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Do insect fungivores that visit polypore cafes aid sporedispersal?

Kristian Seres

Master of biology
Department of plant science

Preface

First I would like to thank my supervisors Tone Birkemoe and Anne Sverdrup-Thygeson for their encouragement and support in my work. I would also like to thank Marius Saunders and Martin Paliocha for help and support with the text. Lastly I would also like to thank my family for being patient and supporting during this hectic year.

This master thesis has been a journey into the exciting world of fungal ecology, and I am very grateful for having the opportunity to write about this topic.

Abstract

Dispersal of wood-decaying fungi has been well studied, but the importance of insects for the dispersal of spores are less documented. In this study I sampled beetles from red belt conk, tinder fungus and aspen bracket by sampling beetles from sporocarps. Several studies have been done on red belt conk and tinder fungus, but not on aspen bracket. Here, I present some species found on aspen bracket that has not been reported previously. My aim was to find out if the beetle community associated with the polypores were host specific, and if they could potentially be good dispersers of spores.

There were unique beetle communities connected to the polypores, and there was an overlap between beetles sampled from conifer and deciduous trees.

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1 Introduction

1.1 Background

The boreal conifer forest of the northern hemisphere is the world's biggest land-based biome, and consists mostly of slow-growing tree species and is characterized by a slow turnover in nutrient cycles. The boreal forest make out a belt that covers most of inland Norway, Sweden and Finland, most of Russia and northern parts of Mongolia, Kazakhstan and Japan, and over to Alaska and Canada. These forests represent diverse ecosystems that harbor many groups of forest-dwelling organisms that are interlinked through several trophic levels. Most of the boreal forest consist of Norwegian spruce (*Picea abies*) and pine (*Pinus sylvestris*), with scattered elements of deciduous trees like birch (*Betula spp.*), goat willow (*Salix caprea*), aspen (*Populus tremula*) and rowan (*Sorbus aucuparia*).

The forest has offered many resources for the human society through history, and it is an important contributor to ecosystem services like e.g. clean air (Escobedo et al., 2011), timber, biofuel (Whalen et al., 2017) and pollination (Potts et al., 2016). Forests and other natural systems contribute widely to ecosystem services on a global scale, and have been valued to be around \$125 trillion/year (Costanza et al., 2014). Many of the forest dwelling species that are under anthropogenic pressure are also important contributors to ecosystem functions and produce services like decomposition of dead wood (Ulyshen, 2016), circulation of nutrients (Manning et al., 2016) and carbon sequestration (Clemmensen et al., 2015).

In Norway, 38% of the land area is covered by forest (12 mill. ha), and out of that, 58% is conifer-dominated forest (Stokland et al., 2014). Most threats to biodiversity in Norwegian forests are anthropogenic causes like land-use change, which represent the main threat for most of the species in the Norwegian Red List of species.

It is important to preserve biodiversity and mitigate species loss to maintain ecosystem function. Many species are not yet fully understood as to what function they may have in the specific ecosystem they are part in. Ecosystem function will not collapse if we lose a certain amount of species, but the consequences if we exceed the threshold in rate of species loss is difficult to predict. Today, there are many global and national initiatives to protect nature and biodiversity, and Norway has committed to several, like the international Convention on Biological Diversity, and national regulations like "Naturmangfoldloven"

Besides anthropogenic disturbances, there are other factors that are not as easy to mitigate. Global change and more extreme variations in climate are other factors that affect species in forest ecosystems (Mina et al., 2017), and has been shown to affect fungal ecology including community composition, fruiting phenology, sporocarp production and dispersal (Andrew et al., 2016). Recent papers like Boddy et al. (2014) and Andrew et al. (2018) has shown that onset and ending of fruiting season are related to geographical location and local bioclimatic factors like mean temperature and precipitation. For example, Kauserud et al. (2012) analyzed

486 autumn fruiting species in Norway, Austria, Switzerland and the United Kingdom, and found that mean annual day of fruiting had become later in all the countries, but interspecific variation in phenological responses was high. Also, some species that are adapted to certain temperature zones are forced to elevate their range as temperatures in lowland areas are becoming less favorable. This change in sporulation time in some fungi may force other species that depend on spores in some way to adapt to these new trends. This could imply a mismatch between sporulation time and flight period in some saproxylic beetles that rely on a provision of spores at a certain time of the season. For the fungi, this means they will miss out the chance to hitchhike to new dead wood with those species.

According to the Norwegian Red List for species 2015, 1122 species (48%) are partly or completely connected to a forest environment. The biggest contributors are fungi (353 species), beetles (230 species), flies (128 species) and lichens (124 species) (Henriksen and Hilmo, 2015). Many of these are highly specialized to different ecological niches like dead wood which we find in old growth forests. Several species benefit on dead wood, the fungi attracts insects that feed on them, and the insects are themselves food for vertebrates like woodpeckers, making it a complex and diverse food web. The amount of dead wood has increased in Norway by almost 50% the last 30 years (Storaunet and Rolstad, 2015), and a result of this has been that some wood dependent species benefited from the increased amounts of habitats, and therefore went out of the Red List of species..

Trees are photosynthetic active organisms that collect energy from sunlight and store it as carbohydrate molecules such as sugars, making them represent a valuable resource for other organisms. However, there are more living cells in a decomposing tree than in a living standing tree. When trees die and eventually fall over, new habitats are made available for several communities of wood-decaying species which all take part in the succession of decomposing the material. The forest decomposers are dependent on a continually supply of new dead wood, not only as a source of food, but also for cover, reproduction (Grotsky et al., 2018) and hibernation. But these resources that newly dead wood offer may be hard to access since they are chemically bounded up and protected by the trees defense system. Different wood-decomposing fungi alter these chemical substances, making them more biological accessible to other species. Compared with undecayed wood, fungal mycelium contains more phosphate and nitrogen relative to carbon, but when the wood is decayed, the nutritional values of the substrate increases (Birkemoe et al., 2018). Similarly, Filipiak et al. (2016) found that concentrations of essential elements such as K, Na, Mg, Zn and Cu in the substrate increased with the rate of wood decay. This shows that addition of mycelium from wood decaying fungi as a supplemental food source is favorable for the development of saproxylic beetles.

The polypores are big consumers of dead wood but some specialists may have very specific requirements to the substrate, like diameter, tree species or succession stage (Berglund et al., 2011), which in turn may be scarce in the habitat. Likewise, specialist species of saproxylic beetles may therefore also be restricted to specific substrates which can be ephemeral at large scales (Jacobsen et al., 2015), which implies longer travel distances to find it. This shows that availability of dead wood in different decay stages is important for biodiversity in forest ecosystems. The supply of coarse woody debris (CWD) is usually provided by some kind of stochastic disturbance in the forest structure. Disturbances can be caused by either abiotic weather-related incidents like storm, flood, drought or fire, or it could be a biotic agent like bark beetles (Marini et al., 2017) or emerald ash borer (Savage and Rieske, 2018) that carry fungal symbionts (Persson et al., 2011) which can attack and kill trees. Disturbances create

patchy structures with gaps in the forest canopy which offers more ecological niches than a monoculture forest, thereby supporting a higher biodiversity of dead-wood dependent species. Retaining dead wood, and so-called woodland key-habitats (Ylisirniö et al., 2016) when managing forests, is therefore some of several factors to include when preserving species richness and forest ecosystem function (Lassauce et al., 2011).

1.2 Dispersal of saproxylic fungi and beetles

Dispersal is a key component in community ecology, and affects species response to environmental change and habitat fragmentation (Jacobsen et al., 2017). Understanding these mechanisms is important in order to preserve ecosystem function and biodiversity in light of the increasing rates of habitat loss worldwide. We can distinguish the main types of movement between active dispersers that generates their own force for the movement, and passive dispersers that relies on an environmental vector like wind or water for movement. Beetles are capable of moving by themselves but polypores are dependent on environmental factors like wind or water currents, hence the polypores may benefit from hitchhiking with the beetles when they seek out newly dead wood to lay their eggs in. Saproxylic fungi have diverse ecology, and their dispersal mode have been assumed to be primarily by air-borne spores (Norros, 2013). However, some species are known to be dispersed also by bark beetles, ambrosia beetles (Scolytinae), ship-timber beetles (Lymexilidea) and wood wasps (Siricidae) (Birkemoe et al., 2018). The biggest difference from randomly dispersing with wind is that an insect-vector allows the fungi to target the dispersal to their preferred substrate. This interaction may benefit the fungi, and make it more robust to habitat fragmentation, as long as the vectors are present in the habitat.

