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박 사 학 위 논 문

제주도 한라산 국립공원내
구상나무(*Abies koreana*) 고사목에
서식하는 절지동물 군집 구조

Community Structure of Arthropods inside Korean
Fir (*Abies koreana*) Snags on Mt. Halla National
Park, Jeju Island, Korea

서울여자대학교 일반대학원

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이 논문을 박사학위 논문으로 제출함

2016 년 7 월

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2016 년 7 월

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ACKNOWLEDGMENTS

I would like to acknowledge the advice and guidance of major Professor Hoonbok, YI. I also thank the members of my graduate committee for their suggestions and encouragement, Professor Chang Seok, LEE; Do Hee, LEE; Chuleui, JUNG and Young Han, YOU.

I would also thanks to the member of our laboratory member for supporting my study.

I would like to specially express my thanks to Professor Jeffrey c. Miller and Andrew Moldenke for assistance in arthropods identification and my family for supporting and encouraging me to complete my Ph.D degree.

1. INTRODUCTION

Forest ecosystems are complex webs of organisms that include plants, animals, fungi, and bacteria (Pearce & Pearce 2001). These ecosystems have many functions such as regulating the hydrological cycle, protecting watersheds and their vegetation, water flows and soils, reduction of CO₂ gas emission impacts, and providing a vast store of genetic information much of which has yet to be uncovered (Pearce and Pearce 2001). Especially, the forest ecosystems have a biggest function by providing the natural habitats for 80% of the world's terrestrial biodiversity (Persson 2013). Even though the forest ecosystems to perform the important functions, these forest ecosystems have decreased due to an occurrence of pests, pollution of environment, anthropogenic and natural ecosystems disturbances as well as climate change (Fahrig 2003; Foley et al. 2005; Linder et al. 2010). Especially, climate change will affect the increase of the temperature in the forests and the decrease of the water storage in the soil of the forests (IPCC 1996; Mitchell 1989). These influence caused the decline of live trees as well as the increase of deadwood proportion in forests. Consequently, these phenomena have changed community structures of the forest dwelling animals including the arthropods (Carroll 2003). Also, these phenomena have more occurred in the subalpine forest than other forest (Koo et al. 2001, Song et al. 2009; 2014).

Generally, deadwood plays a substantial role in several ecological processes in the forest ecosystems (Harmon et al. 1986; Franklin et al.

1997). Deadwood significantly contributes to the total amount of organic material in the forest, thereby affecting the nutrient cycle (Olson 1963; Laiho & Prescott 1999; Swift 1977; Edmonds & Eglitis 1989; Hanula 1993; Schowalter et al. 1998; Yoo & Kim 2002), carbon storage (Laiho & Prescott 1999; Mackensen & Bauhus 1999; Jenisch & Harmon 2002), soil conditioner (McFee & Stone 1966; Tate et al. 1993; Kayahara 1998; Smith et al. 2000), moisture reservoir and refuge from environmental extremes (Amaranthus et al. 1989; Clausen 1964; Means et al. 1996; Margules et al. 1995; Lemckert 1999; Smith et al. 1989; Michaels & Bornemissza 1999; Meggs 2003), provision of physical habitat structure (Buddle 2001; Lee 1995; Butts & McComb 2000; Tallmon & Mills 1994; Bowman et al. 2000; Ecke et al. 2001), nesting and denning sites (Duncan & Taylor 2001), and the substrate for saproxylic and epixylic organisms (Speight 1989; Kirby & Drake 1993; Hallenberg et al. 1994; Hanski & Hammond 1995; Hammond 1997; Dajoz 2000). Nevertheless, deadwood was perceived as a negative element of forest ecosystems, that indicates “mismanagement and wastefulness” of the applied forest management (Stachura et al. 2007). It was regarded as a potential source of biotic pests, mainly insects (Angelstam et al. 2003; Marage & Lemperiere 2005), to the remaining trees in a forest as well as to adjacent stands (Pasierbek et al. 2007). Considering forest workers and visitors, standing deadwoods have been seen as a threat to public safety (Peterken 1996; Thomas 2002) that had to be removed immediately after they had occurred (Pasierbek et al. 2007). Recently, forest managers have accepted deadwood’s value as a contribution to maintaining forest

biodiversity, and management may be altered to maintain or to increase the amounts of deadwood present (Ficher et al. 2015; Vandekerckhove et al. 2012).

Nowadays, domestic forest managers are also considering whether the increasing deadwood removed or not in the forest. The proposed forest management plan for forest managers includes deadwood managements. These management plans include the intermittent thinning and removal of deadwood in the forest to prevent economic damage by pests such as *Bursaphelenchus xylophilous*, bark beetles and longhorn beetles (Korea Forest Service 2010).

Actually, more ecological research data are needed to confirm whether or not the deadwood should be removed in the forest. As well as proper forest management plan should be backed by research results. Because deadwood related to biodiversity of the forest as a natural habitat and food resource. However, the previous research focused on deadwood only in domestic (Kim et al. 2007; Youn 2011; Ko et al. 2014). There was few research about arthropods or wildlife living in the deadwood (Kown 2011; Kim 2012). A study of the interaction between deadwood dwelling wildlife and deadwood is non-existent.

This study is the first to research the Korean fir deadwood-dwelling arthropods community among the decay stages in Korea. It was performed to reveal the needs of deadwood as habitats for biodiversity.

I found the subalpine forests in Korea that have the larger increasing amount of deadwood than other forest. Domestic subalpine forests are Mt. Halla, Mt. Jiri, Mt. Deokyu, and Mt. Gaya. These subalpine forests

have *Abies koreana* Wilson (*A. koreana*; Korean fir) as common species (Kang 1984; Lee and Hong 1995). It is an endemic species in Korea and threatened species of IUCN red list (IUCN 2004). According to a study, it has been reported that the mortality rate of *A. koreana* increases and *A. koreana* is facing critical population declines (Kim et al. 1998, Koo et al. 2001). *A. koreana* has been decreased 18% during 27 years since 1981 in Korea, especially, Mt. Halla has been decreased 34% during 15 years since 1988 (Kim & Lee 2013). Continually, deadwood of *A. koreana* forest has been increased. Mt. Halla has the largest distribution area of *A. koreana* forest (Koh 2003), and the mountain has many Korean fir deadwoods.

The community study of *A. koreana* deadwood-dwelling arthropods was executed in the *A. koreana* forest, Mt. Halla. Generally, arthropod community study is one of a key study in ecological research. Because, arthropods account for the bulk of global organismic diversity, representing almost 60 % of all metazoic species on the earth (Whitfield & Purcell III 2012). Especially, they are the major players in the functioning of ecosystem processes (Weisser & Siemann 2004). Arthropod communities can be highly responsive to temporal and spatial environmental changes over the landscape, including climate (Larocque et al. 2001; Ulyshen & Hanula 2009a,b), habitat alteration (Intachat et al. 1997, Ellis et al. 2001). Small size, rapid population growth, short life cycle, and high mobility make are arthropods useful in detecting fine-scale spatial variation and short temporal changes. In addition to, in assessing habitat quality, arthropod species often serve as indicators of

both undisturbed (Morrison & Marcot 1995) and disturbed ecosystems (González-Megías et al. 2004).

Therefore, this community study of deadwood dwelling arthropods in the *A. koreana* forest would help figure out the importance of deadwood of *A. koreana* forest considering the difference in growth conditions.

The purpose of this study was to understand the importance of various decay levels of deadwood for the arthropod's habitat diversity in forest ecosystems. *Abies koreana* as a Korean endemic species should be conserved from the climate changes and its conservation would be affected to the increase of biodiversity. Although deadwood and arthropods community are attentive research theme in the global, This is the first study regarding Korean fir deadwood dwelling arthropods in Korea. Results of this study will be relevant for developing ecologically sustainable forest management strategies. In addition, it will be used as a basis for the protection and effective management plans of *A. koreana*. In this study to achieve the objective of the study was to verify the setting of the following hypothesis.

Hypotheses

There are many scientific papers dealing with the issues of biodiversity and extinction debt in temperate forests, both of which are partly related to the absence of deadwood (Harmon et al. 1986; Christensen et al. 2005; Müller & Bütler 2010; Vrška et al. 2015).

Domestic deadwoods are only a small proportion of natural levels, but it is also due to other impacts on the forest ecosystem such as prevention

of forest fire and pest control (Kim 2007; Korea Forest Service 2007; Park 2014). In terms of biodiversity, this hypothesis verifies the fact that deadwood increasingly brings biodiversity increasingly in the forest.

H1: Arthropods diversity would be increased along the decay stages.

The second hypothesis is dealing with the functional feeding group of arthropods. Generally speaking, arthropods are highly specialized in their niche requirements. They have the diverse ecological roles such as decomposers, consumers, predators and parasites as well as they have the providing and regulation functions for the ecosystem services (Swift and Anderson 1989; Morris et al. 1991; Miller 1993). The composition of functional feeding group profoundly changes during the wood decay process (Lee et al. 2014). Many predators play an important role in regulating the population of many phytophagous pests (DeBach 1974; Olembo 1991). Therefore, the proportion of higher predators enough can affect to the population of herbivores including pests in the deadwood. So, my second hypothesis is as follows.

H2: The proportion of the herbivores would be higher than the proportion of the predators in the live tree stage and the proportion of the herbivores would be lower than the proportion of the predators in the late decay stage.

Another interesting taxon is bark beetles in deadwood. Although

deadwood is well known as the sources for the bark beetles and other pests (Korea Forest Service, 2010), and bark beetles are commonly recognized as the most mortality agent in coniferous forests (Furniss & Carolin 1977; Dale et al. 2001; Fettig et al. 2007; Hicke et al. 2012, Korea Forest Service, 2010). Bark beetles impact timbers, fiber productions, wildlife populations, biodiversity, endangered species, and cultural resources (Coulson & Schneider 1992; Coulson & Stephen 2006). In short, their impacts affect ecological, economic, social, and political concerns (Smardon & Karp 1993) and are effectively influenced to the past forest management practices (Coulson & Stephen, 2006). Managing and predicting the impacts of bark beetles on forests perfectly requires an understanding about the normal conditional states of the forests (Coulson & Stephen, 2006). Third hypothesis related to pest species abundance at the each decay stage.

H3: Abundance of pest species such as bark beetles would be higher at the early decay stage than live tree stage.

2. Materials and Methods

2.1. Study site

This study was conducted at Korean fir (*Abies koreana* Wilson) areas of Mt. Halla National Park which is located in the center (N 33° 21' 41" E 126° 31' 46") of the Jeju island on the south of the Korean Peninsula (Figure 1). The elevation of Mt. Halla is 1950 m and it is the tallest mountain in South Korea. Mt. Halla has a distinctive climatic conditions, such as often and strong wind, snow storm during the winter season, and changeable temperatures. Korean fir, one of the subalpine coniferous forests, was distributed from 1,300 m to 1800 m of Mt. Halla and the total area of Korean fir was 795.3 ha (Figure 1, Song et al. 2009). This study was executed at three areas which were located on the eastern slope (Seongpanak, SPA; 33° 23' 04.07" N, 126° 37' 07.94" E), western slope (Yeongsil, YS; 33° 20' 24.96" N, 126° 28' 50.58" E), and southern slope (Donnaeko, DNK; 33° 18' 41.51" N, 126° 34' 16.50" E) of Mt Halla (Figure 2). The study areas had three study plots (100 m x 100 m) and the elevation of each study plot was between 1500 m and 1800 m. Each Korean fir study plot had the eight emergence traps (except Seongpanak III which had only seven emergence traps). Totally 71 trap samples were collected bimonthly from April 2013 to July 2014.

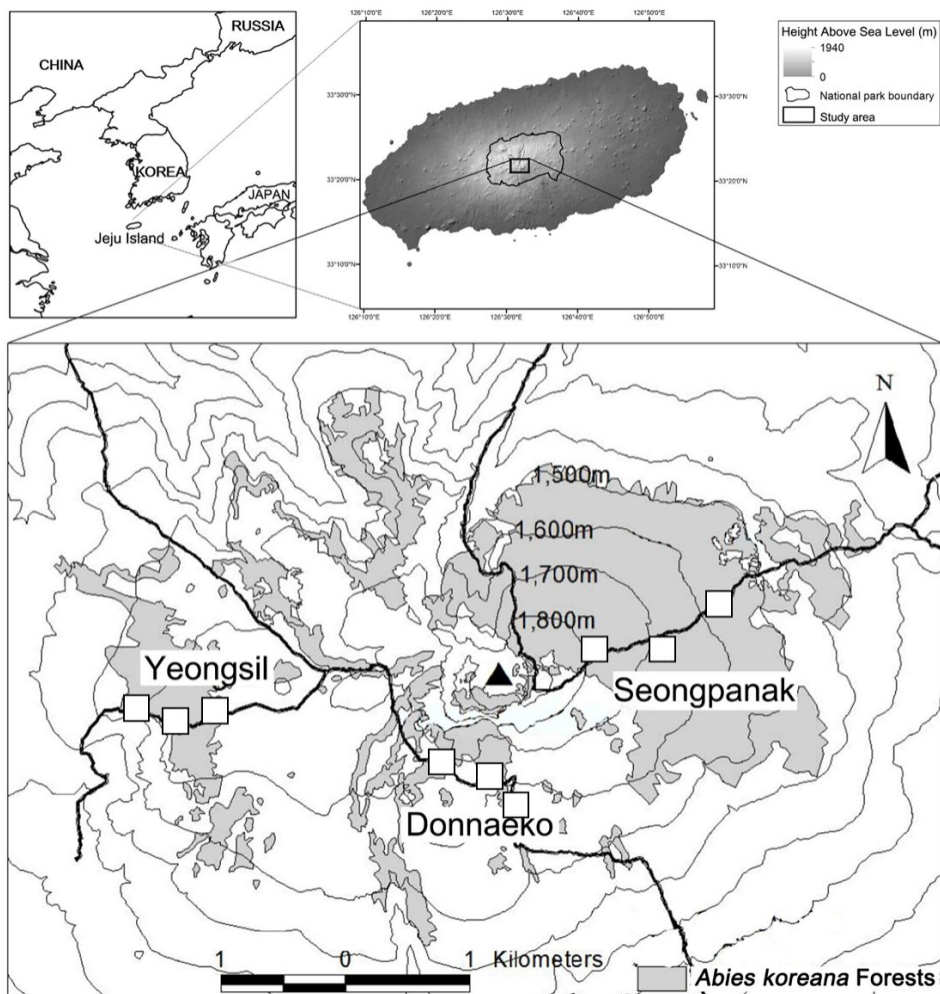


Figure 1. The location map of the three study plots at three study areas (Seongpanak, Yeongsil, Donnaeko) in Mt. Halla (This figure was modified from Song (2011)' s dissertation). The black triangle (▲) is the center of Mt Halla, Baengnokdam.

