*	1	Y	Y
Eucnemidae	*Microrhagus pygmaeus*	1	Y	Y
Hydrophilidae	*Cercyon lateralis*	1	Y	Y
Hydrophilidae	*Cercyon melanocephalus*	1	-	Y
Hydrophilidae	*Megasternum concinnum*	2	Y	Y
Latridiidae	*Cartodere nodifer*	2	Y	Y
Latridiidae	*Cortinicara gibbosa*	4	Y	Y
Latridiidae	*Enicmus transversus*	2	Y	Y
Latridiidae	*Latridius consimilis*	1	Y	Y
Latridiidae	*Latridius minutus*	1	-	Y
Latridiidae	*Stephostethus pandellei*	2	Y	Y
Leiodidae	*Agathidium badium*	3	Y	Y
Leiodidae	*Agathidium nigripenne*	8	Y	Y
Leiodidae	*Agathidium seminulum*	1	Y	Y
Leiodidae	*Anisotoma humeralis*	1	Y	Y
Lymexylidae	*Elateroides dermestoides*	1	Y	Y
Melandryidae	*Orchesia undulata*	3	Y	Y
Melandryidae	*Serropalpus barbatus*	9	Y	Y
Melyridae	*Dasytes sp. 1*	4	-	-
Melyridae	*Dasytes sp. 2*	1	-	-
Melyridae	*Dasytes plumbeus*	5	Y	Y
Monotomidae	*Rhizophagus bipustulatus*	2	Y	Y
Mycetophagidae	*Mycetophagus atomarius*	1	Y	Y
Nitidulidae	*Cychramus luteus*	3	Y	Y
Nitidulidae	*Epuraea pygmaea*	1	Y	Y
Nitidulidae	*Epuraea silacea*	1	-	-
Nitidulidae	*Glischrochilus quadripunctatus*	1	Y	Y
Nitidulidae	*Ipidia quadriplagiata*	1	Y	Y
Orsodacnidae	*Orsodacne cerasi*	2	Y	Y
Ptiliidae	*Acrotrichis intermedia*	1	-	-
Ptiliidae	*Ptenidium nitidum*	1	-	Y
Ptinidae	*Ptinus subpilosus*	1	Y	Y
Salpingidae	*Salpingus planirostris*	11	Y	Y
Salpingidae	*Salpingus ruficollis*	1	-	Y
Scarabaeidae	*Aphodius ater*	3	Y	Y
Scarabaeidae	*Aphodius depressus*	5	Y	Y
Scarabaeidae	*Aphodius equestris*	2	Y	Y
Scarabaeidae	*Aphodius rufipes*	5	Y	Y
Scarabaeidae	*Aphodius rufus*	1	Y	Y
Scarabaeidae	*Serica brunnea*	8	Y	Y
Scirtidae	*Contacyphon phragmiteticola*	1	-	-
Scirtidae	*Elodes elongata*	1	-	-

Scirtidae	*Elodes minuta*	3	Y	Y
Scraptiidae	*Anaspis rufilabris*	2	Y	Y
Scydmaenidae	*Stenichnus godarti*	1	-	Y
Silphidae	*Nicrophorus vespilloides*	2	Y	Y
Staphylinidae	*Amischa analis*	1	Y	Y
Staphylinidae	*Atheta incognita*	1	Y	Y
Staphylinidae	*Atheta ravilla*	1	-	-
Staphylinidae	*Atrecus longiceps*	1	Y	Y
Staphylinidae	*Eusphalerum luteum*	4	Y	Y
Staphylinidae	*Gabrius splendidulus*	1	Y	Y
Staphylinidae	*Haploglossa villosula*	1	Y	Y
Staphylinidae	*Lesteva longoelytrata*	1	Y	Y
Staphylinidae	*Nudobius lentus*	1	Y	Y
Staphylinidae	*Omalium rugatum*	1	Y	Y
Staphylinidae	*Oxytelus sp. 1*	1	-	-
Staphylinidae	*Oxytelus laqueatus*	1	Y	Y
Staphylinidae	*Philonthus cognatus*	1	Y	Y
Staphylinidae	*Phloeopora corticalis*	1	-	Y
Staphylinidae	*Placusa tachyporoides*	9	Y	Y
Staphylinidae	*Quedius cruentus*	2	Y	Y
Staphylinidae	*Quedius maurus*	1	-	Y
Staphylinidae	*Quedius mesomelinus*	17	Y	Y
Staphylinidae	*Quedius xanthopus*	9	Y	Y
Staphylinidae	*Sepedophilus littoreus*	3	Y	Y
Staphylinidae	*Sepedophilus testaceus*	2	Y	Y
Staphylinidae	*Stilicus rufipes*	1	Y	Y
Staphylinidae	*Tachinus rufipes*	4	Y	Y
Staphylinidae	*Tachyporus chrysomelinus*	1	Y	Y
Staphylinidae	*Tetartopeus terminatus*	1	-	-
Tenebrionidae	*Uloma rufa*	5	-	-
Throscidae	*Trixagus carinifrons*	4	Y	Y
Throscidae	*Trixagus dermestoides*	15	Y	Y
Throscidae	*Trixagus leseigneuri*	19	-	-
Throscidae	*Trixagus meybohmi*	4	-	-

* Out of 33 trap-month combinations (11 traps, emptied three times each), based on DNA analysis