Many of the forest dwelling beetles are saproxylic, which means that they are dependent on dead wood in at least one part of their lifecycle, usually the larvae stage. The beetles can be either obligate or facultative saproxylic reflecting their dependence on dead wood. Some saproxylic beetles are also predators that hunt other invertebrates that feed on the sporocarps and inside the spore tubes, while others are fungivorous that feed on mycelia, fruiting bodies or spores. These beetles utilize sporocarps as a breeding place in addition to feeding on the fungi or locate potential prey (Stokland et al., 2012). Analysis of the gut content from three species of saproxylic beetle larvae by PŘIKRYL et al. (2012) actually showed that feeding-guild changed from fungivory to predatory with increased body size. Since many perennial sporocarps are persistent long after their death, some species, for example the family Ciidae, can live for several generations inside these sporocarps before they are completely decomposed.

Saproxylic insects in forest ecosystems are dependent on several factors to be able to disperse and colonize new habitats. Forest landscapes are often fragmented, and in order to disperse over distances, a source population often uses habitat patches or corridors in the forest structure as steppingstones to reach new habitats. This dispersal between populations secures gene flow between populations and prevents bottle-necks or isolation-by-distance to occur.

A recent review paper on dispersal ecology of saproxylic insects by (Komonen and Müller, 2018), found that there are systematic differences in the dispersal abilities of species among ecological groups. For example, they found that the best dispersers are pioneer species such as cerambycids and bark-beetles rather than species associated with wood in later decay-stages.

So, if these pioneer beetles were to get spores from early colonizing fungi attached to their bodies, the fungi may be able to actively target suitable habitats at long distances. In order to make good predictions on insect dispersal, different study methodology like mark-recapture, telemetry, flight mill, genetic differentiation of populations and field experiments are used in combination.

Most polypores are saprotrophs and basidiomycetes and they utilise dead wood as a food source. The hyphae of the fungi grow inside the dead wood, and only the spore producing fruit bodies are visible on the outside. Some polypores are perennial with a hard persistent structure, while others are annual with soft tissue. They are all sessile in which they are bound to a substrate that can either be a trunk, stump or a branch. Since they cannot really move around, once settled, the fungi colonizes and exploits a certain volume of the dead wood. Inside the trunk there can be mycelium from several different fungi present forming populations that change through the decay stages.

The spores of polypore fungi are produced and are situated along the inner wall of hundreds of narrow tubes that make out the hymenium surface. When the spores are mature, and the right environmental conditions are at place, the fungi will release its spores. There are basically three ways the spores are dispersed, and the most common for all fungi is turbulent air that allows wind dispersal, secondly comes dispersal with the help of animals and finally precipitation where the spores are taken with water droplets and carried away (Halbwachs and Bässler, 2015). In addition, when a log has sufficient contact with the forest floor, some polypores are able to perform terrestrial dispersion through mycelial cords (Boddy and Jones, 2008).

The most critical phases of polypore dispersal involve establishment and colonisation of a new suitable substrate which can be ephemeral in both space and time. When a spore lands on a suitable surface, it has to germinate and establish a mycelium. Since the nutritional content of the spore itself is relatively low, the growing mycelium has to quickly acquire additional nutrients through decomposing the surrounding wood. However, this process of establishment is highly dependent on a range of local environmental factors like water content in the wood, temperature and light exposure and presence of other fungi and fungal grazers. The probability of success increases if the fungi can reach the new substrate at an early stage before other species have the chance to colonise it. The best way the fungi can accomplish this is by hitchhiking with early colonizing species.

1.3 Previous research on interactions between saproxylic fungi and beetles

Insects that are capable of dispersing fungal propagules to dead wood through more or less mutualistic interactions are known from several studies (Birkemoe et al., 2018). Recent studies have shown that this may also occur in non-mutualistic relationships.

Jacobsen et al. (2017) did a study where they tested if wood-inhabiting insect species could function as vectors of dispersal for non-mutualistic fungi. They sampled beetles directly from aspen logs or from sticky traps and then rinsed them in sterilized water to separate fungal DNA from their exoskeleton. From 343 beetle individuals, fungal DNA was sampled from 55% of them, where ascomycetes and basidiomycetes constituted 77% and 20% respectively of the sequences. Included here were wood-decaying fungi like red belt conk, tinder fungus and turkey tail. Scanning electron microscopy also revealed that some individuals carried yeast cells, spores and hyphae attached to their exoskeletons. They also found that the fungal

composition was influenced by different beetle genera. This study showed that some wood-inhabiting insects can transfer fungal material to recently dead wood, hence the wood-decaying fungi may benefit from targeted animal-mediated dispersal.

Many studies have been published on interactions between forest dwelling beetles and perennial polypores in boreal forests, and especially the north European countries. Several different methodologies have been used, like free-hanging window traps or trunk-window traps pitfall traps (Milberg et al., 2014), polypore-baited traps (Jonsell and Nordlander, 1995), rearing of dead and living sporocarps, hand collecting from dead (Hågvar and Steen, 2013) and living sporocarps. Some of the polypores in my study have been thoroughly examined before, like the red belt conk and tinder fungus, but only a few on aspen bracket. Several studies like Hågvar and Økland (1997) and Jacobsen et al. (2017) have proposed that there is a positive relationship between saproxylic beetles and decomposing polypore species with regards to spore distribution.

1.4 Research objective

Dispersal of organisms is pronounced in different ways, and is an important phase in nearly all species community dynamics. Wood-decaying fungi and wind-dispersed plants may both be constrained by abiotic factors like loss of wind or habitat fragmentation. However, positive interactions with other species from different trophic levels have been frequently observed. The objective of my thesis was to investigate the relationship between the spore-producing hymenium area of the polypores and the abundance and diversity of saproxylic beetle species found on the surface of the sporocarps.

With my study, I wanted to find out if the saproxylic beetles collected from the sporocarps could potentially be good spore-dispersers for perennial wood-decaying fungi.

Secondly, I wanted to find out if the saproxylic beetles collected in my study were host specific in the sense that they tend to feed on, and share host-tree preference with the polypore species they were collected from. If the beetles have their larval stage in the same tree species as the fungi grow on, they will transfer spores to a preferable substrate for the fungi. And if the tree has recently died, chances are there are no other fungi present and probability for successful colonization increases for the fungi.

Thirdly, I wanted to find out if there were specific faunas of beetles related to the three polypores in my study, and if so, I wanted to know if these faunas are found in other parts of the boreal forest. Finally, I wanted to find out if the abundance and species richness of beetles collected from polypores change through the season.

Therefor I present the following research questions:

- i) How does the spore producing area of a polypore relate to the abundance and species richness of saproxylic beetles visiting that polypore?
- ii) Are the beetles that visit the polypores host-tree specific? Will e.g. beetles that utilize one specific tree species as their breeding habitat be found feeding on polypores on the same tree species?
- iii) Are there specific beetle communities related to the polypore species in my study?
- iv) Do the abundance and species richness of beetles differ through the season?

2 Materials and Methods

2.1 Research design

The objective of my fieldwork was to collect adult beetles from the polypore surface through a summer season. Before the fieldwork started, I visited many areas to find suitable study sites. I wanted to find polypores that mainly grow on one specific tree species and one that grows on both conifer and deciduous trees.

The site had to have a high density of coarse woody debris (CWD) and the chosen polypore, and it had to be located within a maximum driving range of about half-hour from Ås centrum in order to keep a reasonable timeframe. I also put a limit on 30 minutes walking distance from the parking place.

Some of the study sites were divided in sub-patches, with about 5-10 minutes walking distance between them. This was done in order to get a sufficient number of the selected polypore in close proximity.

Fieldwork was conducted in four different sites situated southeast of Oslo. Each site included between 5 – 10 logs or stumps, containing between 2 – 13 sporocarps each.

In total, I sampled 175 sporocarps during the season, and the highest amount of sporocarps belonged to red belt conk with 44% of the sporocarps, tinder fungus had 30% of the sporocarps and aspen bracket had 26% of the sporocarps (Table 2.1). Due to difficulties in finding enough sporocarps from each species at each site, the sampling numbers were uneven and are not directly comparable.

Table 2.1 shows numbers of logs and stumps from each tree category and numbers of sporocarps sampled from them at the different study sites. (Tree categories: CON=conifers, DEC=deciduous)

	Dølerud		Nordre Pollen		Vardåsen		Eldor		SUM
	Substrate	Sporocarps	Substrate	Sporocarps	Substrate	Sporocarps	Substrate	Sporocarps	Sporocarps
Red belt conk	CON log: 0 CON stump: 2 DEC stump: 2	0 13 4	CON log: 1 CON stump: 5	5 21			CON log: 1 CON stump: 4	9 25	14 59 4
Tinder fungus	DEC log: 4 DEC stump: 0	34 0	DEC log: 1 DEC stump: 3	2 17					36 17
Aspen bracket	DEC stump: 1	3			DEC log: 2 DEC stump: 4	18 24			21 24
SUM	CON log: 0 CON stump: 2 DEC log: 4 DEC stump: 3	0 13 34 7	CON log: 1 CON stump: 5 DEC log: 1 DEC stump: 3	5 21 2 17	CON log: 0 CON stump: 0 DEC log: 2 DEC stump: 4	0 0 18 24	CON log: 1 CON stump: 4 DEC log: DEC stump:	9 25 0 0	14 59 54 48

Sampling was usually done between 10:00 and 22:00, and consequently light conditions varied throughout the season, but flashlights were used when necessary. I avoided collecting during days with rainy and windy condition, since I assumed the beetles avoided this weather for flight. Collecting during night was not done due to practical reasons.