A.



B.



C.



Figure 2. The three study areas which were located on the (A) Seongpanak (SPA), (B) Yeongsil (YS), and (C) Donnaeko (DNK) of Mt Halla.

2.2. Experimental design

This study was designed to compare the community of arthropods by one live tree and the three-different decay stages of Korean fir. I studied about the live tree and snag-dwelling arthropods. I used tree-decay stage system to identify the decay levels of *A. koreana*. Generally, the five class decay system has been used to describe the extent of decay in deadwood. This system is based on a variety of tree characteristics, including the presence or absence of bark and fine twigs, bole shape, wood texture, etc. (Rose et al. 2001). The five class system was modified and refined into three decay stage system by combining 1 – 2 class (early decay stage), and combining 4 – 5 class (late decay stage). A simplified system of three structural classes has been developed based on the premise that fewer classes were sufficient to describe wildlife use and easier to apply in the field (Rose et al. 2001). Therefore I used three decay stage system to divide *A. koreana* deadwood decay classes.

The full design was consisted of emergence traps, three decay stage system of Korean fir (*A. koreana*) live tree and snags in the three experimental blocks on Mt. Halla. Figure 3 showed the characteristic of each decay stage. Live tree stage has green color leaves. Early decay stage has bark, small branch, and brown color leaves. Middle decay stage has not leaves, just has a few branch. Late decay stage has no leaves and branch, only has a few bark and branch of the trail (Table 1).

I used the emergence traps to collect the live tree and the snag-dwelling arthropods in *A. koreana* forest ecosystems. Within each block, I installed 24 emergence traps: eight traps in each study plot. An emergence trap was enclosed with a 1m x 2m wide strip cloths around the live tree and the snag trunks, and the trap was positioned at the height level of 1.0m ~ 1.5m from the ground (Figure 4). A black plastic fabric barrier was used to be enclosed the trees and snags. Along the borders of the trap, staples and a wire were used to secure the fabric to a wide strip where the bark achieved a close fit from the cloth. A hole was made at the bottom of cloths to hold a cap which is for the transparent plastic container. The volume size of plastic container was 250 ml, and the container was half-filled with 50% attenuated ethylene glycol (Kim 2012). Bimonthly, I collected the arthropod samples.

Table 1. Criteria of distinction for decay stage at the five decay class system (USDA forest service 1979) and three decay stages system.

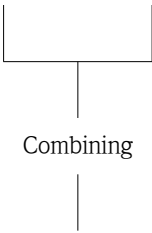
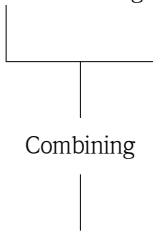
Five decay class system	Class 1	Class 2	Class 3	Class 4	Class 5
Bark	intact	intact	trace	absent	absent
Twigs < 3cm	present	absent	absent	absent	absent
Texture	intact	intact to partly soft	hard, large pieces	small, soft, blocky pieces	soft and powdery
Shape	round	round	round	round to oval	oval
Color of wood	original color	original color	original color to faded	light to faded brown or yellow	fade to light yellow or gray
Three decay stage system					
	Combining			Combining	
	Early decay stage (ED)		Middle decay stage (MD)	Late decay stage (LD)	



Figure 3. Photos of the live tree and the three decay stage snags. A is the live Korean fir (green color, many leaves), B is the early decay stage snag (bark and branch are intact, low leaves), C is the middle decay stage snag (Bark is trace, no leaves, branch is few), D is the late decay stage snag (Bark and Brach are no exist or few, no leaves).

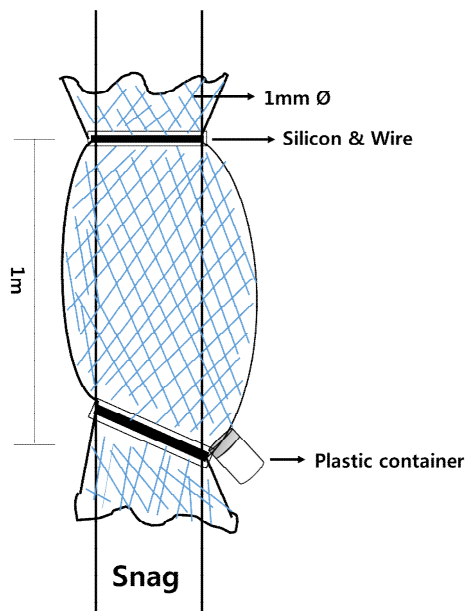


Figure 4. A scheme and a photo of an emergence trap. An emergence trap was consisted of a black plastic fabric (1mmØ) with the sampling bottle half-filled with ethylene-glycol. The height of emergence trap on a snag was one meter, and it is located over one meter from ground.

2.3. Abiotic characteristics of deadwoods

I measured and recorded the possible influence of other variables besides the type of arthropods. These variables included the presence or absence of bark, leaves, and branch, also included diameter at the breast height (DBH), deadwood standing shape, coverage of the deadwood, decay stage (live, early, middle, late). coverage of the deadwood has been divided into 1-5 type (all open, 1/4 open, half open, 3/4 open, all close).

2.4. Sorting and identification of arthropods

The arthropod samples were transported to the laboratory and preserved with 80% ethyl alcohol. All arthropods sample were sorted into collecting date, and I counted and identified to the family level or species level based on morphological taxonomy references (ESK & KSAE, 1994; Lee 1998; Kim 2001; Namgung 2004; Tripplehorn & Johnson 2005; Zhang 2013, KBR webpage).

2.5. Functional feeding groups

The deadwoods provides food and habitat for various organisms. Functional feeding groups are a classification approach that is based on eating food type rather than taxonomic group. The same acquisition of food type in different species can result in the ingestion of a wide

range of food items. The benefit of this method is that instead of hundreds of different taxa to be studied, a small number of groups of organisms can be studied collectively based on the way they function and process energy in the forest ecosystem. Individuals are categorized based on their mechanisms for obtaining food and not specifically on what they are eating. I used the functional feeding groups for arthropods community analyses. The Functional feeding groups divided into ten groups based on type of food. Table 2 explains the definition of each functional feeding group. For examples, *Polygraphus nobuchi* belong to the xylophagous that feed on dying or newly deadwood. I classified the remains of arthropods species based on table 2 (Kappes & Topp 2004; Karpa et al. 2007; Sharkey 2007; Gullan & Cranston 2009). The classified species list is shown in the appendix 1.

Table 2. Ten functional feeding groups and each definition.

Functional feeding group		Definition
Herbivore	Phytophagous	This group includes arthropods which feed on plant matter and possess biting/ chewing mouthparts.
	Xylophagous	Eating dying or newly dead wood, also including ambrosia eaters.
	Saprophagous	Arthropods feeding on dead and decaying plant or animal matter by using enzymes to first liquefy the material, which is subsequently ingested.
	Fungivore	Arthropods feeding on fungi.
	Sap sucker	This group includes organisms which feed on plant matter and possess piercing/sucking mouthparts.
Omnivore		This group is a consumption classification for animals that have the capability to obtain energy and nutrients from materials originating from plant and animal origin.
Predator		This broad group comprises arthropods which feed on other arthropods, irrespective of the mode of feeding.
Parasitoid		This group includes arthropods which feed in or on another living animal for a relatively long time during one or all of their life-stages.
Detritivore		This group is heterotrophs that obtain nutrients by consuming detritus (decomposing plant and animal parts as well as feces)
Uneaten group		When the adults, mouthpart is degenerated, they can not eat anything.
Unknown		Identification impossible

Table 3. Freshness of preferred prey at the each functional feeding group.

Fresh	→			Decayed
Predator	Parasitoid			
Phytophagous	Xylophagous	Saprophagous		Detritivore
Sap-sucker				
Omnivore	Fungivore			

2.6. Statistical analyses

The species diversity was measured by α diversity. In general, α diversity is a measure of microhabitat diversity within a homogeneous community (Cody 1985). To calculate each decay stage diversity, the total number of species (γ diversity) was divided by the average number of species (α diversity) per decay stage and site. The Shannon–Weiner diversity index was calculated, with evenness included, as well as the Simpson diversity index (McCune and Grace 2002).

This experimental design was randomized design. Each study plot considered in the statistical analyses in this study was based on a nested experimental design. Given the randomized design of the experiment, I initially evaluated responses of individual taxa and groups to block and decay stage treatments using a split plot in a time approach by analyses of variance (ANOVAs), with 2 df for block, 3 df for treatment (decay stages). ANOVA was used for test the differences in mean abundance, mean species richness, and mean species diversity for the arthropod community in blocks and decay stages (SAS Institute 2000).

The arthropods communities with the pooled data of each block were analyzed by conducting non-metric multidimensional scaling (NMS) with PC-ORD program version 6.2 (McCune and Grace 2002).

The pooled main matrices for each arthropod sample had high β diversity, moderate to extreme row and column skewness, and a high coefficient of variation among the sums of the columns (species) in the matrix. Thus, rare species that occurred in <5% of the samples were

deleted, and the data were transformed by taking logarithms. The Sorensen distance measure was used for all analyses. The transformed data were used for ordination analysis at this point.

Non-metric multidimensional scaling (NMS) (Mather 1976; Kruskal 1964; Clarke 1993) is an iterative method based on rank distances between sample units. It is useful for ecological gradient studies because of its general robustness and lack of assumptions about the distribution or type of data. Therefore, NMS was used to determine the number of factors structuring the complex arthropod community structure and to qualitatively summarize the overall distribution of species assemblages across the gradients of different decay stage levels and blocks.

I used 14 variables to determine which of the variables had high correlation coefficients. The variables we used for NMS analysis are seven categorical variables (Block, study plot, decay stage, season, altitude, coverage, DBH) and seven quantitative variables (Mean, arthropod abundance, species richness, four community indices). Sorensen distances were used in species space.

Indicator species analysis (ISA)

Indicator species analysis used to elucidate the indicator species for collected each arthropods community in the study blocks by Pc-ord (Clarke and Gorley 2006). The Dufrêne & Legendre (1997) analysis can be used for either quantitative or binary data and begins by calculating the average abundance of each species in each group. This average is then divided by sum of average abundances across all groups. The

resulting value indicates how the abundance of that species is distributed among the group. These IV (Indicate value) range from 0 (No indication) to 100 (Perfect indication).

Multi-response permutation procedures (MRPP)

MRPP is a nonparametric procedure for testing the hypothesis of no difference between two or more groups of entities (McCune and Grace 2002). MRPP provides little more than the test statistic, a measure of “effect size”, and a p-value. Effect size provided by the Chance-corrected within-group agreement (A). MRPP is a permutation-based randomization procedure. It begins by constructing a distance matrix using my distance measure choice Sorensen distances. The sample units belonging to a given group are identified from my data group (4 decay stage, 3 blocks) coding variable and the distances among them are averaged. This is repeated for each group, producing the observed ‘within-group’ average distances for each. These distances are then weighted, usually by the relative size of the group. The resulting p-value from MRPP indicates the probability of having obtained as low an average within-group sample unit distance as my actually observed. The resulting A-value from MRPP indicates the homogeneity of within-group. When all items are identical within group, $A=1$. If heterogeneity within groups, then $A=0$. The multi-response permutation procedure (MRPP) was used to compare similarity between each group and determine the statistical significance of NMS between arthropods communities in each block and decay stage in this study.

3. Results

3.1. Overall deadwood-dwelling arthropods community structure

I collected 69,674 arthropods individuals during the study period (from April 2013 to July 2014), except for larvae individuals. These consisted of 6 classes, 23 orders, 99 families, and 224 species. Average arthropod abundance of each species among the decay stages (L, ED, MD, LD) was shown in Appendix 1. The species with the largest individual number was *Formica japonica* with 30,286 individuals and it comprised of 43.47% from the total individuals. The species with the second large individual number was *Tomocerus* sp. (common name: springtail) with 11,386 individuals and it comprised of 16.34% from the total individuals (Table 4). The species with the third large individual number was *Polygraphus nobuchii* (common name: bark beetle) with 6,067 individuals, and it comprised 8.71% of the total individuals. Myrmecinae sp. with 3,639 individuals comprised of 5.22% from the total individuals. Other species was caught by less than 5% of the total individuals and all taxa.

Table 4. Abundance and proportion of arthropod species in the top ten dominant species.

Class	Order	Family	Species	Abundance	Proportion	Cumulative Percentage
Insecta	Hymenoptera	Formicidae	<i>Formica japonica</i>	30,286	43.47%	43.47%
Entognatha	Collembola	Isotomidae	Tomocerus #1	11,386	16.34%	59.81%
Insecta	Coleoptera	Scolytidae	<i>Polygraphus nobuchii</i>	6,067	8.71%	68.52%
Insecta	Hymenoptera	Formicidae	<i>Myrmica kotokui</i>	3,639	5.22%	73.74%
Entognatha	Collembola	Isotomidae	Tomocerus #4	3,432	4.93%	78.67%
Entognatha	Collembola	Sminthuridae	Sminthuridae #1	2,869	4.12%	82.78%
Arachnida	Opiliones	Opilionidae	Opilionidae #1	1,011	1.45%	84.24%
Arachnida	Sarcoptiformes	Acaridae	Acaridae #1	982	1.41%	85.64%
Insecta	Hemiptera	Aphididae	Aphididae #3	747	1.07%	86.72%

Decay stages : L, ED, MD, LD

In the live trees (L), 17,625 individuals (6 classes, 18 orders, 81 families, 154 species) were caught. In the early decay stage (ED), 19,193 individuals (6 classes, 19 orders, 80 families, 156 species) were caught and in the middle decay stage (MD), 9,348 individuals (6 classes, 19 orders, 75 families, 152 species) were caught. In the late decay stage (LD), 23,508 individuals (6 classes, 20 orders, 81 families, 170 species) were caught.

The mean abundance and the mean species richness per trap in the live tree stage was 259.19 ± 32.334 and 15.71 ± 0.996 , respectively. In the early decay stage, the mean abundance and the mean species richness per trap was 262.92 ± 39.923 and 14.48 ± 0.879 . In the middle decay stage, the mean abundance and the mean species richness per trap was 129.83 ± 12.728 and 13.53 ± 0.806 . In the late decay stage, the mean abundance and the mean species richness per trap was 340.67 ± 77.271 and 17.13 ± 1.216 (Table 5). The mean abundance and mean species richness per trap was higher in the late decay stage than in the middle decay stage and other decay stages. The mean abundance and mean species richness per trap between the live tree stage and the early decay stage was similar. The total abundance was significantly different among each decay stage (L, ED, MD, LD, $P < 0.0143$) by examining the Duncan test, but the total species richness was not significantly different among the decay stages ($P < 0.0579$).