The sites Dølerud and Vardåsen were surveyed eight times and Eldor and Nordre Pollen seven times. I followed the same path each time, in order to have a good routine. I chose to

sample beetles only from living sporocarps which grew on both fallen logs and stumps, but there had to be a minimum distance of 10 cm between the polypore and the forest floor in order to make visual inspection and collection possible

2.2 Study areas

The four study sites were a mix of old and young managed forests and nature reserves, and varied in tree species composition and age classes. Also sun exposure varied since some of the logs were situated in canyons with lots of shade, while others were in more open forest. All the sites had large amounts of dead wood in different decay stages, but differed in vegetation. Some areas were dominated by tall grass and herbaceous plants, while others were dominated by low growing shrubs like bilberry (*Vaccinium myrtillus*), lingonberry (*Vaccinium vitis-idaea*) and heather (*Calluna vulgaris*). The bedrock at the sites is similar, and consists mostly of gneiss which is most common in this part of the country.

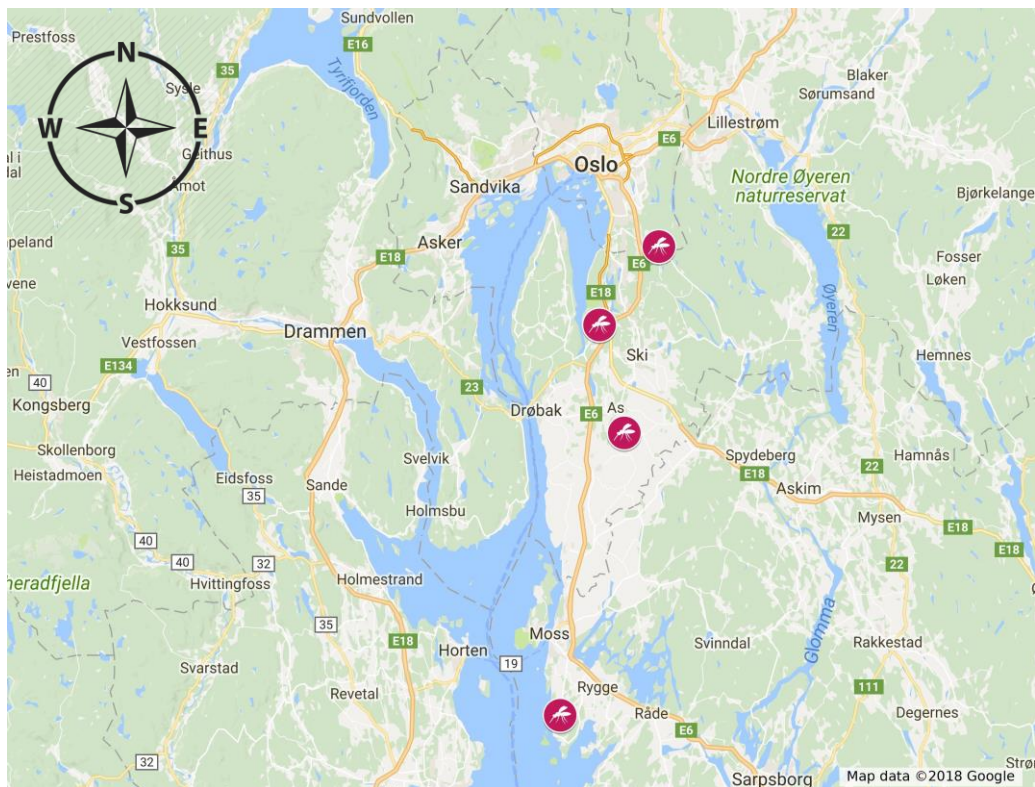


Figure 2.1 Map showing locations of the four study sites. From the top: Dølerud, Nordre Pollen, Eldor and Vardåsen.

Dølerud

The first site was situated in “Spinneren friluftslivområde” (Lat. 59.83, Long. 10.88, 190-270 masl.) which was preserved in 2013 (Markaloven §11 “Eventyrskogsparagrafen”) and stretches over 3,5 km² inside the Østmarka forest area in Oslo municipality. The geology gives this landscape its characteristic north-south ridges and valleys. The forest is mostly dominated by Norway spruce, with pine dominating on the ridges and deciduous trees like birch, goat willow (*Salix caprea*) aspen (*Populus tremula*) and rowan scattered around. The bottom vegetation at this site was affected by the lack of light due to canyons and dense canopy cover, and consisted mostly of short grass. Most of the tinder fungus was located in a narrow and shady canyon with a little stream called Sølvdoblabekken running through it. All the sub-patches had a little stream running close by. This productive conifer-forest has a variation in both topography and vegetation and has a relatively high amount of dead wood of different tree species. I chose this site because it contained many sporocarps of tinder fungus and sporocarps of red belt conk on black alder.

Four threatened fungi were included in the Norwegian Red List for Species from this site; *Hypocrea alutacea* (In Norwegian: kjerneklubbe), *Ramaria botrytis* (In Norwegian: rødtuppsopp), *Gomphus clavatus* (In Norwegian: fiolgubbe) and *Mycena alba* (In Norwegian: krembarkhette).

Nordre Pollen

The second site was located in Nordre Pollen nature reserve in Ås municipality (Lat. 59.75, Long. 10.76, 1-144 masl.), which was established in 2005 and consists of 814 daa. This forest area covers a narrow and steep valley with a small stream running through it and its surroundings. The forest is a mix between old stands of Norway spruce and pine. Some deciduous trees like black alder (*Alnus glutinosa*) bird cherry (*Prunus padus*), European ash (*Fraxinus excelsior*) (VU) and littleleaf linden (*Tilia cordata*) can be found in warmer locations in the valley. The vegetation here is a mix between tall herbaceous species and ferns in wet areas and low growing shrubs (*Vaccinium spp*) in dryer ones.

At this site, there were three findings of threatened fungi in the Norwegian Red List for Species (2015); *Perenniporia subacida* (In Norwegian: dynekjuka) (EN), *Antrodiella citrinella* (In Norwegian: gul snyltekjuka) (VU), *Sceletocutis brevispora* (In Norwegian: klengekjuka) (VU).

Vardåsen

The third site was located in Vardåsen nature reserve in Rygge municipality (Lat. 59.35, Long. 10.68, 1-89 masl.). The reserve covers an area of 893 daa and was preserved in 1993. The forest consists of Norway spruce in moist areas and pine in dryer areas. There has been some forestry activity in the northeast part in the 80's and some selective felling in mid-1900, and the oldest Norwegian spruce trees are from mid-1800 (Miljødirektoratet, 2010). This forest contained deciduous trees like the common birch, goat willow and rowan, but also oak (*Quercus sp.*) and European beech (*Fagus sylvatica*) in addition to a high amount of aspen, especially in the east part of the reserve. The vegetation at this site was dominated mostly by low growing shrubs (*Vaccinium spp*) mixed with short grass. I chose this site because of the high amount of aspen with aspen bracket (*Phellinus tremulae*) growing on it.

According to the Norwegian Red List for Species (2015), there were four threatened fungi at this site; *Polyporus umbellatus* (In Norwegian: skjermkjuka) (VU), *Hydnellum mirabile* (In Norwegian: ørstebunnpigg) (VU), *Ramaria lutea* (In Norwegian: ruskorallsopp) (VU) and *Ramaria rufescens* (In Norwegian: bruntuppkorallsopp) (VU).

Eldor

The last site was located in the Eldor forest in Ås municipality (Lat. 59.64, Long 10.81, 120 masl.) which was a young managed forest. The forest here was dominated by Norway spruce with some deciduous trees like birch, goat willow and rowan in smaller amounts. There were a high degree of wind-fallen Norwegian spruce, and there was an old clearcutting nearby that consisted of small birch in dense regrowth. The vegetation was dominated by grass and low growing shrubs (*Vaccinium spp*) in a mix. I chose this site because of the high density of red belt conk sporocarps. The topography of the site includes many small cliffs, and the whole area is frequently used for recreation by locals. I chose this site because there was a high amount of Norway spruce wind falls and a high density of red belt conk in it. There were no findings of threatened species according to The Norwegian Red List of Species at this site.

2.3 The Polypores examined in this study

All of the polypore species in my study belongs to the division basidiomycete, and are perennial and fomitoid, which means their fruit bodies are very hard, with a thick context and several annual layers. They are very robust when alive and can stay attached to the tree surface for many years after their death (Schigel et al., 2004). They are all commonly distributed in the boreal forest.

We can classify decomposer fungi into white-rot and brown-rot species according to their enzymatic composition in which they utilise to break down the woody structure (Ryvarden and Melo, 2014). White-rot fungi produce cellulase and lignase which breaks down lignin, cellulose and hemicellulose, leaving no stabile end product. Only about ten percent of the basidiomycete wood-decaying polypores are brown-rot fungi, and they appear mostly on conifer trees like Norway spruce *P. abies* (Gran) which has a higher content of lignin (27-35%) than deciduous trees that have 19-24% lignin. Brown-rot fungi selectively decompose cellulose and hemicellulose in the material, leaving out lignin (Ryvarden and Melo, 2014). This process gives the trunks the characteristic brown-coloured and most often cubic appearance. The end product from brown-rot fungi is extremely stabile and can remain unchanged in the soil for hundreds of years. In boreal forest ecosystems, where it can constitute up to 30% of the upper soil layer, contributing with soil properties like water capacity, ion-exchange capacity and pH buffer, in addition to carbon sequestration.

The three polypore species, red belt conk (*Fomitopsis pinicola*), tinder fungus (*Fomes fomentarius*) and aspen bracket (*Phellinus tremulae*) are commonly distributed throughout the Fennoscandian boreal forest. They are all perennial decomposers with a very hard and persistent structure.

Red belt conk

Red belt conk (In Norwegian: rødbrandkjuke) is a perennial brown-rot fungus which most often grows on Norway spruce (Figure 2.1), but can also be found growing on deciduous trees like birch and aspen (Ryvarden and Melo, 2014). It was chosen as a representative for brown-rot species growing on conifers since it most commonly grows on Norway spruce. The red belt conk is typically foot-shaped to shelf-shaped, it can be up to 30-40 cm wide and long and 10 cm thick at the basis, and the hat surface is uneven and covered with a resinous skin which colour can vary from deep red in the centre and yellow-like on the. The pore surface has 3-5 pores pr. mm. and has a whitish colour when young, while it gets a more yellow to brown colour when old.



Figure 2.1 shows the polypore species included in the study; red belt conk on Norwegian spruce (left), tinder fungus on birch (middle) and aspen bracket on aspen. (Photo: Egil Michaelsen (left), George Chernilevsky (middle), Kristin Vigander (right)).

Tinder fungus

Tinder fungus (In Norwegian: knuskkjuke) is a perennial white-rot fungus (Figure 2.1), and it was chosen because it is the most common white-rot fungi that grow on deciduous trees and most often on birch which is basically found in every forest in Norway. The pore surface, with 3-4 pores pr. mm, is grey-white at first and later become browner with age (Ryvarden and Melo, 2014). The sporocarp is most often white-grey to brown, has a foot-shape look and a characteristic marbled mycelium core inside.

Aspen bracket

Aspen bracket (In Norwegian: ospeildkjuke) is also a perennial white-rot decomposer which often grows at branch scars of aspen (Figure 2.1), and can be up to 15 cm thick and 20 cm wide. The upper surface becomes blackened and rimose, resembling charcoal, while the pore surface is purplish to dark reddish brown with 5-7 pores per mm (Ryvarden and Melo, 2014). The substrate is especially aspen but has also been recorded from white poplar (*P. alba*) and grey poplar (*P. canescens*).

2.4 Insect Sampling

The objective was to collect beetles that potentially could spread spores, either by directly feeding on the hymenium surface, or just attracted to the sporocarp for hunting other insects. The beetles were collected from both top and bottom side of the polypores by gently brushing the insects off the surface with a wetted stick or by an entomological aspirator. If some species were very abundant, like *Gyrophana boleti* or *Cis glabratus*, only 2 specimens were collected and the rest was counted. All beetles were then placed in a container with preservative liquid (70% alcohol) and the containers were given a tag with information of site and log number. When the fieldwork was finished, the sampled beetles were sent to identification by a taxonomic expert, Sindre Ligaard. All samplings were carried out between 29. May to 30. September 2017.

2.5 Data analyses

Prior to performing any analysis, I had to compile an ecological matrix with information on host preferences for the beetles. This was done by accessing information from existing published material accessed online.

All data analysis was performed using R version 3.5.0., R commander version 2.4-4 and RcmdrPlugin.NMBU version 1.8.8.

3 Results

In total, I collected 36 species of beetles, from 12 families and 28 genera. They were manually collected from three species of polypores, from four different locations during the time period from 29. May to 30. September 2017.

3.1 Distribution of beetle species in this study

Aspen bracket harbored 75% of the species while red belt conk had 71% in contrast to tinder fungus that had 38% of the species. Vardåsen Nature Reserve was the location with most species (18) and 54 specimens divided by polypore species, followed by Dølerud with 17 species and 459 specimens. Nordre Pollen had eleven species and 1209 specimens, and Eldor had five species and 1255 specimens (Table 3.1). *G. boleti* was the most frequent species on red belt conk, *Boletophagus reticulatus* was most frequent on tinder fungus and on aspen bracket, *Scaphisoma boleti* was the most dominant species.

The beetle species collected in this study

Seven predator species were collected on aspen bracket, four on red belt conk and one on tinder fungus. Staphylinidae was by far the biggest family of beetles in the insect sample and was represented by 14 species (39%) within eleven genera, and *G. boleti* (Figure 3.1) was the most frequent observed (2868 observations) species in this family.

The second biggest family was Ciidae with five species (14%) from two genera, and with *C. glabratus* (Figure 3.1) as the most frequent (30 observations).

Most of the beetle species (68%) were fungivorous, but ten species (28%) were predators, that may hunt other invertebrates on the hymenium surface, but only in 42% of the observations were they found together with another beetle species.



Figure 3.1 shows the two most abundant beetle species sampled in my study. a) *G. boleti*, b) aggregation of *G. boleti* on hymenium surface of red belt conk, c) *C. glabratus*. (Photo: entomologie-stuttgart.de (left and right), G. Drange (middle)).

Table 3.1 Number of individuals of beetle species observed on the different polypores and locations. The two latter columns state the tree category in which the beetles were collected (Coll.) from, and host category at larvae development stage obtained from the literature (Host). The categories are: DEC=Deciduous, CON=Conifer, MIX=Mix of both conifer and deciduous trees.

Family	Species	Polypores			Study areas				Sum	Coll	Host
		Red belt conk	Aspen bracket	Tinder fungus	Vardåsen	Nordre Pollen	Dølerud	Eldor			
Ciidae	<i>Cis bidentatus</i>	0	5	0	5	0	0	0	0	DEC	MIX
	<i>Cis glabratus</i>	29	0	1	0	7	1	22	30	MIX	MIX
	<i>Cis jaquemartii</i>	0	0	2	0	1	1	0	2	DEC	DEC
	<i>Cis quadriens</i>	1	0	0	0	0	1	0	1	CON	MIX
	<i>Ennearthron cornotum</i>	0	5	1	5	0	1	0	1	DEC	MIX
Cryptophagidae	<i>Atomaria wollastoni</i>	2	0	0	0	0	2	0	2	CON	CON
	<i>Pteryngium crenatum</i>	3	0	0	0	2	1	0	3	CON	MIX
Erotylidae	<i>Triplax russica</i>	0	5	0	5	0	0	0	0	DEC	DEC
	<i>Tritoma bipostulata</i>	0	0	1	0	0	1	0	1	DEC	DEC
Latridiidae	<i>Corticaria longicollis</i>	1	0	0	0	0	1	0	1	CON	MIX
	<i>Corticaria gibbosa</i>	1	0	0	0	0	0	1	1	CON	MIX
Leiiodidae	<i>Agathidium nigripenne</i>	0	0	1	0	0	1	0	1	DEC	MIX
	<i>Anisotoma humeralis</i>	1	0	0	0	1	0	0	1	CON	MIX
Melandryidae	<i>Abdera flexuosa</i>	0	1	0	1	0	0	0	0	DEC	MIX
Monotomidae	<i>Rhizophagus dispar</i>	0	1	0	1	0	0	0	0	DEC	MIX
Nitidulidae	<i>Epurea variegata</i>	1	1	0	1	0	0	1	1	MIX	DEC
	<i>Epurea unicolor</i>	0	1	0	1	0	0	0	0	DEC	DEC
	<i>Ipidia binotata</i>	1	0	0	0	1	0	0	1	CON	MIX
Staphylinidae	<i>Acrulia inflata</i>	0	1	0	1	0	0	0	0	DEC	MIX
	<i>Agaricochara latissima</i>	0	4	0	4	0	0	0	0	DEC	DEC
	<i>Bolitochara mulsanti</i>	0	1	0	1	0	0	0	0	DEC	MIX
	<i>Euryusa castanoptera</i>	1	0	0	0	0	1	0	1	DEC	DEC
	<i>Gyrophæna affinis</i>	0	0	1	0	0	1	0	1	DEC	MIX
	<i>Gyrophæna boleti</i>	2818	3	5	3	1183	410	1230	2823	MIX	MIX
	<i>Gyrophæna poweri</i>	0	2	0	2	0	0	0	0	DEC	DEC
	<i>Leptusa pulchella</i>	2	1	0	1	1	1	1	3	MIX	MIX
	<i>Lordithon lunulatus</i>	0	1	1	1	0	0	0	0	DEC	MIX
	<i>Phyllodrepa linearis</i>	0	2	0	2	0	0	0	0	DEC	MIX
	<i>Proteinus atomarius</i>	1	0	0	0	0	1	0	1	CON	MIX
	<i>Scaphisoma boleti</i>	4	11	0	11	4	0	0	4	MIX	MIX
	<i>Scaphisoma boreale</i>	0	7	0	7	0	0	0	0	DEC	DEC
	<i>Sepedophilus testaceus</i>	0	2	0	2	0	0	0	0	DEC	MIX
Tenebrionidae	<i>Bolitophagus reticulatus</i>	0	0	30	0	6	24	0	30	DEC	DEC
Trogossotidae	<i>Peltis ferruginea</i>	12	0	0	0	2	10	0	12	CON	MIX
	<i>Thymalus limbatus</i>	1	0	0	0	1	0	0	1	CON	MIX
	SUM individuals	2880	54	43	54	1209	459	1255	2973		
	SUM species	17	18	9	18	11	18	5			