In the Seongpanak area, mean species richness was the highest in the late decay stage, and mean species richness was similar in other decay

stages (L, ED, MD) ($P = 0.0009$; Table 6, Figure 5). Mean species richness in the Yeongsil was the highest in the live tree decay stage ($P=0.0020$; Figure 5). Mean species richness in the Donnaeko was no statistical difference among decay stages (Figure 5). Mean abundance of the each block (Seongpanak, Yeongsil, Donnaeko) was the significant difference among the decay stages. Mean abundance of the Seongpanak and Yeongsil was gradually reduced, and was shown the trends to increase at the late decay stage (Table 6, Figure 5-6). Mean abundance of the Donnaeko was the highest in the late decay stage ($P = 0.0038$; Figure 5).

Effect of block and decay stage

Two factors (block (B), decay stage (D)) and their interactions were compared amongst mean abundance and mean species richness (Table 7). Only 9 taxa were differed significantly by block, mean abundance of only 14 taxa varied significantly among the decay stages; nine of these instances were also significant by B x D interaction. Mean abundance of 13 taxa was affected by B x D interaction.

Table 5. The mean abundance and the mean species richness per trap in the each decay stage (L: Live tree stage, ED: Early decay stage, MD: Middle decay stage, LD: Late decay stage). Each number in mean abundance is mean abundance $\pm$ standard error, and each number is mean species richness is mean species richness $\pm$ standard error. Duncan test was applied to compare each stage in abundance and species richness.

	Decay stages (Mean $\pm$ SE)				P-value
	L	ED	MD	LD	
Mean abundance	259.19 $\pm$ 32.33 ^{ab}	262.92 $\pm$ 39.92 ^{ab}	129.83 $\pm$ 12.73 ^b	340.67 $\pm$ 77.27 ^a	0.0143*
Mean species richness	15.71 $\pm$ 0.99 ^{ab}	14.48 $\pm$ 0.88 ^{ab}	13.53 $\pm$ 0.81 ^b	17.13 $\pm$ 1.22 ^a	n.s.

n.s. No Significant

*Significant at $p \leq 0.05$

Duncan's test is proc ANOVA, Duncan's multiple range test. (a, b, and ab mean different group.)

Table 6. The mean abundance and the mean species richness of arthropods at each decay stage (per trap). (L: Live tree stage, ED: Early decay stage, MD: Middle decay stage, LD: Late decay stage). Results of ANOVA tests were given as P values. Every number is consisted of Mean $\pm$ SE.

	L	ED	MD	LD	P value
Mean abundance	Seongpanak	250.17 $\pm$ 51.06	142.75 $\pm$ 16.58	268.40 $\pm$ 40.91	0.0487*
	Yeongsil	458.40 $\pm$ 67.26	114.96 $\pm$ 19.87	136.96 $\pm$ 17.34	<.0001***
	Donnaeko	102.21 $\pm$ 19.87	131.79 $\pm$ 28.53	613.17 $\pm$ 209.71	0.0038**
Mean species richness	Seongpanak	15.25 $\pm$ 1.17	15.79 $\pm$ 1.18	23.45 $\pm$ 2.70	0.0009***
	Yeongsil	21.50 $\pm$ 1.81	12.38 $\pm$ 1.29	16.76 $\pm$ 1.61	0.0020**
	Donnaeko	11.33 $\pm$ 1.58	12.42 $\pm$ 1.63	12.25 $\pm$ 1.50	n.s.

n.s.No Significant
 *Significant at p $\leq$ 0.05
 **Significant at p $\leq$ 0.01
 ***Significant at p $\leq$ 0.001

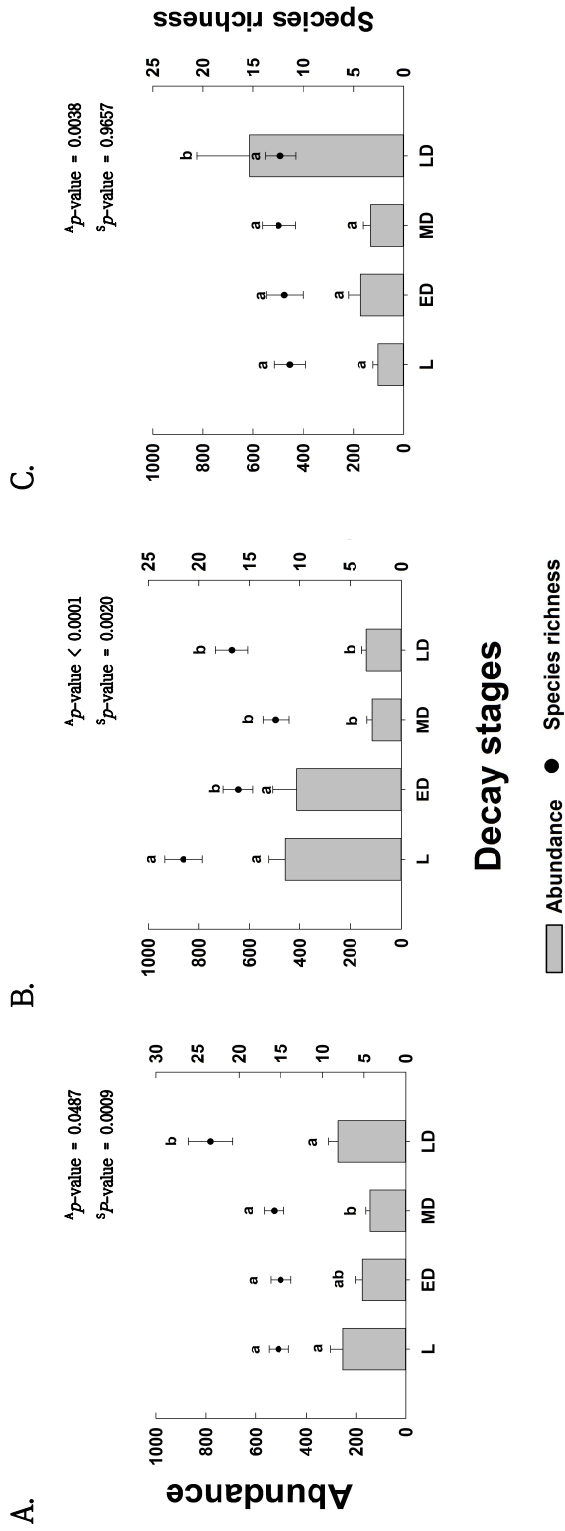


Figure 5. The mean abundance and the species richness in the three study area (A. Seongpanak, B. Yeongsil, C. Donnaeko). Left Y axis is the mean abundance and right Y axis is the mean species richness. X axis is the decay stages (L: live tree stage, ED: early decay stage, MD: middle decay stage, LD: late decay stage). Gray bars of the graph represented the mean abundance. black points showed the mean species richness. ($^A p\text{-value}$: analysis of variance for mean abundance, $^S p\text{-value}$: analysis of variance for mean species richness)

Table 7. ANOVA table for block (B) and decay stages (D) on the mean abundance and the mean species richness of arthropods in this study during the study periods, April 2013 and July 2014. The number in parenthesis indicates degrees of freedom (DF).

Variable	Block (B) (2)	Decay stages (D) (3)	(B x D) (6)
Abundance	n.s.	0.0086**	<.0001***
Species richness	<.0001***	0.0360*	0.0010***

n.s. No Significant

* Significant at $p \leq 0.05$

** Significant at $p \leq 0.01$

*** Significant at $p \leq 0.001$

3.2 Analysis of community indices among the decay stages

The graphs of the community indices among the decay stages in the Seongpanak (SPA) were shown in figure 8. Mean species richness was the highest in the late decay stage, but other stages were similar ($P = 0.0009$). The evenness index (E) was significantly different ($p = 0.0251$). Evenness of middle decay stage was the highest in the decay stages. Evenness of early and late decay stages showed similar values. Shannon's diversity index (H) was no statistical difference, but dominant index (D') was significant difference ($p = 0.0293$). Dominant index of middle decay stage was the highest, but dominant index of early decay stage was the lowest.

The graphs of the community index among the decay stages in the Yeongsil (YS) were shown in figure 8. Mean species richness (S) in the Yeongsil was decreased from the live tree stage to the middle decay stage, and then it was increased at the late decay stage ($p = 0.0020$). The evenness (E), Shannon's diversity index (H) and dominant index (D') were increased among the decay stages, but there were not statistical difference except the evenness value ($p = 0.0036$).

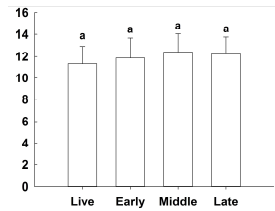
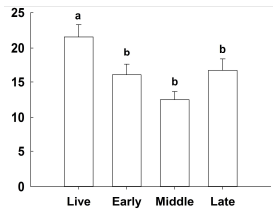
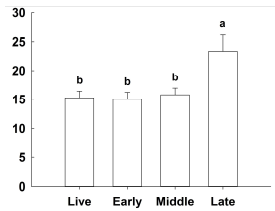
Community index results of the decay stages in the Donnaeko (DNK) were shown in Figure 8. Mean species richness (R) was not statistical difference, and all of the evenness (E), shannon' diversity index (H) and dominant index (D') were the lowest in the late decay stage. Evenness was significantly different, but dominant index and Shannon's diversity index were not statistically different.

a. Species Richness (S)

$P = 0.0009^*$

$P = 0.0020^*$

n.s.

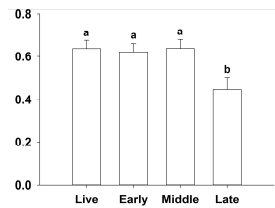
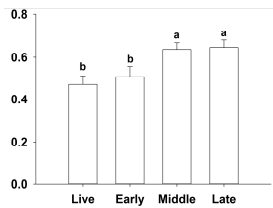
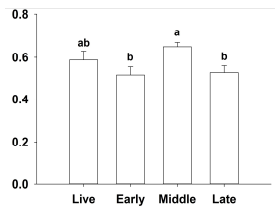


b. Evenness (E)

$P = 0.0251^*$

$P = 0.0036^*$

$P = 0.0057^*$

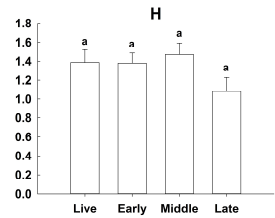
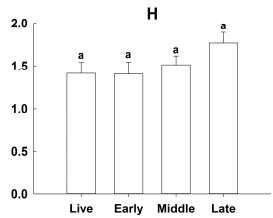
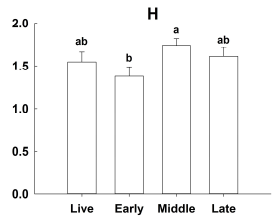


c. Shannon's Diversity Index (H)

n.s.

n.s.

n.s.

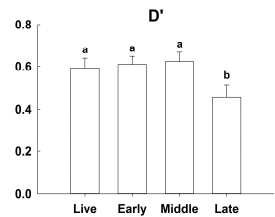
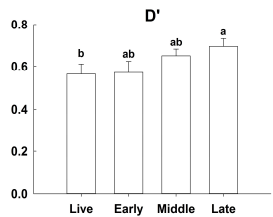
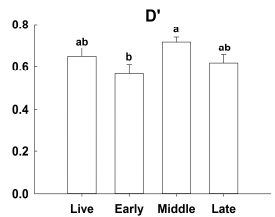


d. Dominant Index (D')

$P = 0.0293^*$

n.s.

n.s.



Seongpanak

Yeongsil

Donnaeko

*significant at $p \leq 0.05$, *n.s.*: no significant

Figure 6. The graphs showed the community indices (a. species richness, b. evenness, c. Shannon diversity index, d. dominant index) among the decay stages (L: live tree stage, ED: early decay stage, MD: middle decay stage, LD: late decay stage) in the three blocks (Seongpanak, Yeongsil, Donnaeko).

3.3. Proportion of functional feeding groups among the decay stages

112 taxa herbivores consisted of phytophagous (Byrrhidae, Chrysomelidae of Coleoptera, Cecidomyiidae and Drosophilidae of Diptera, Tenthredinidae of Hymenoptera; 15 taxa), xylophagous (Bostrichidae, Cerambycidae, Curculionidae, Lyctidae, Pyrochroidae, Scolytidae and Sphindidae of Coleoptera, Siricidae of Hymenoptera; 26 taxa), saprophagous (Elateridae, Melandryidae, Monotomidae, Nitidulidae, Ostomidae and Ptiliidae of Coleoptera, Lauxaniidae and Sphaeroceridae of Diptera, Limnephilidae of Trichoptera, Oniscidae of Isopoda, Julidae of Juliformia ; 23 taxa), fungivores (Ciidae, Leiodidae, Scaphidiidae and Scarabaeidae of Coleoptera, Mycetophilidae of Diptera, Aradidae of Hemiptera, 1 taxa of Thysanoptera; 10 taxa), Sap-sucker (Phoridae, Tephritidae of Diptera, Anthocoridae, Aphididae, Lachnidae, Lygaeidae, Microphysidae, Miridae, Pentatomidae, Pseudococcidae, Tingidae of Hemiptera, Cercopidae, Cicadellidae, Fulgoridae and Psyllidae of Homoptera, 5 taxa of Lepidoptera, 1 taxon of Psocoptera; 38 taxa).

15 taxa omnivores consisted of Collembola (Dicyrtomidae, Hypogastruridae, Isotomidae, Sminthuridae; 8 taxa), Dermaptera (Forficulidae; 1 taxon), Diptera (Lonchaeidae; 1 taxon), Hymenoptera (Formicidae, 5 taxa). 53 taxa predator consisted of Acarina (Acaridae, Bdellidae, Camisiidae, Euphthiracaridae, Galumnidae, Trombidiidae; 14 taxa), Araneae (Clausenidae, Lycosidae, Cybaeidae, Gnaphosidae, Micryphatidae, Salticidae, Theridiidae; 8 taxa), Opilliones (Opilionidae, 1 taxon), Coleoptera (Centharidae, Coccinellidae, Harpalidae, Leiodidae,

Pselaphidae, Staphylinidae; 19 taxa) Diptera (Empididae, Psychodidae, Rhagionidae, Scathophagidae, Tipulidae; 9 taxa), Hemiptera (Reduviidae; 1 taxon), Neuroptera (1 taxon), Lithobiida (1 taxon), Pseudoscorpionida (1 taxon). 30 taxa parasitoid consisted of Diptera (Chloropidae; 1 taxon), Hymenoptera (Ceraphronidae, Cynipidae, Diapriidae, Eulophidae, Ichneumonidae, Megaspilidae, Proctotrupidae, Pteromalidae, Scelionidae; 29 taxa). 7 taxa detritivores consisted of 1 taxon Tenebrionidae of Coleoptera, Diptera (Bibionidae, Calliphoridae, Sciaridae; 5 taxa), 1 taxon Rhaphidophoridae of Orthoptera. 6 taxa etc. group consisted of degenerated mouth parts (Chironomidae of Diptera; 6 taxa) and unknown 1 taxon.