Beetle fauna on the polypore species

The most abundant beetle species found on aspen bracket was *S. boleti* and *S. boreale* with eleven and seven specimens respectively and on tinder fungus *B. reticulatus* was most frequently observed (30 specimens).

On red belt conk, the most abundant species was *G. boleti*, *Cis glabratus* and *Peltis ferruginea*. There was a clear overweight by *G. boleti* with 2818 observations compared with the latter two species that had only 29 and twelve observations respectively.

Red belt conk had the highest number of observations compared with number of sporocarps (2880), followed by aspen bracket (54 observations) and tinder fungus with 43 observations. The large difference in observation numbers is caused by *G. boleti* which utilizes this polypore as its habitat (Staniec et al., 2016).

Only two species (*G. boleti* and *Leptusa pulchella*) were found on every polypore species (Figure 3.2), red belt conk and aspen bracket shared five species with the others and tinder fungus shared four species. Aspen bracket had 13 unique species, tinder fungus had five specific species and red belt conk had twelve specific species, but included here is also an observation of *Euryusa castanoptera* which was collected from a sporocarp that grew on grey alder.

Five species, *G. boleti*, *C. glabratus*, *S. boleti*, *L. pulchella* and *Epuraea variegata*, were found on both conifer and deciduous trees, and one species, *E. cornotum*, was only found on tinder fungus and aspen bracket.

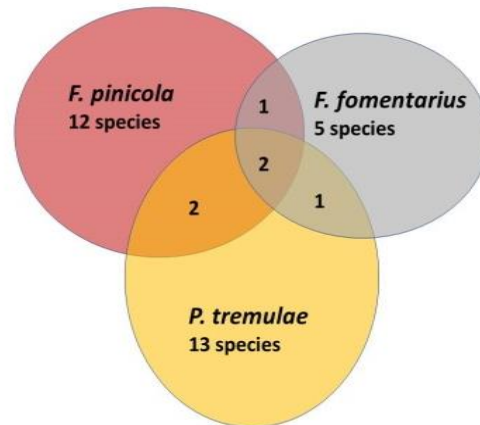


Figure 3.2: Venn diagram showing number of unique and shared beetle species between the three polypores.

3.2 Hymenium surface

The hymenium surface was measured for all sporocarps and summed up for each polypore species at each site (Table 3.2). The area of the hymenium was calculated using the following formula: $b \times h \times \frac{1}{2}$, where b and h are the diameter in E/W and N/S direction of the polypore.

Table 3.2 shows the summarized hymenium surface (in cm^2), together with sum of logs, sporocarps and beetles for each polypore species at each site.

	NordrePollen		Dølerud			Eldor	Vardåsen
	Red belt conk	Tinder fungus	Red belt conk	Tinder fungus	Aspen bracket	Red belt conk	Aspen bracket
Hymenium surface (cm^2)	1570	566	1019	2177	48	1421	997
Sum logs	6	4	3	4	1	5	6
Sum sporocarps	34	19	17	34	3	35	43
Sum species	9	5	11	8	0	5	18
Sum individuals	885	7	423	36	0	1255	54

The relationship between the hymenium surface and abundance of species and individuals are illustrated in figure 3.3. Performing Linear regression analysis revealed no clear relationship between hymenium surface and number of individuals ($p=0,4818$) and species ($p=0,4105$) when all polypore species were put together, but the p-value was lower when analyzed for

species without *G. boleti* ($p=0,1265$). However, a stronger connection was detected when analyzing species ($p=0,0674$) and individuals ($p=0,0564$) for aspen bracket alone, possibly indicating a trend.

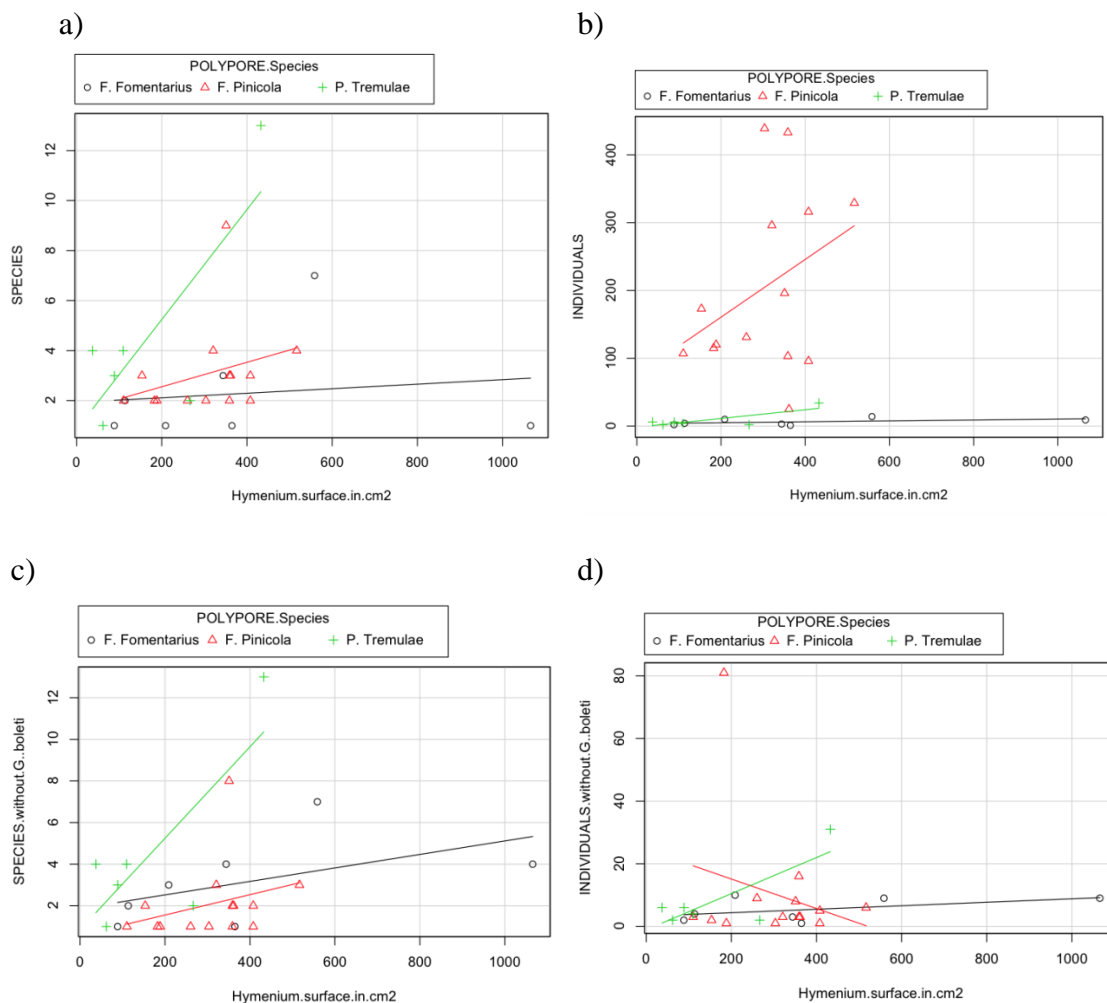


Figure 3.3: Scatterplot shows the relationship between hymenium surface and the number of beetles observed for all polypore species. a-b) is included *G. boleti*, and c-d) is excluded *G. boleti*.

3.3 Preferences and tree association

20 species (55% of all species) from eight families were collected from three species of deciduous trees, eleven species (31%) from eight families was collected from one species of conifer tree (Norway spruce), and only five species (14%) from three families were observed on both deciduous and conifer trees.

All of the beetles collected were categorized as saproxylic except one, *Proteinus atomarius*, which is a predator usually found in rotten organic matter. One of the species (*Malthodes spp.*) was left out of the ecological analysis, since DNA analysis was necessary for species identification, leaving 35 species in the sample matrix.

From the total of 34 saproxylic species, 63% were obligate saproxylic.

Of the beetles that were collected from deciduous trees, nine (26%) of these use deciduous trees for larval development, and eleven (57%) had mixed host trees (Table 3.3). In contrast,

nine species were collected from conifer trees, but only one of these had conifer as host tree and eight (23%) had mixed host trees. Only six species were found on both conifer and deciduous trees, and five of these species (14%) had mixed host trees.

Table 3.3 shows number of beetle species and the tree category they were collected from, compared with the host tree category obtained from the literature. The highlighted cells shows number of matching species with the literature.

Host tree (literature)	Collected from		
	Conifer	Deciduous	Mix
Conifer	1	0	0
Deciduous	0	9	1
Mix	8	11	5
Sum	9	20	6
% of total	26	57	17

3.4 Observation time

Most of the beetles were collected early in the season, in June, with 1311 specimens at the first survey, but if we discard *G. boleti*, most individuals (41) were found during the second survey. *C. glabratus* had the highest number of specimens (18) in survey 3. Red belt conk and aspen bracket had most visits early in the summer, while tinder fungus had small seasonal variation in visits. The highest number of observed individuals was at survey 2 and 3, and the highest number of species was collected from aspen bracket in survey two, but in survey tree, no species was collected (Figure 3.4).

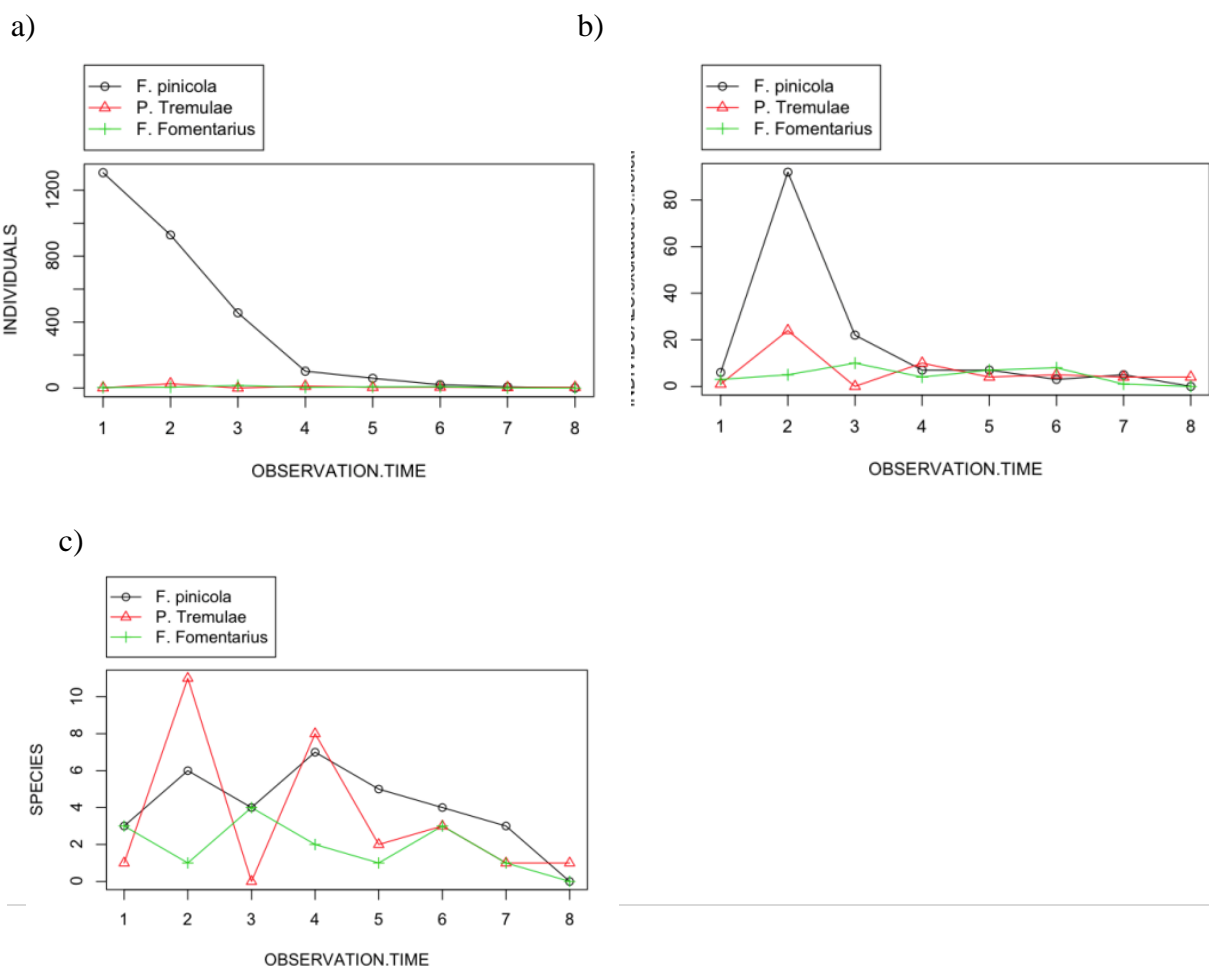


Figure 3.4 shows the numeric distribution (with (a) and without (b) *G. boleti*), and species richness (c) of beetles in each host fungi through observation time 1-8. The number of sporocarps sampled were not equal, therefore the numbers are not directly comparable.

Again, the abundance of *G. boleti* was disproportional compared with the other species on all the study sites except Vardåsen which did not include red belt conk. *G. boleti* was the only species that was found on almost every survey through the season (Appendix table 2).

4 Discussion

Saproxyllic beetles are known to visit the hymenium surface of polypores either for feeding or predation, and when they do, they may get spores attached to their exoskeleton, which they in turn may carry and deposit in a new suitable habitat (Birkemoe et al., 2018).

This interaction between wood-decaying fungi and saproxyllic beetles has benefits for both parts. The sporocarp itself functions as shelter and breeding ground for some species, and through enzymatic decomposition, the fungi facilitate the wood making nutrients available for the beetles that in return spread propagules for the fungi.

4.1 Hypothesis 1

My first hypothesis was that there is a relationship between the hymenium surface area of the sporocarps, and the abundance and species richness of the beetle fauna collected there. The hymenium surface of the polypore would then function as a proxy for the amount of spores available as food for beetle species. If the surface area was large, I would expect more beetles to be found as opposed to a smaller surface area.

This hypothesis was not confirmed, I did not find a significant correlation between the surface area size of the sporocarps and the abundance and species richness of the beetle fauna. Since almost all of the species I collected were fungivorous, I could not confirm that provision of spores attracted beetles from other functional groups.

Possible reasons for this lack of correlation may be several. There were plenty of dead wood with sporocarps from the selected polypores at all sites. At the sites Vardåsen and Eldor, the dead wood that was surveyed was denser than at the other sites. Since there were so many sporocarps in close proximity, there could be less competition for spores, or the cost of flight is so low that the beetles can choose freely between sporocarps. Another possibility could be that other sporocarps on other logs nearby had an attractational effect, resulting in fewer individuals visiting “my” sporocarps. Many of the tinder fungus sporocarps that had no visitors were young, and thereby emit a different chemical signal than older sporocarps which often attracts more visitors.

4.2 Hypothesis 2

In my second hypothesis I asked the question if the beetles collected in my study were host-specific. Would e.g. beetles that utilise deciduous trees as their breeding habitat be found on

sporocarps that grow on deciduous trees? I asked this to find out in what degree the beetle species were potential spore distributors in the same habitat as the fungus. To answer this, I compiled a matrix with ecological information regarding host preference accessed from publications published online (Appendix table 1). I found support for this hypothesis. All of the beetles I collected were found on polypores that shared the same host-tree category in agreement with known literature.