The mean species richness of the fungivore, omnivore and predator groups among the decay stages were significant difference (Table 8, Figure 9). The rest of functional feeding groups had no statistical difference in the decay stage, except for these three groups. Fungivore species tended to increase in accordance with the decay stage. Omnivore species were higher in the early decay stage and the middle decay stage than the live tree stage and the late decay stage. Predator species were lowest in the early decay stage, but generally they were tended to increase according to the process of the decay stages.

The mean abundances of the xylophagous, omnivore, and predator groups according to the process of decay stages were statistically different (Table 8, Figure 10). The mean abundance of xylophagous group was higher in the early decay stage than in other stages. The mean abundance of omnivore group was shown the opposite trend of

species richness, it was lower in the early decay stage and the middle decay stage than in the live tree stage and in the late decay stage. The mean abundance of predator group was the highest in the middle decay stage, and was similar in the live tree stage and in the late decay stage.

Table 8. The proportion (%) of the mean abundance and the mean species richness at each functional feeding group (FFG) in accordance with the live tree stage and the three decay stages (L: Live tree stage, ED: Early decay stage, MD: Middle decay stage, LD: Late decay stage).

FFG	Proportion of mean abundance (%)					Proportion of mean species richness (%)				
	L	ED	MD	LD	p-value	L	ED	MD	LD	p-value
Phytophagous	0.66	0.43	1.27	0.65	n.s.	4.49	3.69	4.11	4.99	n.s.
Xylophagous	11.32	20.93	2.40	0.57	0.0026**	8.24	7.19	5.75	5.41	n.s.
Saprophagous	0.63	1.81	3.26	0.88	n.s.	6.18	7.38	6.47	7.28	n.s.
Fungivore	0.11	0.06	0.87	0.30	n.s.	0.56	0.57	1.54	1.86	0.0031**
Sap-sucker	2.18	7.19	1.31	1.60	n.s.	9.74	10.32	7.60	8.63	n.s.
Omnivore	77.15	62.05	77.61	87.86	0.0109*	28.37	31.41	30.70	29.02	0.0339*
Predator	6.50	5.40	10.56	6.79	0.0454*	30.52	26.96	31.72	32.32	0.0056**
Parasitoid	0.55	0.57	0.74	0.32	n.s.	5.52	5.39	5.24	4.57	n.s.
Detritivore	0.37	0.64	0.74	0.65	n.s.	3.00	3.60	2.87	3.05	n.s.
Uneaten group	0.51	0.91	1.24	0.37	n.s.	3.28	3.31	3.90	2.79	n.s.
Unknown	0.01	0.01	0.01	0.01	n.s.	0.09	0.19	0.10	0.08	n.s.

n.s. No significant

*Significant at $p \leq 0.05$

**Significant at $p \leq 0.01$

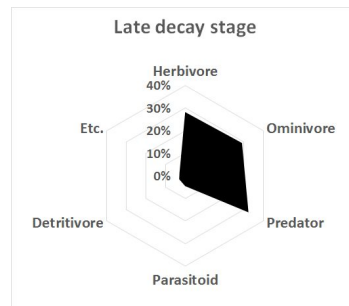
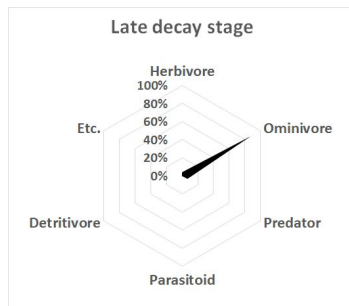
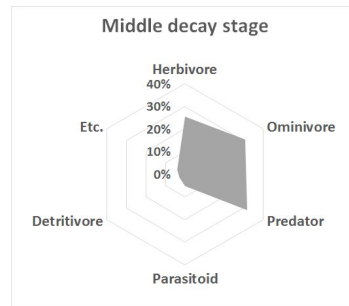
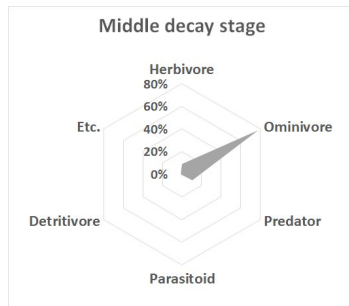
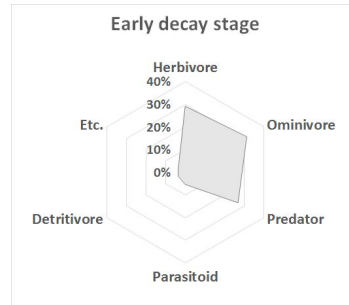
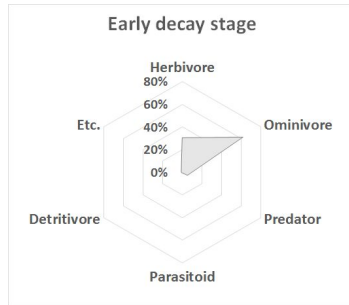
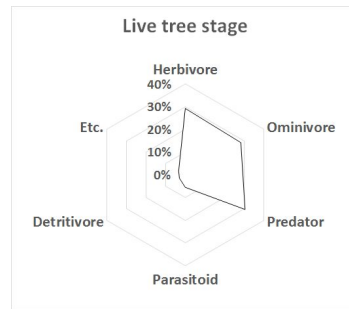
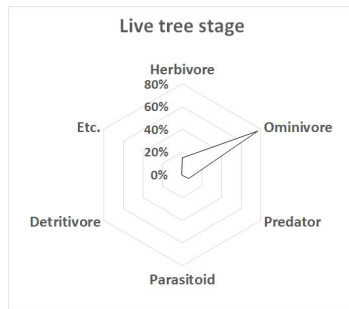


Figure 7. The proportion (%) of the mean abundance and the mean species richness at the five functional feeding groups (herbivore, omnivore, predator, parasitoid, detritivore) in accordance with the live tree stage and the three decay stages.

Seongpanak

The mean species richness of the five functional feeding groups in the Seongpanak was significantly different. The functional feeding groups were phytophagous, saprophagous, omnivore, predator, and detritivore (Table 9, Figure 8). The mean species richness of phytophagous species was the highest in the late decay stage, and there was similar between the live tree stage and the middle decay stage ($p = 0.0191$). The mean species richness of saprophagous and omnivore were the highest in the late decay stage, and there were shown the similar proportion in other decay stages ($p = 0.0002$ and 0.0037). Although detritivore's graph shape was similar to phytophagous group's, the proportion values were big different between in the live tree stage and in the early decay stage, but there was no significant difference between in the live tree stage and in the early decay stage from Duncan's PROC test. The mean species richness of predator was the lowest in the early decay stage ($p = 0.0018$).

The results of the mean abundance proportions between functional feeding groups in the Seongpanak showed in the Table 9, Figure 8. The mean abundance between omnivore and detritivore groups was statistically different ($p = 0.0499$ and $p = 0.0065$). The mean abundance of omnivore was the highest in the live tree stage, and the lowest in the middle decay stage. The mean abundance of detritivore was the highest in the late decay stage, the mean abundance of other stages were not statistically different from Duncan's PROC test.

Yeongsil

Table 9 and figure 8 showed the proportion (%) of the species richness at the functional feeding group of Yeongsil in accordance with decay stage. There was statistical difference proportion of the species richness in the phytophagous, saprophagous, omnivore and predator. Phytophagous and saprophagous were the highest in the live tree stage. Saprophagous was decreased among the decay stages, but phytophagous was higher in the late decay stage than in the early and middle decay stage. Omnivore was the highest in the live tree stage, and the lowest in the middle decay stage. Predator was decreased from in the live tree stage to middle decay stage, and then increased as much as live tree stage at the late decay stages. Table 9 and figure 8 shown the proportion (%) of the arthropods abundance at the functional feeding group of Yeongsil in accordance with decay stage. Only two group, xylophagous and omnivore were significant difference between tree decay stages. Xylophagous was the highest in the early decay stage, and abundance of in the middle and late decay stage were very lower than early decay stage. Omnivore abundance was decreased from live tree stage to middle decay stage, and there were similar values between middle decay stage and late decay stage.

Donnaeko

Table 9 and figure 8 shown the proportion (%) of the species richness at the functional feeding group of Donnaeko in accordance with decay stage. There was no significant difference in the each functional feeding

group among the decay stages. In the omnivore and degenerated mouth parts groups abundance was statistically different between tree decay stages (Table 9 and Figure 8). omnivore abundance was significantly the highest in the late decay stage, and there was no significant difference in the live tree, early and middle decay stage. In contrast, Degenerated mouth parts abundance was the highest in the live tree stage, and the other stages abundance was no statistically significant differences.

Table 9. The proportion (%) of the mean abundance and the mean species richness at each functional feeding group (FFG) in accordance with the live tree stage and the three decay stages (L.: Live tree stage, ED: Early decay stage, MD: Middle decay stage, LD: Late decay stage) on the three study area.

FFG	Seongpanak					Yeongsil					Dernaeko					
	L	ED	MD	LD	p-value	L	ED	MD	LD	p-value	L	ED	MD	LD	p-value	
Mean Abundance	Phytophagous	0.75	0.97	1.34	1.47	n.s.	0.61	0.29	1.27	0.99	n.s.	0.65	0.24	1.20	0.27	n.s.
	Xylophagous	8.41	14.56	1.81	1.49	n.s.	15.50	30.16	4.24	0.82	0.0087**	2.81	0.69	1.42	0.18	n.s.
	Saprophagous	0.72	6.09	6.39	1.96	n.s.	0.51	0.49	0.94	1.40	n.s.	0.86	0.90	1.90	0.37	n.s.
	Fungivore	0.23	0.21	0.38	0.56	n.s.	0.04	0.02	2.25	1.02	n.s.	0.04	0.00	0.19	0.03	n.s.
	Sap-sucker	1.33	1.65	1.49	4.68	n.s.	1.92	5.99	1.30	3.01	n.s.	5.26	17.00	1.11	0.14	n.s.
	Omnivore	80.96	67.05	73.53	73.68	0.0499*	74.89	56.62	76.66	76.90	0.0004***	76.27	72.28	82.86	95.58	0.0030**
	Predator	6.81	7.15	12.00	12.43	n.s.	5.22	4.07	9.35	13.26	n.s.	10.52	7.36	10.05	3.23	n.s.
	Parasitoid	0.40	0.61	0.47	0.63	n.s.	0.41	0.51	1.01	0.76	n.s.	1.43	0.69	0.79	0.11	n.s.
	Detritivore	0.10	0.87	0.55	2.22	0.0065**	0.50	0.63	1.56	0.91	n.s.	0.57	0.40	0.22	0.02	n.s.
	Uneaten group	0.28	0.80	2.01	0.89	n.s.	0.37	1.22	1.41	0.88	n.s.	1.59	0.13	0.25	0.06	0.0402*
Unknown	-	0.02	0.03	-	n.s.	0.01	0.01	-	0.06	n.s.	-	-	-	-	-	
Mean Species richness	Phytophagous	3.28	5.56	3.96	5.76	0.0191*	5.81	3.21	4.38	5.01	0.0335*	4.04	1.92	4.03	3.74	n.s.
	Xylophagous	7.92	8.33	5.54	5.54	n.s.	8.14	8.03	6.79	5.25	n.s.	8.82	4.21	5.03	5.44	n.s.
	Saprophagous	6.28	7.78	8.18	10.23	0.0002***	6.74	7.34	4.71	3.58	0.0240*	5.15	6.90	6.04	7.82	n.s.
	Fungivore	0.55	1.11	1.85	2.13	n.s.	0.80	0.46	1.68	1.67	n.s.	0.37	0.00	1.01	1.70	n.s.
	Sap-sucker	9.29	10.00	8.18	9.59	n.s.	10.00	10.55	6.73	9.55	n.s.	9.93	10.34	7.72	5.78	n.s.
	Omnivore	30.60	30.00	29.29	26.23	0.0037**	24.42	27.98	30.30	26.01	0.0076**	31.62	39.08	32.89	37.76	n.s.
	Predator	33.61	22.78	32.19	28.36	0.0018**	29.53	30.50	28.62	37.71	0.0014**	27.94	26.82	34.23	30.95	n.s.
	Parasitoid	4.64	6.11	3.43	4.69	n.s.	6.05	4.36	7.74	4.77	n.s.	5.88	6.13	5.03	4.08	n.s.
	Detritivore	1.09	4.17	2.64	5.12	0.0008***	4.88	3.44	4.04	2.63	n.s.	2.57	3.07	2.01	0.34	n.s.
	Uneaten group	2.73	3.89	4.49	2.35	n.s.	3.49	3.90	5.05	3.58	n.s.	3.68	1.53	2.01	2.38	n.s.
Unknown	-	0.28	0.26	-	n.s.	0.23	0.23	-	0.24	n.s.	-	-	-	-	-	

n.s. No significant

*Significant at $p \leq 0.05$

**Significant at $p \leq 0.01$

***Significant at $p \leq 0.001$

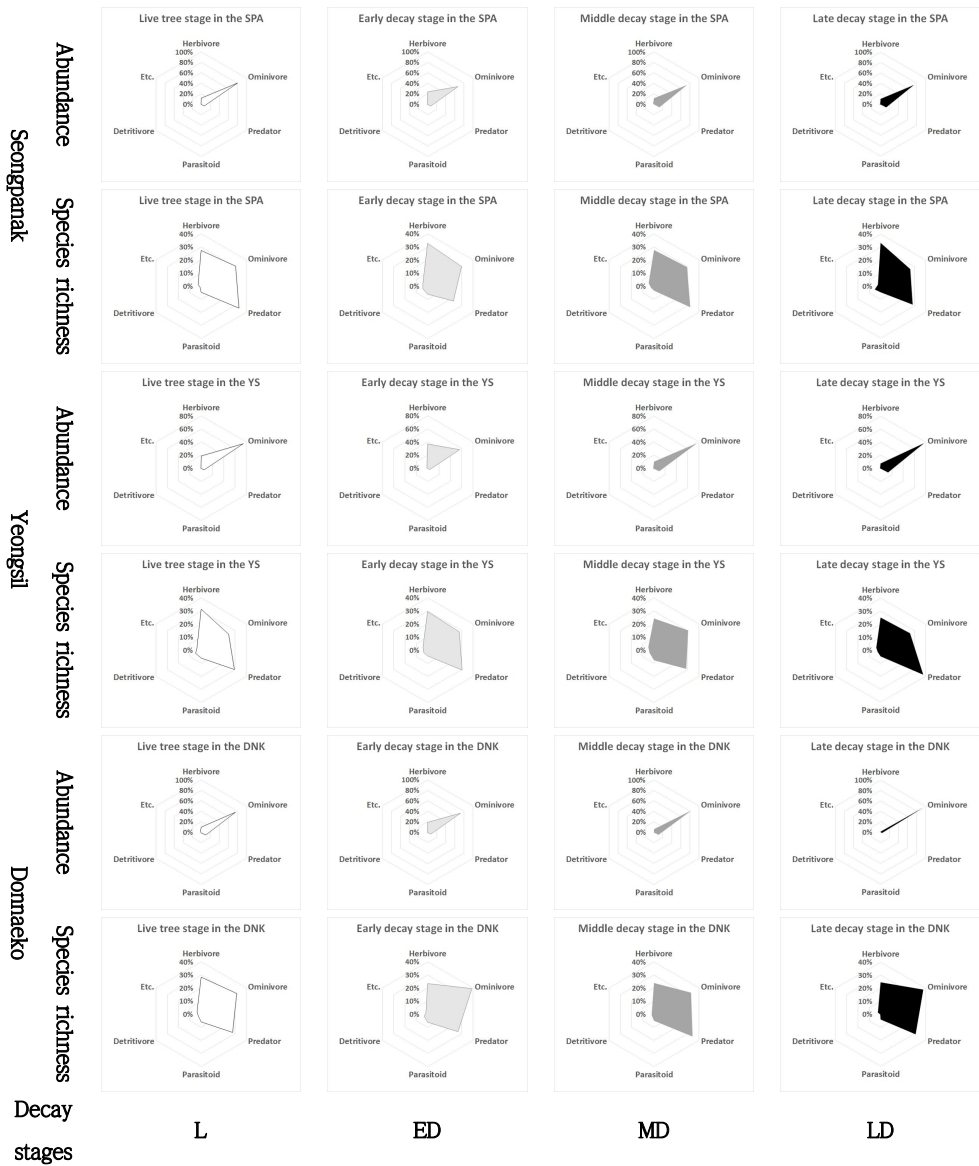


Figure 8. The proportion (%) of the mean abundance and the mean species richness at the five functional feeding groups (herbivore, omnivore, predator, parasitoid, detritivore) in accordance with the live tree stage and the three decay stages.