Some volatiles emitted from different polypore hosts can attract beetles to the sporocarps and could explain the broadness of polyphagy amongst fungivorous beetles (Schigel, 2016). These chemical signals may thus play an important role in directing adult beetles that are in search of new patches to colonize (Fäldt et al., 1999).

A study from Virginia, USA where they collected beetles from sporocarps manually and with waxed paper, reported an increase of beetle diversity with increasing age of sporocarps, suggesting that age-related changes in the chemical structure supported the increase in species diversity (Epps and Arnold, 2018).

Many saproxylic beetles actually feed on the wood that is colonized by, and on the fungi that is colonizing and decomposing the wood itself. (Johansson et al., 2006) did an experiment where they tested the attraction of beetles to volatiles emitted from both mycelia and sporocarps of six polypore species in four old-growth spruce forests in northern Sweden using baited window traps. Their results indicated that some beetle species could discriminate volatiles from mycelium and sporocarps of both the same and other species of polypores, e.g. they found that the predator *L. lunulatus* preferred sporocarps of red belt conk.

When trying to explain host-tree preferences among saproxylic beetles, the trees defense system and its chemical and physical properties are key factors to examine. Trees are characteristic by large size and longevity, collecting energy through years of photosynthesis making them a massive opportunity of resources for other organisms. But the trees have developed a variation of protective mechanisms after being constantly challenged over millions of years by different pathogens and grazers.

This differences in lignin makes conifer lignin more resistant to degradation by microbes than lignin found in deciduous trees and may therefore be important for the host-tree preference among white-rot and brown-rot fungi since they decompose lignin differently.

Saproxylic organisms have been forced through evolution to adapt to the trees defense systems, making it an arms race to overcome obstacles. In a host tree with low defense investments we would expect to find a high degree of generalist species, and in host trees with high investment in defense we would expect to find more specialists.

True specialist (monophagous) saproxylic beetles use only one single tree species or genus, whilst specialized saproxylic beetles (oligophagous) are restricted to one family or closely related families, and generalists can use a broad range of species from several families or orders.

4.3 Hypothesis 3

In my third hypothesis I asked if there were specific beetle communities related to the polypore species in my study. To answer this question, I compared my results with the results from other similar studies from the boreal forest that involved the same polypore species. Most of the beetle species found on the polypores does not necessarily breed in the respective polypore species. The substrate for their larval stage is often dead wood or fungi associated with decaying woody material.

Several studies have explored, with varying sampling methods, the beetle fauna of red belt conk and tinder fungus, but very few on aspen bracket. (Hågvar, 1999) did a study on red belt conk and tinder fungus in Østmarka Nature Reserve using the same methodology as me, and of the 61 beetle species collected, we shared 26% from nine families. Red belt conk harbored 44% of the species in this study, which is similar to my findings of 49%. However, 74% of the species, compared to my 26%, were found on tinder fungus. This may be explained by favorable sporulation conditions early in the summer, or that 23% of the species in this study were only collected at night and were presumably night active. Also, nearly half of the species (43%) were present both day and night. The number of sampled sporocarps was uneven, 100 sporocarps of red belt conk was sampled in contrast to 40 sporocarps of tinder fungus. The high number of beetle species compared with fewer sporocarps sampled clearly indicates a higher attraction to tinder fungus. Since 63% of the species found on red belt conk are capable of breeding in coniferous wood, and 86% of the species from tinder fungus are capable of breeding in deciduous wood, it may be argued that fungal odours functions as a guidance for the beetles (kairomone effect) in search of breeding habitats. The overlap of beetle species between the two polypores he collected from was 18%, while I had a 14% overlap between red belt conk and tinder fungus. This indicates that several species do not distinguish between polypore species that usually are found on either conifer or deciduous trees. Also, in this study, the most numerous species was *G. boleti* which could totally dominate the hymenium surface of some red belt conk sporocarps.

Hågvar and Økland (1997) did a study on attraction of beetles to living sporocarps of red belt conk in Østmarka forest area using trunk-window traps Kaila (1993) which consists of a plastic window attached in a vertical split cut of a living sporocarp, and with a collection funnel below. In addition, they also used a free-hanging window trap to compare the results to the background “air-plankton fauna”. The authors report that nine species from seven families caught in the trunk-window traps, were common with my findings on red belt conk, and they were all observed sitting on the hymenium surface.

In Sweden, Jonsell and Nordlander (1995) did a trapping experiment near Uppsala where they tested the attraction to fungal odors of tinder fungus and red belt conk using window traps baited with chopped fruiting bodies. Out of the 96 species represented by at least 15 individuals, 29% significantly showed an attraction to odours from the sporocarps, and eleven species preferred only red belt conk and six species preferred only tinder fungus.

Several studies have been done in Finland. Schigel (2011) did a study where 176 beetle species from 116 polypore species were collected from both the surface of the sporocarps and reared from living and dead sporocarps. Twelve percent of the species in this study was also found in my study, however not on the same polypore species. Twelve species (7%) were found to visit red belt conk, twenty-five (14%) were found on tinder fungus and five (3%)

were found on aspen bracket, compared to 17, nine and 18 species respectively from my study.

There was no match between the beetle species in my study and the beetle five species collected from 209 sporocarps of aspen bracket in this study, however, the author group aspen bracket in a subgroup together with *P. igniarius*, *P. laevigatus*, *P. lundellii* and *P. populicola*. If we look at similarities with this group as a whole, only three species, *C. bidentatus*, *Rhizophagus dispar*, *Acrulia inflata* and *Leptusa pulchella*, were found as visitors. All these species were in my study collected solely from aspen bracket, except for *L. pulchella* that was found on all the polypore species. This may indicate that there is a certain fauna having a preference for these polypore taxa, even though the paper did not offer information to explain the low number of species compared to my findings.

Komonen et al. (2004) also did a study where they compared beetle species assemblages across Finland, Sweden and Norway, but they only looked at red belt conk and they used rearing methods with both living and dead sporocarps. They found that the four fungivorous species I found in my study, *C. glabratus*, *C. quadriens*, *C. jacquemartii* and *C. bidentatus*, were all rather frequently found in Finland, Sweden and Norway, but *E. cornotum* was only found in Sweden. *C. glabratus* was the most abundant species in this study with occurrence on 70% of the sporocarps on average, while in my study it was the third most abundant species after *B. reticulatus* and *G. boleti*.

Nikitsky and Schigel (2004) did a collection and rearing study from different parts of the Moscow region where they found 61 polypore species that harbored 261 species of beetles, and 102 (39%) of them were found on tinder fungus. *C. glabratus* was found but reported as “untypical host”, which was the same in my case, I collected one from tinder fungus but the rest (29 specimens) was found on red belt conk. A total of 16 (16%) species from tinder fungus matched my findings, five of these I collected from tinder fungus, three from red belt conk and eight from aspen bracket. This gives a thirteen percent match regarding preference for deciduous trees. On red belt conk, 21% of the species they collected were common with my findings including the abundant *G. boleti*.

Krasutskii (2007) did a study in the forests of the Urals and Trans Urals where he collected and reared beetles from red belt conk sporocarps. Four (13%) species were common with my findings, but I only collected two of them (*P. crenatum* and *E. variegata*) from red belt conk.

4.4 Notes on beetle (families) in this study

One of the most abundant families collected was the specialized family Ciidae. This cosmopolitan family consists of over 500 described species and is known to be truly fungivorous and they develop in polypore fruit bodies and feed on spores or fungal tissue (Stokland et al., 2012). Most of the larvae in this family have a narrow host-fungus range, but a few are highly polyphagous, like for instance *E. cornotum*, which I collected from tinder fungus and aspen bracket has been reported to utilize 20 different polypore species (Nikitsky and Schigel, 2004). *C. glabratus* and *C. jacquemartii* from the “*jacquemartii*” group are reported to have systematic relations with the polypore genera *Fomes* (tinder fungus), *Fomitopsis* (red belt conk), *Phellinus* (aspen bracket) and *Ganoderma* (artist’s fungus) and have a host preference of hard fruit bodies. This was partly in line with my results. *C. jacquemartii* was only found on *Fomes*, and *C. glabratus* was found on both *Fomes* and *Fomitopsis*. *C. glabratus* is reported to be a rare forest species which develops in moistened sporocarps on spruce.

Økland (1995) did a rearing study in Østmarka Nature where he found that *C. glabratus* and *C. quadriens* had strong host specificity to red belt conk and *C. jaquemartii* and *B. reticulatus* with tinder fungus, which also corresponds with my results. Jonsell and Nordlander (1995) did a study on the attraction of beetles to odours of red belt conk and tinder fungus with fresh and old sporocarps and found the same species as Økland (1995) breeding in the sporocarps.

Triplax russica has been reported to be monophagous on chaga mushroom (*Inonotus obliquus*) (Nikitsky and Schigel, 2004), but I sampled it only once on aspen bracket. However, there were a lot of chaga mushroom often growing together with aspen bracket on the same log at the Vardåsen location. The chaga mushroom is actually the closest relative (Ryvarden and Melo, 2014) to the genus *Phellini*, but it does not have the conspicuously sporocarps like the other species in this study, instead they grow a rather hidden sporocarp that emerges from under the bark of the tree (Schigel et al., 2006) which in turn makes it difficult to detect. With a lot of chaga mushroom at the location, it would be expected to find visiting species like *T. russica* feeding on a sporocarp nearby.

The host preference of the monophagous *B. reticulatus* has been well documented by e.g. Jonsell et al. (2003) Midtgaard et al. (2013), and corresponded well with my findings (88% occurrence on all the sampled birch logs) on tinder fungus. This species is also reported to be a strong competitor for resources (Rukke, 2002) which may explain the relative abundance of this species on tinder fungus. This species was observed several times hiding behind the sporocarps and sometimes copulating on the hymenium surface, as also reported by Nilsson (1997).

Only one beetle species from my sample (*Atomaria wollastoni*) was reported to have conifers as their only preferred host tree.

5 Conclusion

Many beetle species have overlapping host preferences with the polypore species they visit. Chemical signals emitted by polypores functions as guidance for some species in search of breeding habitat. Some species are generalists and have no clear preference for either conifer or deciduous trees as habitats. My results show however that there are unique beetle communities connected with certain polypore species. Most beetles collected in my study were fungivorous, and their importance as spore dispersers were not clearly established. Future research should be aimed at finding unique communities that are related to polypores and may thus be good spore dispersers.

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Appendix

Table 1 Shows the ecological information regarding the species in this study

Family	Species	Saproxyllic	Functional group	Larvae fungy	Larvae stage	Collected from	Polypore collected from
CIIDAE	<i>Cis bidentatus</i>	OBL	F	x	MIX	DEC	PT
"	<i>Cis glabratus</i>	OBL	F	x	MIX	MIX	MIX
"	<i>Cis jaquemartii</i>	OBL	F	x	DEC	DEC	FF
"	<i>Cis quadriens</i>	OBL	F	x	MIX	CON	FP
"	<i>Ennearthron cornotum</i>	OBL	F	x	MIX	DEC	MIX
CRYPTOPHAGIDAE	<i>Atomaria wollastoni</i>	OBL	F	x	CON	CON	FP
"	<i>Pteryngium crenatum</i>	OBL	F	x	MIX	CON	FP
EROTYLIDAE	<i>Triplax russica</i>	OBL	F	x	DEC	DEC	PT
"	<i>Tritoma bipostulata</i>	OBL	F	x	DEC	DEC	FF
LATRIDIIDAE	<i>Corticaria longicollis</i>	FAC	F	U	MIX	CON	FP
"	<i>Corticaria gibbosa</i>	FAC	F	x	MIX	CON	FP
LEIODIDAE	<i>Agathidium nigripenne</i>	FAC	F	U	MIX	DEC	FF
"	<i>Anisotoma humeralis</i>	OBL	F	U	MIX	CON	FP
MELANDRYIDAE	<i>Abdera flexuosa</i>	OBL	F	x	MIX	DEC	PT
MONOTOMIDAE	<i>Rhizophagus dispar</i>	FAC	P	x	MIX	DEC	PT
NITIDULIDAE	<i>Epurea variegata</i>	OBL	F	x	DEC	MIX	MIX
"	<i>Epurea unicolor</i>	FAC	P	U	DEC	DEC	PT
"	<i>Ipidia binotata</i>	FAC	P	U	MIX	CON	FP
STAPHYLINIDAE	<i>Acrulia inflata</i>	FAC	P	U	MIX	DEC	PT
"	<i>Agaricochara latissima</i>	OBL	F	x	DEC	DEC	PT
"	<i>Bolitochara mulsanti</i>	OBL	P	U	MIX	DEC	PT
"	<i>Euryusa castanoptera</i>	OBL	P	U	DEC	DEC	FP
"	<i>Gyrophaena affinis</i>	FAC	F	U	MIX	DEC	FF
"	<i>Gyrophaena boleti</i>	OBL	F	x	MIX	MIX	MIX
"	<i>Gyrophaena poweri</i>	FAC	F	x	DEC	DEC	PT
"	<i>Leptusa pulchella</i>	OBL	P	x	MIX	MIX	MIX
"	<i>Lordithon lunulatus</i>	FAC	P	U	MIX	DEC	PT
"	<i>Phyllocrepa linearis</i>	OBL	P	U	MIX	DEC	PT
"	<i>Proteinus atomarius</i>	-	P	U	MIX	CON	FP
"	<i>Scaphisoma boleti</i>	OBL	F	x	MIX	MIX	MIX
"	<i>Scaphisoma boreale</i>	FAC	F	x	DEC	DEC	PT
"	<i>Sepedophilus testaceus</i>	FAC	F	x	MIX	DEC	PT
TENEBRIONIDAE	<i>Bolitophagus reticulatus</i>	OBL	F	x	DEC	DEC	FF
TROGOSSITIDAE	<i>Peltis ferruginea</i>	OBL	F	x	MIX	CON	FP
"	<i>Thymalus limbatus</i>	OBL	F	x	MIX	CON	FP

Table 2 Shows the distribution of beetles through the season.

Species	Survey 1	Survey 2	Survey 3	Survey 4	Survey 5	Survey 6	Survey 7	Survey 8	SUM
<i>Malthodes</i> sp.	0	0	0	1	0	0	0	0	1
<i>Cis bidentatus</i>	0	5	0	0	0	0	0	0	5
<i>Cis bidentatus</i>	0	7	18	2	3	0	0	0	30
<i>Cis glabratus</i>	0	0	1	1	0	0	0	0	2
<i>Cis jaquemartii</i>	0	1	0	0	0	0	0	0	1
<i>Cis quadriens</i>	0	0	0	2	0	1	3	0	6
<i>Ennearthron cornotum</i>	0	0	0	0	2	0	0	0	2
<i>Atomaria wollastoni</i>	0	1	1	1	0	0	0	0	3
<i>Pteryngium crenatum</i>	0	3	0	2	0	0	0	0	5
<i>Triplax russica</i>	0	0	0	0	0	1	0	0	1
<i>Tritoma bipostulata</i>	0	0	0	0	1	0	0	0	1
<i>Corticaria longicollis</i>	0	0	0	1	0	0	0	0	1
<i>Corticaria gibbosa</i>	1	0	0	0	0	0	0	0	1
<i>Agathidium nigripenne</i>	1	0	0	0	0	0	0	0	1
<i>Anisotoma humeralis</i>	0	1	0	0	0	0	0	0	1
<i>Abdera flexuosa</i>	0	1	0	0	0	0	0	0	1
<i>Rhizophagus dispar</i>	0	0	0	1	0	1	0	0	2
<i>Epurea variegata</i>	0	0	0	1	0	0	0	0	1
<i>Epurea unicolor</i>	0	0	0	0	0	1	0	0	1
<i>Ipidia binotata</i>	0	0	0	0	0	1	0	0	1
<i>Acrulia inflata</i>	0	0	0	0	0	0	0	4	0
<i>Agaricochara latissima</i>	0	0	0	1	0	0	0	0	1
<i>Bolitochara mulsanti</i>	0	0	0	0	0	0	1	0	1
<i>Euryusa castanoptera</i>	1	0	0	0	0	0	0	0	1
<i>Gyrophaena affinis</i>	1301	919	439	96	52	17	2	0	2826
<i>Gyrophaena boleti</i>	0	0	0	0	0	0	0	0	0
<i>Gyrophaena poweri</i>	0	2	0	0	0	0	0	0	2
<i>Leptusa pulchella</i>	0	1	0	0	1	1	1	0	4
<i>Lordithon lunulatus</i>	1	0	0	0	0	0	0	0	1
<i>Phyllodrepa linearis</i>	0	1	0	1	0	0	0	0	2
<i>Proteinus atomarius</i>	0	0	0	0	0	1	0	0	1
<i>Scaphisoma boleti</i>	0	7	0	2	2	0	0	0	11
<i>Scaphisoma boreale</i>	0	1	0	1	2	3	4	0	11
<i>Sepedophilus testaceus</i>	0	2	0	0	0	0	0	0	2
<i>Bolitophagus reticulatus</i>	1	5	8	3	7	6	0	0	30
<i>Peltis ferruginea</i>	5	2	4	1	0	0	0	0	12
<i>Thymalus limbatus</i>	0	1	0	0	0	0	0	0	1
SUM	1311	959	471	117	70	33	11	4	2973



Norges miljø- og biovitenskapelige universitet
Noregs miljø- og biovitenskapelige universitet
Norwegian University of Life Sciences

Postboks 5003
NO-1432 Ås
Norway