3.4 Indicator species analysis (ISA)

Results of the Dufrêne & Legendre (1997) indicator species analysis examined the responses of individual species to decay stage variables abundance in the each block (Seongpanak, Yeongsil, Donnaeko). Indicator values (IV) were summarized with the decay stages in Table 10 shows only significant taxa with p-value less than 0.05.

Twenty arthropods species were statistically significant chosen as indicators for the Live tree stages. Among these 20 taxa, Araneae and Opiliones had each 1 taxon (Opilionidae and Salticidae each 1 taxon), Coleoptera had 10 taxa (Cantharidae 1 taxon, Chrysomelidae 2 taxa, Curculionidae 2 taxa, Harpalidae 1 taxon, Nitidulidae and Scolytidae each 1 taxon, Staphylinidae 1 taxon), Dermaptera had 1 taxon (Forficulidae), Diptera had 1 taxon (Tipulidae 1 taxon), Hemiptera had 2 taxa (Anthocoridae and Lachnidae), Homoptera had Cicadellidae 1 taxon, Hymenoptera had 4 taxa (Eulophidae 1 taxon, Formicidae 2 taxa, Ichneumonidae 1 taxon). Herbivore group of the twenty indicators was higher species than other functional feeding groups [nine herbivores (phytophagous 2taxa, xylophagous 3 taxa, saprophagous 1 taxon, Sap-sucker 3 taxa), six predators, three omnivores, two parasitoids]. Early decay stage had 7 taxa of arthropods as indicators. 1 taxon was Dicyrtomidae of Collembola. 3 taxa were Coleoptera (Monotomidae, Scolytidae, Tenebrionidae). 2 taxa were Hemiptera (Lachnidae, Miridae), and 1 taxon was Formicidae of Hymenoptera. Like live tree stage, Herbivore group (4 taxa) was higher species than omnivore (2 taxa) and

detritivore (1 taxon). Middle decay stage had only 3 arthropods taxa as indicators. Among these 3 taxa, 1 taxon Lycosidae of Araneae, 1 taxon Acaridae of Sarcoptiformes, 1 taxon Staphylinidae of Coleoptera. There was only predator group as indicators. Twenty-three taxa of arthropods for the late decay stage were significant indicators. Two taxa were Cybaeidae and Micryphatidae of Araneae, and three taxa were Sarcoptiformes (two taxa of Euphthiracaridae, 1 taxon of Galumnidae). One taxon was Isotomidae of Collembola, and six taxa were Coleoptera (Byrrhidae, Cantharidae, Cerambycidae, Elateridae, Melandryidae, Nitidulidae). Diptera had 4 taxa as indicators (each 1 taxon of Drosophilidae and Lonchaeidae, 2 taxa of Sciaridae). Homoptera had 2 taxa as indicators (Cicadellidae and Psyllidae), Hymenoptera had 6 taxa as indicators (Diapriidae 2 taxa, Formicidae 3 taxa, Ichneumonidae 1 taxon). Eight taxa of total indicator for the late decay stage were herbivores (phytophagous 2 taxa, xylophagous 1 taxon, saprophagous 3 taxa, Sap-sucker 2 taxa). Predators and omnivore were each 5 taxa of the indicators, detritivores were 2 taxa, parasitoid was three taxa. Eight taxa for the Live tree stage, one taxon for Middle decay stage, and fifteen taxa for Late decay stage, have low p-values (0.01). One taxon for the live tree stage, [Formica japonica (IV=57.7)] and three taxa for the late decay stage, [Oribotritia of Euphthiracaridae (IV=37.7), Tomocerus #2 of Isotomidae (IV=50.0), Chalciosphaerium #1 of Byrrhidae (IV=53.2)] have especially low p-values (0.001).

3.5 Results of multi-response permutation procedures (MRPP)

I found that there was difference of species composition among the three blocks (Seongpanak, Yeongsil, Donnaeko) from the results of MRPP ($P = 0.000$, $A = 0.020$). Also species composition according to decay stages (L, ED, MD, LD) was statistically different ($P = 0.000$, $A = 0.010$).

Table 10. Indicator species of each decay stage (Total abundance). Monte Carlo test of significance of observed maximum indicator value (IV) for each species in the Mt. Halla area. (FFG: functional feeding group, Degrees of freedom: decay stage d.f. = 3,^aSpecies with two or more maxgroup. ^bIV: Observed Indicator value. SPA is Seongpanak, YS is Yeongsil, DNK is Donnaeko. *Significant at $P \leq 0.05$. **Significant at $P \leq 0.01$. ***Significant at $P \leq 0.001$.)

Stages	Species Name			FFG	IV ^b
Live tree stage	Arachnida	Opiliones	Opilionidae #1	Predator	YS (28.2*)
	Insecta	Araneae	Phidippus #1	Predator	YS (27.7*)
		Coleoptera	<i>Asiopodabrus fragiliformis</i>	Predator	YS (20.0**)
			Altica #1	Phytophagous	YS (23.0*)
			<i>Syneta adamsi</i>	Phytophagous	YS (22.3**)
		Curculionidae	<i>Anthonomus rectirostris</i>	Xylophagous	YS (13.4*)
			<i>Hylobius haroldi</i>	Xylophagous	YS (14.3*)
			<i>Asaphidion semilucidum</i>	Predator	SPA (16.9*), YS (20.7*)
		Harpalidae	^a <i>Carpophilus chalybeus</i>	Saprophagous	YS (10.0*)
		Nitidulidae	^a <i>Polygraphus nobuchii</i>	Xylophagous	DNK (24.2*)
		Scolytidae	<i>Tachinus sibiricus</i>	Predator	YS (15.5*)
		Staphylinidae	<i>Forficula scudderi</i>	Omnivore	YS (16.0*), DNK (13.9*)
		Forficulidae	<i>Tipula taikun</i>	Predator	SPA (26.5**), YS (27.2**)
		Tipulidae	Anthocoridae #3	Sap-sucker	DNK (20.8**)
		Anthocoridae	^a Cinara #1	Sap-sucker	SPA (21.4**)
		Lachnidae	Cicadellidae #1	Sap-sucker	YS (16.2*)
		Cicadellidae	Eulophidae #4	Parasitoid	YS (11.8*)
		Eulophidae	^a <i>Formica japonica</i>	Omnivore	YS (57.7***)
		Formicidae	^a <i>Myrmica kurokii</i>	Omnivore	YS (33.7**)
		Ichneumonidae	Ichneumonidae #1	Parasitoid	YS (10.0*)
Early decay stage	Entognatha	Collembola	Ptenothrix #1	Omnivore	DNK (19.9*)
	Insecta	Dicyrtomidae	<i>Monotoma longicollis</i>	Saprophagous	YS (17.9*)
		Monotomidae	^a <i>Polygraphus nobuchii</i>	Xylophagous	YS (39.5*)
		Scolytidae	<i>Misolampidius chejuensis</i>	Detritivores	DNK (11.8*)
		Tenebrionidae	^a Cinara #1	Sap-sucker	DNK (22.5*)
		Lachnidae	Miridae #1	Sap-sucker	SPA (13.3*)
		Miridae	^a <i>Myrmica kurokii</i>	Omnivore	SPA (28.5*)
		Formicidae			
		Hymenoptera			

Table 10. Indicator species of each decay stage (Total abundance). Monte Carlo test of significance of observed maximum indicator value (IV) for each species in the Mt. Halla area. (FFG: functional feeding group, Degrees of freedom: decay stage d.f. = 3, ^aSpecies with two or more maxgroup, ^{IV}: Observed Indicator value. SPA is Seongpanak, YS is Yeongsil, DNK is Donnaeko. *Significant at $P \leq 0.05$. **Significant at $P \leq 0.01$. ***Significant at $P \leq 0.001$.)

Stages	Species Name			FFG	IV ^a
Middle decay stage	Arachnida	Araneae	Lycosidae	Lycosidae #1	SPA (13.7*)
		Sarcoptiformes	Acaridae	Acaridae #1	SPA (17.9**)
	Insecta	Coleoptera	Staphylinidae	Staphylinidae #2	DNK (25.6*)
	Arachnida	Araneae	Cybaeidae	Cybaeidae #1	YS (31.4**)
			Micryphatid	Micryphatidae #1	DNK (18.7**)
		Sarcoptiformes	Euphthiracaridae	Oribotritia	SPA (24.1**), YS (37.7****)
			Galumnidae	galumnidae #1	YS (17.5*)
	Entognatha	Collembola	Isotomidae	Tomocerus #2	SPA (50.0****)
	Insecta	Coleoptera	Byrrhidae	Chalciosphaerium #1	SPA (53.2****)
			Cantharidae	<i>Asiopodabrus fragiliformis</i>	SPA (29.8**)
			Cerambycidae	<i>Leptura annularis</i>	SPA (23.5**)
			Elateridae	<i>Melanotus castanipes</i>	SPA (12.9*)
			Melandryidae	<i>Orchesia imitans</i>	SPA (12.9*)
			Nitidulidae	^a <i>Carpophilus chalybeus</i>	SPA (26.2**)
		Diptera	Drosophilidae	Drosophila #1	SPA (18.8**)
			Lonchaeidae	Protearomyia #1	SPA (10.0*)
			Sciariidae	Bradyia #1	SPA (26.6**)
			Sciariidae	Bradyia #2	SPA (10.0*)
	Homoptera		Cicadellidae	Cicadellidae #3	SPA (17.6*)
			Psyllidae	Psyllidae #1	SPA (29.9**)
Late decay stage	Hymenoptera		Diapriidae	Diapriidae #3	SPA (10.0*)
			Diapriidae	Diapriidae #4	SPA (15.7**)
			Formicidae	^a <i>Formica japonica</i>	DNK (74.8**)
			Formicidae	^a <i>Myrmica kotokui</i>	DNK (35.8*)
			Formicidae	^a <i>Myrmica kurokii</i>	DNK (19.9*)
			Ichneumonidae	Ichneumonidae #2	SPA (10.0*)
				Parasitoid	

Table 11. Results of Multi-response permutation procedures (MRPP). d.f is degree of freedom.

Variable (d.f)	A - value	P-value
Blocks (3)	0.021	0.000
Decay stage (4)	0.010	0.000
Tree characteristics		
Bark (3)	0.004	0.005
Leaf (3)	0.006	0.000
Branch (4)	0.005	0.003
Statu (3)	0.003	0.015
Cover (4)	0.011	0.000

3.6 Nonmetric multidimensional scaling (NMS)

Nonmetric multidimensional scaling (NMS) was performed on a dataset consisting of 224 morphospecies captured in this study using PC-ORD (McCune and Mefford 2006).

Seongpanak (SPA) was analyzed by using the 171 species in the 92 traps. The results of Seongpanak NMS explained approximately 32.8% of variance for axis 1 and approximately 24.7% of variance for axis 2. The species richness and tree DBH showed increasing tendency along axis 1. The evenness (E) and Dominant index (D') showed increasing tendency along axis 2. Arthropods community of the decay stages in the Seongpanak was similar between early decay stage and middle decay stage (Figure 9). There was significant difference between the decay stages ($A = 0.028$, $P = 0.000$).

Yeongsil (YS) was analyzed by using the 173 species in the 96 traps. The results of Yeongsil NMS explained approximately 26.6% of variance for axis 1 and approximately 26.3% of variance for axis 2. The species richness, Shannon's diversity index and Dominant index (D') showed increasing tendency along axis 1. Arthropods community of the decay stages in the Yeongsil showed a shape overlapping each the portion (Figure 9). There was significant difference between the decay stages ($A = 0.032$, $P = 0.000$).

Donnaeko (DNK) was analyzed by using the 149 species in the 94 traps. The results of DNK NMS explained approximately 34.6% of variance for axis 1 and approximately 23.4% of variance for axis 2. The species

richness showed increasing tendency along axis 1. Arthropods community of the decay stages in the DNK showed a shape overlapping almost part of each decay stage cloud (Figure 9). But there was no significant difference between the decay stages ($A = 0.006$, $P = 0.074$).

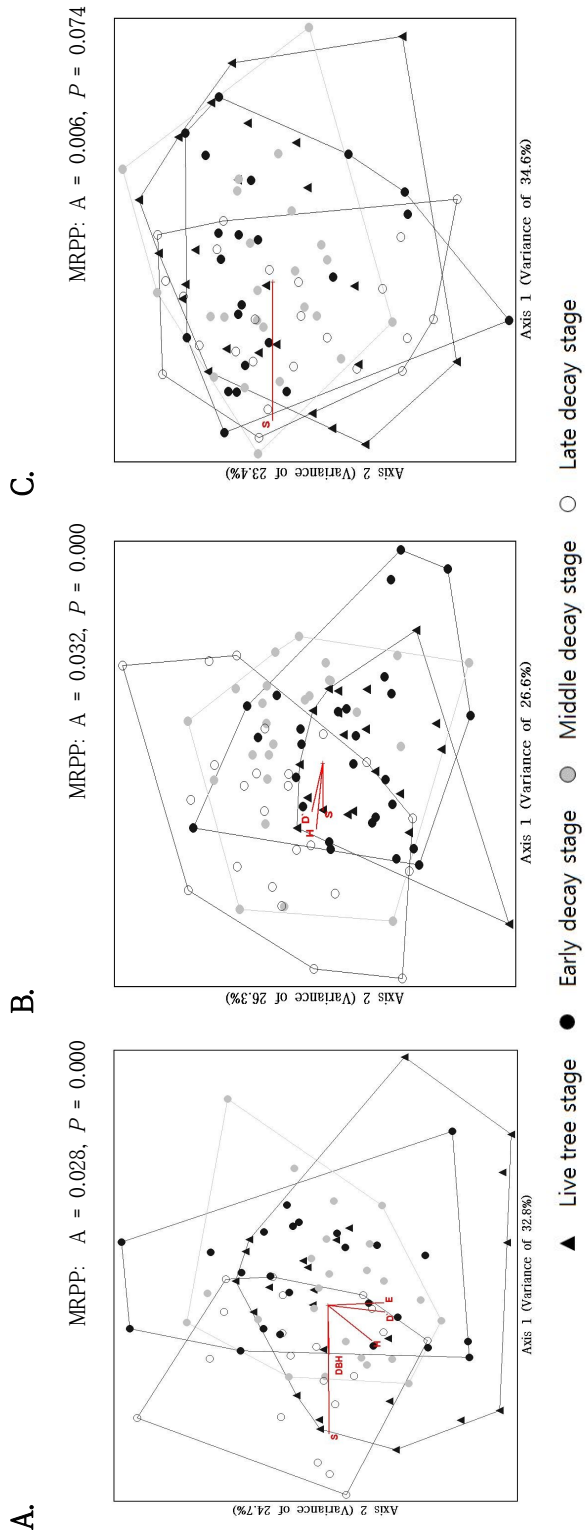


Figure 9. Non-metric Multidimensional Scaling (NMS) plot of the total collected arthropods according to decay stages (Live tree, early, middle, late) in three study areas from April 2013 to July 2014. S: species richness, DBH: diameter at the breast height, H: shannon's diversity index, D' : dominant index, E: evenness index.

3.7 Identified species only in each stage of decay stages

Seven taxa were identified in the tree of only live tree stage and six taxa of them were singleton. Fifteen taxa were identified in the tree of only early decay stage and thirteen taxa of them were singleton. Eleven species were identified in the only middle decay stage, eight species of them were singleton. Twenty-three taxa were identified in the only late decay stage, among them, seventeen taxa were singleton (Table 12).

Table 12. Arthropod species found only in each stage among one the live tree stage and the three decay stages.

Scientific Name		Feeding functional group	No. of Individuals
Live tree stage		7 species	
Coleoptera	Chrysomelidae	Chrysomelidae #1	1
	Melandyridae	Melandyra #1	1
Diptera	Bibionidae	<i>Bibio pseudoclavipes</i>	2
Hemiptera	Pentatomidae	Pentatomidae #3	1
Hymenoptera	Pteromalidae	Pteromalidae #1	1
Thysanoptera	Unclassified	Thysanoptera #1	1
Araneae	Theridiid	Theridiidae #1	1
Early decay stage		15 species	
Coleoptera	Cerambycidae	<i>Pidonia puziloi</i>	1
	Curculionidae	Curculionidae #2	1
	Harpalidae	<i>Pterostichus raptor</i>	1
	Leiodidae	Anisotoma #1	1
	Melandyridae	Orchesia #1	1
	Ptiliidae	Ptiliidae #1	1
	Pyrochroidae	<i>Pseudopyrochroa laticollis</i>	1
	Calliphoridae	Calliphoridae #1	1
	Chironomidae	Stenochironomus #1	2
	Ichneumonidae	Ichneumonidae #5	1
Diptera	Siricidae	Siricidae #1	1
	Siricidae	Siricidae #2	1
Hymenoptera	Unclassified	Moth #1	1
	Unclassified	Moth #2	1
Lepidoptera	Unclassified	Unknown	1
Acarina	Unclassified		6

Table 12. Arthropod species found only in each stage among one live tree stage and three decay stages.

Scientific Name		Feeding functional group	No. of Individuals
Middle decay stage		11 species	
Coleoptera	Chrysomelidae	Altica #2	Phytophagous 1
		Galerucinae #1	Phytophagous 1
		Galerucinae #2	Phytophagous 1
	Ostomidae	Ostomidae #1	Saprophagous 1
Hemiptera	Aphididae	Aphididae #2	Sap-sucker 1
Homoptera	Cercopidae	Cercopidae #1	Sap-sucker 1
Hymenoptera	Formicidae	Lasius #2	Omnivore 2
	Siricidae	Siricidae #3	Xylophagous 3
Lepidoptera	Unclassified	Moth #4	Sap-sucker 1
		Moth #5	Sap-sucker 1
Trichoptera	Unclassified	Trichoptera #1	Saprophagous 3
Late decay stage		23 species	
Coleoptera	Byrrhidae	Chalciosphaerium sp	Phytophagous 1
Coleoptera		<i>Simplocaria bicolor</i>	Phytophagous 1
	Coccinellidae	Coccinella #1	Predator 1
	Curculionidae	Curculionidae #3	Xylophagous 6
		Curculio #1	Xylophagous 2
		Curculio #2	Xylophagous 1
		<i>Curculio hallasanensis</i>	Xylophagous 1
	Lyctidae	<i>Lyctus brunneus</i>	Xylophagous 2
	Scaphidiidae	Scaphidium #2	Fungus Feeder 1
	Staphylinidae	Staphylinidae #3	Predator 1
		Tachyporinae #1	Predator 1

Table 12. Arthropod species found only in each stage among one live tree stage and three decay stages.

Scientific Name		Feeding functional group	No. of Individuals
Diptera Hemiptera	Tipulidae	Predator	1
	Aradidae	Fungus Feeder	1
	Miridae	Sap-sucker	1
		Sap-sucker	2
		Sap-sucker	1
Hymenoptera		Parasitoid	2
		Parasitoid	11
		Herbivore	1
		Predator	1
		Sap-sucker	1
Neuroptera		Saprophagous	1
Psocoptera		Predator	1
Trichoptera			
Acarina			
	<i>Limonia margarita</i>		
	aradidae #1		
	Miridae #2		
	Miridae #3		
	Miridae #5		
	Ceraphronidae #1		
	Ichneumonidae #2		
	Tenthredinidae #1		
	Neuroptera #1		
	Psocus #1		
	Limnephilidae #1		
	Bdellidae #2		

4. DISCUSSION

Deadwoods are surely clarified as very important elements in the forest ecosystems through several studies (Irmeler et al. 1996; Dudley and Vallauri 2005; Brin et al. 2011; Verkerk et al. 2011; Lassauce 2012; Delph et al. 2014). Although some study of deadwoods was conducted in vegetation dynamics and vegetation mortality (Lim et al. 2006; Song et al. 2014), this is the first study regarding Korean fir deadwood dwelling arthropods in Korea. This study is dealing with the arthropod composition inside *A. koreana* deadwood in the Mt. Halla with the three hypotheses.

Deadwood-dwelling arthropods

Through this study, it was found 224 species of 22 orders in the live tree and the deadwood of *A. koreana*. Coleoptera of them was 75 species and the 33.5% proportion of the total species (Figure 10). *Polygraphus nobuchii* was the highest abundant species among Coleoptera order, and the species accounted for 77.8% (6,067 individuals) of the total Coleoptera abundance. Staphylinidae #2 (Staphylinidae), Altica #1 (Chrysomelidae) showed the second highest abundance, but they had a proportion less than 5% of the total species. *Polygraphus nobuchii* was the highest abundance (50.24 ± 18.79) in the early decay stage among the live tree stage and other two decay stages, 25.51 ± 9.09 individuals found in the live tree stage were the next higher (Figure 11). Two species of ambrosia beetle were collected in this study, the species

abundances were confirmed by 0.8% and 0.1% of the percentage of each species with less than 100 individuals. According to the Kwon et al. (2011), the occurrence patterns of bark beetles living on deadwoods of *Quercus serrata* and *Carpinus laxiflora* were the highest in the early decay stage and the live tree stage. Although Kwon et al. (2011) and this study have only a difference of tree species, but both studies were never independent. Typically, bark beetle is known as pests that attack the bark of trees, most of bark beetles will not move onto living trees, and they will only utilize the stressed trees or the newly dead trees (Peltonen 1999). It is also expected gradually to increase the damages caused by climate changes (Kamata et al. 2002; Choi 2011). Although it has been performed an intermittent thinning or removed deadwoods in the forest as a way to prevent the spread of bark beetle pests around the world (Houston 1981; Hagar 2007), this primary pest management way is bringing the results to be undermined even when the forests must be preserved. A long-horned beetle is a well-known pest as a wood-boring insect, total 60 individuals of 5 species were collected in this study, and the highest abundance was in the live tree stage, but specific species (*Leptura anularis*) was the highest abundance in the late decay stage (Figure 12).

The species richness of Hymenoptera was the higher order than other orders of arthropods. It had 17.0% species richness proportion of the total, and the abundance of Hymenoptera was 34,513 individuals, as the highest order among the other orders (Figure 10). The higher abundances of Hymenoptera belong to the Formicidae family, the sum of

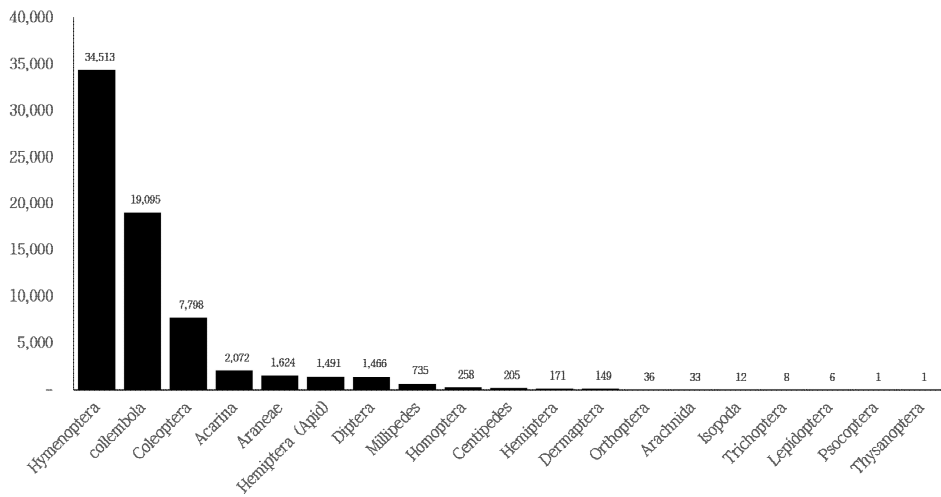
three high abundance was about 99.0% proportion in the total Hymenoptera abundance. Figure 13 showed the *Formica japonica* abundance of per trap among the decay stages. *Formica japonica* was the highest species in the late decay stage (204.54 ± 71.38), it was higher in the live tree stage (113.16 ± 23.51), and it was followed in the early decay stage (64.10 ± 14.04) and in the middle decay stage (33.53 ± 7.48) order.

In this study, I found five ant species, four of which were forest forager. The other species was *Formica japonica*, a grassland forager. According to Kwon et al. (2014), the expansion of exposed open habitats is a major cause to increase the grassland foragers in the forest ecosystems. This may explain why the species is most abundant in the forest ecosystems. Recently, the study blocks in the Mt. Halla were disturbed by climate changes such as heavy rains, heavy wind, and heavy drought, and it caused to increase many Korean fir deadwoods with increasing open areas in the forest.

35 species of Diptera were accounted for 15.6% of the total species richness (Figure 10). Coleoptera and Hymenoptera had the certain species with a proportion of 50% or more. The dominant species of Diptera, *Stenochironomus* #2 (Chironomidae), was low proportion 18.1% of the total Diptera abundance. The other species of Diptera had 0.1% ~ 18.1% proportion of total abundance. When Chironomids became to the adult insects, their mouth parts are degenerating, and they never eat any foods. Nevertheless, *Stenochironomus* #2 (Chironomidae) showed the highest abundance among Diptera species. Generally, Chironomids live

everywhere there is moisture or water. Some researchers found them in wetlands, lakes, streams, damp soil and moss, and around waterfalls on slick rock surfaces. Some specialize in surviving in rock depressions or in tree holes where water is temporarily (Armitage et al. 2012). Therefore, roles of deadwoods have to serve as a habitat as well as to give food resources of arthropods.

a.



b.

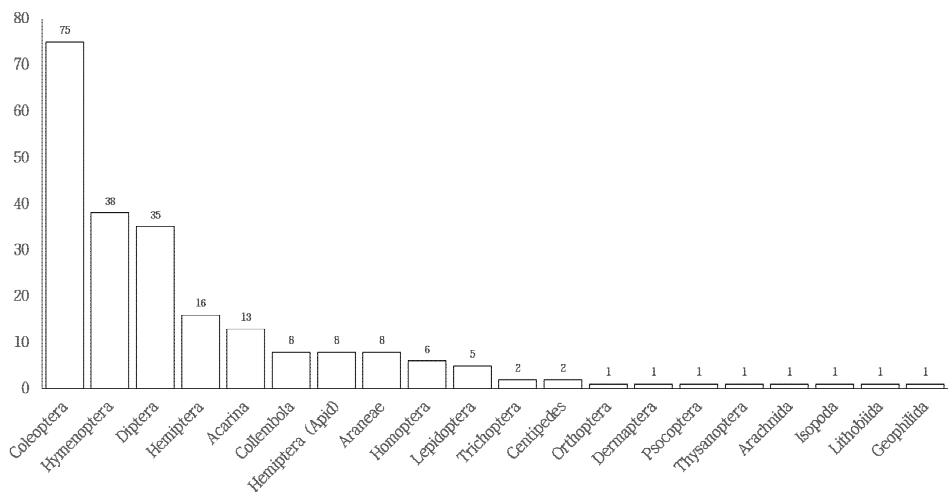


Figure 10. Total abundance of each order (a) and total species richness of each order (b) in the arthropod community.

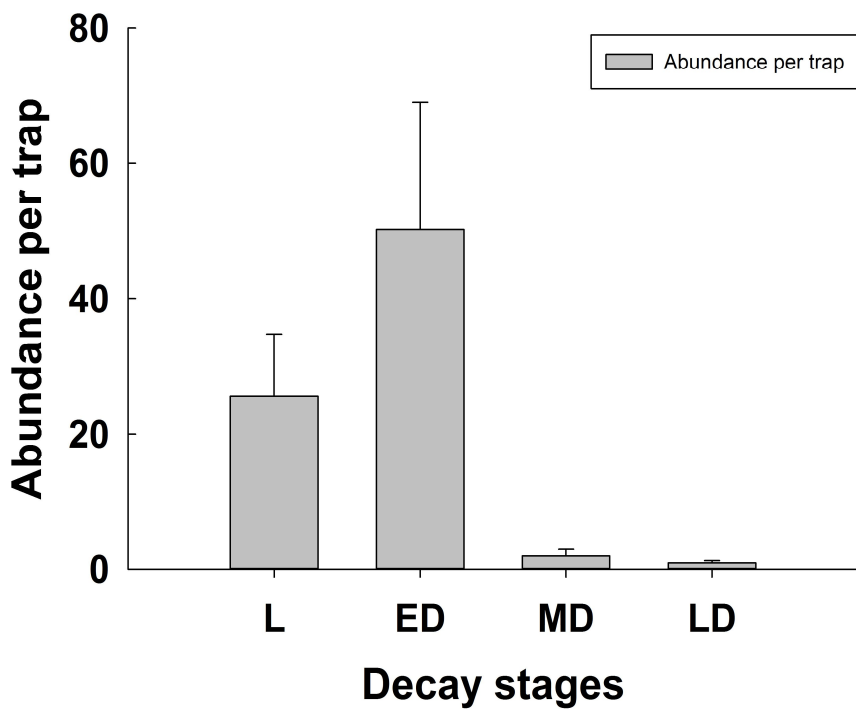


Figure 11. Mean abundance of *Polygraphus nobuchii* per trap among the live tree stage and the three decay stages. (L: live tree stage, ED: early decay stage, MD: middle decay stage, LD: late decay stage)

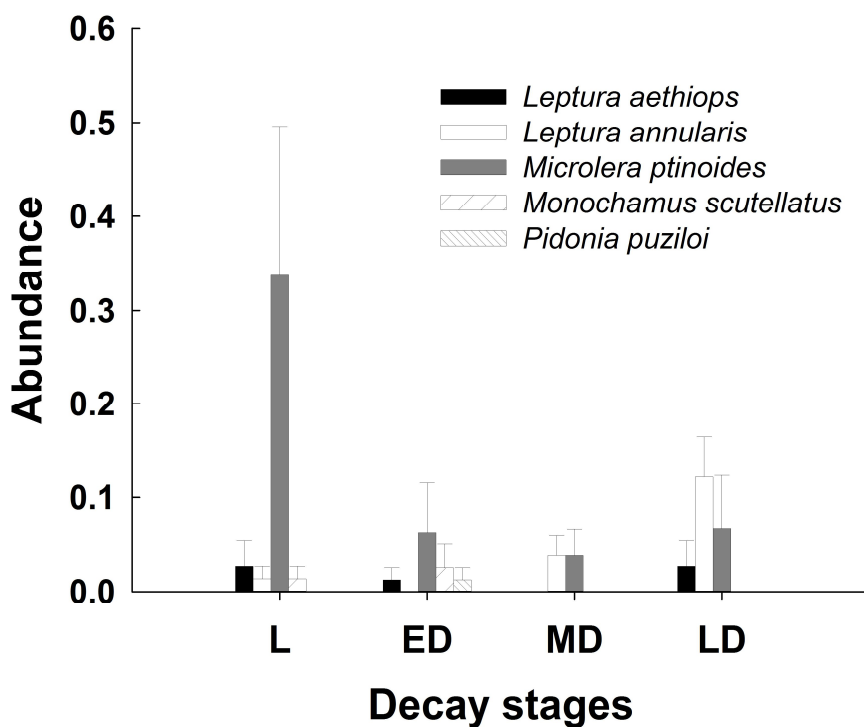


Figure 12. Mean abundance of Cerambycidae per trap among the live tree stage and the three decay stages. (L: live tree stage, ED: early decay stage, MD: middle decay stage, LD: late decay stage)

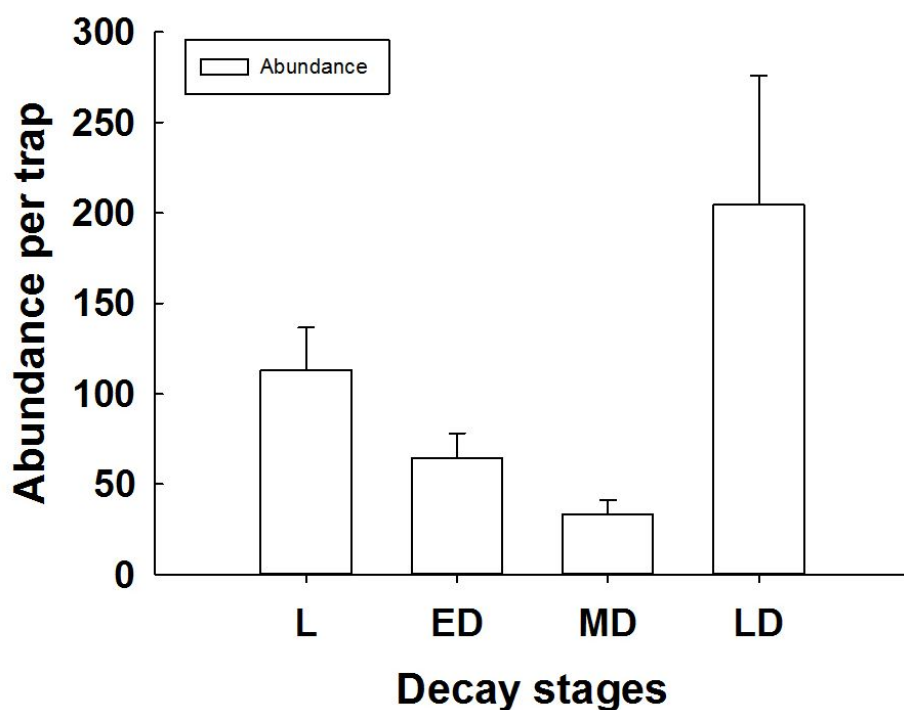


Figure 13. Mean abundance of *Formica japonica* per trap among the live tree stage and the three decay stages. (L: live tree stage, ED: early decay stage, MD: middle decay stage, LD: late decay stage)

Species diversity of arthropods at the each decay stage

In this study, I applied the same experimental design in the three study blocks (Seongpanak, Yeongsil, DNK) located in Mt. Halla. In the combined data analysis of the three study blocks, species richness was the highest in the late decay stage. It decreased in order from live tree stage, early decay stage to middle decay stage. Abundance results were similar to species richness, but Shannon's diversity index was the highest in the middle decay stage, causing a certain species to be dominant in the other decay stage. However, there was none statistically significant among the decay stages. The results were conducted by community analysis by areas. All three areas showed a difference of species diversity to decay stages, but there was no statistical difference. Evenness across all three areas showed statistically significant differences between the decay stages as the graph patterns of evenness were different among the three areas.

Functional feeding groups

Arthropods species were divided into groups of ten to functional feeding groups. Among the groups, the combined pythophagous, xylophagous, saprophagous, fungivore, Sap-sucker groups were classified into herbivore group. The remaining group was used as divided groups existing.

Most species's proportion of functional feeding groups for deadwood dwelling arthropods were not statistically different between decay stages. Few functional feeding groups were significant difference. Predator's

proportion were 32.32% in the late decay stage, higher than the early decay stages, it showed statistically different ($p = 0.0056$). The proportions of predator species on the decay stages except the early decay stage was the highest than other functional feeding groups. the proportion of herbivore species on the early decay stages was the higher than the proportion of predator. The proportion of predator in the area of Seongpanak and Yeongsil among the three areas was higher in the late decay stage. It showed a decrease and increase of the U-shaped graph. But, Donnaeko study area was not significantly difference of all functional feeding groups among the decay stages.

Many species associated with deadwood do not live on the deadwood directly, but on other species that consume deadwood (Jonsson et al. 2005). In this study, indicator species of *A. koreana* live tree was total twenty species, among them, nine species were herbivores, three species were omnivores, six species were predator, two species were parasitoids. Early decay stages had four herbivore species and two omnivore species and one detritivore species. Middle decay stage had three predator indicator species. Most indicators identified in the late decay stage. Total twenty three species were identified, among them, eight species were herbivores, five species were omnivores, five species were predators, three species were parasitoids, two species were detritivores. During most decay stages, except immediately after tree death before the fungal community has developed, a large number of herbivores feed on fungal mycelium (Esseen et al. 1997). In turn, many parasitic insects live on wood living insects (Kenis et al. 2007). In this study result, there was

a change functional feeding group of indicator species among the decay stages. Among the decay stages, phytophagous and Sap-sucker groups emerged from the live tree stage, xylophagous emerged from early decay stage. Predator who feed on the micro insect emerged from middle decay stage. Saprophagous, detritivores, and parasitoids emerged from the late decay stage.

According to the findings of Paletto and Tosi (2010) and Yoo & Kim (2002), the moisture content of deadwood decreased from the early decay stage, after which it increased rapidly to the late decay stage. This behavior can be explained by a natural loss of moisture after death and a successive reabsorption of atmospheric humidity (rain, snow) in advanced decay stages. Abundance pattern of certain species identified in this study is similar pattern of humidity curves of dead stages. Especially Formicidae is mostly similar (Figure 13). However, the abundance of same species in the each area have different pattern. Seonpanak and Yeongsil, Donnaeko are same *A. koreana* forest, but environmental characteristics such as slope, intensity of the wind and light, soil condition are different among the area. The different results of this study among the three areas are related to this reason.

Environment of Seongpanak is the most common, the length of the tree was the longest and growing condition was good. Yeongsil is the worst growing environment among the three areas, the length of the tree was the shortest, The roots are vulnerable to high winds cause by soil condition is made with rock. Donnaeko environment is similar to Seongpanak, but DBH of *A. koreana* was lower than the other areas and

intensity of light was stronger than the other area. In this study, only the characteristic of the deadwood was analyzed arthropods communities with decay stage of deadwood and live tree.

5. CONCLUSION

The importance of deadwood for arthropods including other animals has been emphasized in several studies (Ratcliffe 1993; Siitonen & Martikainen 1994; Martikainen 2001, Siitonen 2001; Kerby et al. 1998). From those research, the accumulation of deadwood in the forest may be important for the biodiversity of forests, and thus, the deadwood should conserve in the same forest ecosystems except the safety problem. From my study, I found the impact of deadwood on arthropod community and it is true that it is not the priority to remove the deadwood to keep the forests. The deadwood left in the forests is not likely to increase pests such as bark beetles as well as not likely to increase the tree mortality. I identified the arthropod indicator species among the live tree stage and the three decay stages. As previously mentioned, indicator species analysis was also considering only the live tree and the three decay stages in the deadwood, but all of other environmental elements did not apply. Although this indicator species analysis result has still deficient data, I would suggest this result for the upcoming study about indicator species of deadwood would surely be used as basic data.

The purpose of this study was to understand the importance of various decay levels of deadwood for the arthropod's habitat diversity in forest ecosystems. *Abies koreana* as a Korean endemic species should be conserved from the climate changes and its conservation would be affected to the increase of biodiversity. The expected things from this

study are as follow. The ecological role of deadwoods in the forest can be more identified, the forest pest problems such as bark beetles and nematode in the forest can be ecologically controlled, and the basic data can be shared with a broad research for similar topics. My research results will be relevant for developing the ecologically sustainable forest management strategies and I expect these results will be used as the basic data for the forest management plans of *Abies koreana*.

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APPENDIX

Appendix 1. The mean abundance with standard error per trap of each species in the live tree stage and the three decay stages. (FFG: Functional feeding group, Sig.: significant, D is decay stage, B is block, A is altitude SE: standard error)

FFG / Class	Classification		Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
	Order	Family		Species	Mean ±SE	Mean ±SE	Mean ±SE	Mean ±SE	Mean ±SE	Mean ±SE	
Phytophagous Insecta	Coleoptera	Byrrhidae	Chalciosphaerium #1	-	-	-	-	-	-	0.01±0.01	
			Chalciosphaerium #2	0.16±0.06	0.05±0.03	0.19±0.13	0.28±0.12				
			Chalciosphaerium #3	-	-	0.01±0.01	0.03±0.02				
		Chrysomelidae	<i>Simplocaria bicolor</i>	-	-	-	-	0.01±0.01	0.01±0.01		
			Altica #1	1.11±0.34	0.53±0.21	0.68±0.28	1.15±0.37				
			Altica #2	-	-	0.01±0.01	-				
			Altica #3	0.07±0.04	0.06±0.03	0.03±0.03	0.05±0.03				
			Chrysomelidae #1	0.01±0.01	-	-	-				
			Galerucinae #1	-	-	0.01±0.01	-				
	Diptera	Galerucinae #2	-	-	0.01±0.01	-					
		<i>Syneta adamsi</i>	0.11±0.05	0.01±0.01	0.03±0.02	0.01±0.01					
		Cecidomyiidae #1	-	-	-	-					
	Hymenoptera	Cecidomyiidae	Cecidomyiidae #2	-	0.05±0.03	0.17±0.09	0.16±0.08				
			Cecidomyiidae #3	0.07±0.04	0.24±0.14	0.37±0.26	0.22±0.10				
			Drosophila #1	0.07±0.03	0.11±0.05	0.05±0.03	0.16±0.05				
	Xylophagous Insecta	Coleoptera	Bostrichidae	Tenthredinidae #1	-	-	-	-	0.01±0.01		
Ambrosiodmus #1				0.07±0.03	0.16±0.06	0.41±0.37	0.18±0.08				
Curculionidae		Ambrosiodmus #2	0.05±0.04	0.03±0.03	-	0.01±0.01					
		<i>Leptura aethiops</i>	0.03±0.03	0.01±0.01	-	0.03±0.03					
		<i>Leptura annularis</i>	0.01±0.01	-	0.04±0.02	0.12±0.04					
		<i>Microdera pinioides</i>	0.34±0.16	0.06±0.05	0.04±0.03	0.07±0.06					
		<i>Monochamus scutellatus</i>	0.01±0.01	0.03±0.03	-	-					
		<i>Pidonia puziloi</i>	-	0.01±0.01	-	-					
Curculionidae		<i>Anthonomus rectirostris</i>	0.20±0.09	0.05±0.04	0.06±0.05	0.07±0.04					
		<i>Barinomorphus antennatus</i>	0.03±0.02	0.03±0.02	0.01±0.01	0.03±0.02					

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FFG / Class	Classification		Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
	Order	Family		Mean	SE	Mean	SE	Mean	SE	Mean	SE
Saprophagous	Diplopoda	Lycidae	D, B, A	0.05	±0.03	-	-	-	-	0.01	±0.01
				-	-	0.01	±0.01	-	-	-	-
				-	-	-	-	-	-	0.08	±0.06
				-	-	-	-	-	-	0.03	±0.03
				-	-	-	-	-	-	0.01	±0.01
				-	-	-	-	-	-	0.01	±0.01
				0.03	±0.02	-	-	0.01	±0.01	-	-
				0.07	±0.04	0.05	±0.03	0.08	±0.03	0.09	±0.04
				0.34	±0.13	0.05	±0.03	0.08	±0.04	0.04	±0.04
				0.07	±0.04	0.04	±0.02	0.12	±0.06	0.01	±0.01
	Insecta	Elateridae	B	0.18	±0.06	0.08	±0.03	0.04	±0.02	0.07	±0.04
				-	-	-	-	-	-	0.03	±0.02
				-	-	0.01	±0.01	-	-	-	-
				25.51	±9.09	50.24	±18.79	1.92	±0.97	0.91	±0.34
				-	-	0.01	±0.01	0.05	±0.03	0.18	±0.10
				-	-	0.01	±0.01	-	-	-	-
				-	-	0.01	±0.01	-	-	-	-
				-	-	-	-	0.04	±0.03	-	-
				-	-	-	-	-	-	-	-
				-	-	-	-	-	-	-	-
Saprophagous	Diplopoda	Lycidae	A	0.23	±0.08	0.22	±0.09	0.51	±0.29	0.68	±0.29
				0.54	±0.16	3.35	±2.02	3.04	±0.71	1.07	±0.21
				0.09	±0.03	0.08	±0.06	0.06	±0.03	0.19	±0.07
				0.03	±0.02	0.01	±0.01	0.01	±0.01	0.03	±0.03
				0.08	±0.06	0.08	±0.04	0.03	±0.02	-	-
				0.07	±0.06	0.06	±0.04	0.01	±0.01	-	-
				0.12	±0.08	0.05	±0.03	0.01	±0.01	0.07	±0.04
				0.01	±0.01	-	-	-	-	-	-
				-	-	-	-	-	-	-	-
				-	-	-	-	-	-	-	-

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FFG / Class	Order	Classification		Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
		Family	Species		Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE
Fungivore Insecta	Malacostraca	Coleoptera	Orchesia #1		-	0.01±0.01	-	-	-	-	-	-
			<i>Orchesia imitans</i>	B, D	0.07±0.04	0.09±0.04	0.06±0.05	0.47±0.14	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02
			<i>Monotoma longicollis</i>	B, D	0.08±0.04	0.19±0.07	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02
			Monotomidae #1		-	0.01±0.01	0.05±0.04	-	-	-	-	-
			<i>Carpophilus chalybeus</i>		0.09±0.07	0.03±0.02	0.03±0.02	0.07±0.04	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02
		Diptera	<i>Lasiodactylus pictus</i>		-	0.03±0.02	-	0.04±0.02	0.01±0.01	0.04±0.02	0.04±0.02	0.04±0.02
			Nitidulidae #1		0.04±0.02	0.16±0.08	-	-	-	-	-	-
			Ostomidae #1		-	-	0.01±0.01	-	-	-	-	-
			Ptiliidae #1		-	0.01±0.01	0.03±0.02	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01
			Homoneura #1		0.01±0.01	-	-	0.08±0.05	0.08±0.05	0.08±0.05	0.08±0.05	0.08±0.05
	Tricoptera	Sphaeroceridae	Sphaeroceridae #1		0.01±0.01	0.01±0.01	-	-	-	-	-	-
			Sphaeroceridae #2		0.01±0.01	0.01±0.01	-	-	-	-	-	-
		Limnephilidae	Limnephilidae #1		-	-	-	-	-	-	-	-
		Unidentified	Trichoptera #1		-	-	-	-	-	-	-	-
		Oniscidae	Trichoptera #2		-	-	-	-	-	-	-	-
Fungivore Insecta	Malacostraca	Coleoptera	Oniscidae #1		0.04±0.03	0.01±0.01	0.09±0.06	0.04±0.03	0.04±0.03	0.04±0.03	0.04±0.03	0.04±0.03
					-	-	-	-	-	-	-	-
					-	-	-	-	-	-	-	-
					-	-	-	-	-	-	-	-
					-	-	-	-	-	-	-	-
		Diptera	<i>Cis serripilosus</i>		0.03±0.03	0.01±0.01	0.05±0.04	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01
			Anisotoma #1		-	0.01±0.01	-	-	-	-	-	-
			Scaphidium #1		-	-	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01
			Scaphidium #2		-	-	-	-	-	-	-	-
			Scaphidium #3		0.19±0.13	0.08±0.08	0.92±0.64	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01
	Hemiptera	Thysanoptera	<i>Serica angulata</i>		-	-	-	-	-	-	-	-
			Mycetophilidae #1	B	0.01±0.01	0.03±0.02	0.15±0.07	0.18±0.08	0.18±0.08	0.18±0.08	0.18±0.08	0.18±0.08
			Mycetophilidae #2		0.01±0.01	0.01±0.01	-	-	-	-	-	-
			Aradidae #1		-	-	-	-	-	-	-	-
			Thysanoptera #1		0.01±0.01	-	-	-	-	-	-	-

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FFG / Class		Classification		Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
Order	Family	Species	Mean±SE		Mean±SE	Mean±SE	Mean±SE	Mean±SE				
Sap-sucker	Insecta	Diptera	Phoridae	Megaselia #1	0.65±0.23	0.35±0.13	0.22±0.11	1.74±1.30				
				Megaselia #2	0.41±0.15	0.56±0.18	0.42±0.13	0.32±0.09				
		Hemiptera	Tephritidae	<i>Phora holosericea</i>			0.04±0.03	0.01±0.01				
				Tephritidae #1	0.04±0.02	-	-	0.03±0.02				
				Aphididae #1	0.08±0.05	0.15±0.13	0.04±0.03	0.12±0.06				
		Aphididae	Aphididae #2	-	-	0.01±0.01	-					
			Aphididae #3	1.31±0.78	7.47±6.50	0.14±0.07	0.66±0.41					
			Aphididae #4	-	0.15±0.15	0.01±0.01	-					
			Aphididae #5	0.18±0.08	0.16±0.09	0.04±0.03	0.07±0.03					
			Macrosiphum #1	0.07±0.07	0.15±0.07	0.05±0.03	0.09±0.04					
		Lachnidae	Cinara #1	0.47±0.17	7.41±7.15	0.05±0.03	0.03±0.02					
			Lygaeidae #1	0.20±0.10	0.08±0.03	0.04±0.02	0.09±0.04					
		Microphysidae	<i>Loricula pilosella Miyamoto</i>	0.05±0.03	0.03±0.02	0.03±0.02	0.04±0.02					
			Miridae #1	0.04±0.02	0.06±0.03	0.03±0.02						
		Miridae	Miridae #2	-	-	-	0.01±0.01					
			Miridae #3	-	-	-	0.03±0.02					
			Miridae #4	-	0.01±0.01	-	0.01±0.01					
			Miridae #5	-	-	-	0.01±0.01					
			Pentatomidae #1	-	0.01±0.01	-	0.03±0.03					
		Pentatomidae	Pentatomidae #2	0.01±0.01	0.03±0.03	-	0.01±0.01					
			Pentatomidae #3	0.01±0.01	-	-	-					
Pseudococcicidae #1	0.04±0.03		0.11±0.11	0.05±0.04	0.04±0.03							
Homoptera	Tingidae	Acalypta #1	0.49±0.43	0.04±0.02								
	Cercopidae	Cercopidae #1	-	-	0.01±0.01	-						
	Cicadellidae	Cicadellidae #1	0.18±0.11	0.08±0.05	0.12±0.05	0.03±0.02						
		Cicadellidae #2	0.05±0.04	0.16±0.10	0.09±0.07	0.08±0.04						
		Cicadellidae #3	0.14±0.07	0.15±0.06	0.04±0.02	0.50±0.33						

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		Family	Species		Mean±SE		Mean±SE		Mean±SE		Mean±SE	
Lepidoptera		Fulgoridae	Fulgoridae #1	B	0.05±0.03		0.10±0.05		0.04±0.03		0.07±0.05	
		Psyllidae	Psyllidae #1		0.19±0.10		0.15±0.06		0.09±0.04		1.24±0.75	
		Unidentified	Moth #1		-		0.01±0.01		-		-	
			Moth #2		-		0.01±0.01		-		-	
			Moth #3		-		-		0.01±0.01		0.01±0.01	
			Moth #4		-		-		0.01±0.01		-	
			Moth #5		-		-		0.01±0.01		-	
Psocoptera		Amphipsocidae	Psocus #1		-		-		-		0.01±0.01	
Omnivore	Entognatha	Collembola	Ptenothrix #1		0.35±0.16		4.30±3.80		0.05±0.03		0.24±0.09	
			Hypogastrura #1		0.03±0.03		-		0.01±0.01		-	
			Hypogastrura #2		0.77±0.32		1.19±0.53		0.85±0.24		1.57±0.47	
		Isotomidae	Tomocerus #1	B	41.81±5.72		40.29±5.83		31.71±3.76		37.45±6.15	
			Tomocerus #2		1.39±0.41		1.73±0.48		1.47±0.59		2.07±0.59	
			Tomocerus #3		1.03±0.36		0.63±0.18		0.51±0.20		0.39±0.16	
	Insecta	Smynthridae	Tomocerus #4	A	11.74±4.96		9.70±5.05		10.04±5.40		13.73±6.19	
			Smynthridae #1		9.23±3.40		6.52±2.40		11.00±3.10		11.51±2.64	
			<i>Misolampidius chejudoensis</i>		0.19±0.06		0.13±0.06		0.26±0.10		0.32±0.11	
			Forficula scudderi		1.32±0.99		0.25±0.08		0.24±0.14		0.45±0.13	
			Protearomyia #1		-		0.03±0.02		-		0.03±0.02	
			Anthocoridae #1		0.11±0.06		0.03±0.02		-		0.04±0.03	
Hymenoptera		Formicidae	Anthocoridae #1		0.01±0.01		0.01±0.01		0.01±0.01		0.01±0.01	
			Anthocoridae #2		-		-		0.01±0.01		0.01±0.01	
			Anthocoridae #3		0.49±0.42		-		-		0.09±0.09	
			<i>Formica japonica</i>		113.16±23.51		64.10±14.04		33.53±7.48		204.54±71.38	
			Lasius #1		0.01±0.01		-		-		0.01±0.01	
			Lasius #2		-		-		0.03±0.02		-	

Appendix 1. The mean abundance with standard error per trap of each species in the live tree stage and the three decay stages. (FFG: Functional feeding group, Sig.: significant, D is decay stage, B is block, A is altitude SE: standard error)

FFG / Class	Order	Classification		Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
		Family	Species		Mean	SE	Mean	SE	Mean	SE	Mean	SE
Predator Arachnida	Unidentified Araneae	Unidentified	<i>Myrmica kotokui</i>	B	10.16	±3.91	22.96	±12.36	4.88	±1.27	10.39	±2.15
			<i>Myrmica kurokii</i>		1.00	±0.26	0.92	±0.24	0.33	±0.13	0.93	±0.27
			Unidentified Acarina		-		0.08	±0.08	-		-	
			Cybaeidae #1	B	0.55	±0.21	0.46	±0.14	0.40	±0.11	0.97	±0.27
			Gnaphosidae #1		0.01	±0.01	0.05	±0.04	0.05	±0.04	0.22	±0.16
	Opiliones	Unidentified	Lycosidae #1		0.43	±0.21	0.18	±0.07	0.15	±0.05	0.43	±0.12
			Micryphatidae #1		0.65	±0.39	0.06	±0.03	0.19	±0.07	0.46	±0.09
			Micryphatidae #2		0.15	±0.12	0.09	±0.05	0.04	±0.02	0.04	±0.04
			Phidippus #1		0.01	±0.01	-		-		-	
			Therididae #1		4.14	±1.24	2.92	±1.70	3.37	±0.99	3.58	±2.08
	Pseudoscorpionida Sarcoptiformes	Unidentified	Opilionidae #1	B	1.09	±0.31	0.54	±0.22	0.40	±0.16	0.58	±0.15
			Pseudoscorpionida #1	D	0.05	±0.03	-		0.17	±0.07	0.22	±0.11
			Acaridae #1	D	1.88	±0.41	2.68	±0.65	2.06	±0.34	7.95	±1.72
			Camisiidae #1		0.01	±0.01	0.01	±0.01	0.17	±0.11	0.05	±0.03
			Euphthiracaridae	D	0.18	±0.08	0.20	±0.10	0.58	±0.16	2.46	±0.57
	Sarcoptiformes Trombidiformes	Galumnidae	galumnidae #1	B	1.01	±0.52	0.86	±0.32	1.28	±0.41	2.64	±0.92
			Bdellidae #1		0.24	±0.24	1.39	±1.27	0.04	±0.03	0.05	±0.03
			Bdellidae #2		-		-		-		0.01	±0.01
			Bdellidae #3		0.22	±0.13	0.08	±0.03	0.12	±0.09	0.27	±0.15
			Trombididae		0.50	±0.28	0.27	±0.12	0.22	±0.10	0.24	±0.07
	Trombidiformes	Trombididae	Trombididae #1		0.01	±0.01	0.04	±0.03	0.01	±0.01		
			Trombididae #2	B, D	-		0.03	±0.02	-		0.03	±0.03
			Trombididae #3		0.34	±0.09	0.22	±0.11	1.06	±0.77	0.43	±0.10
			Trombididae #4	B	0.04	±0.02	0.03	±0.02	0.01	±0.01	0.11	±0.06
			Trombididae #5		0.01	±0.01	0.01	±0.01	-		-	
			Trombididae #6		-		-		-		-	

Appendix 1. The mean abundance with standard error per trap of each species in the live tree stage and the three decay stages. (FFG: Functional feeding group, Sig.: significant, D is decay stage, B is block, A is altitude SE: standard error)

FFG / Class	Classification			Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
	Order	Family	Species		Mean	SE	Mean	SE	Mean	SE	Mean	SE
Chilopoda	Geophilomorpha	Geophilidae	Geophilomorpha #1		0.04	±0.03	0.06	±0.03	0.01	±0.01	0.09	±0.03
	Lithobiomorpha	Lithobiidae	Lithobiidae #1		0.72	±0.28	0.52	±0.11	0.58	±0.11	0.73	±0.15
Insecta	Coleoptera	Cantharidae	<i>Asiopodabrus fragiliformis</i>		0.24	±0.12	0.09	±0.08	0.03	±0.03	0.07	±0.04
		Coccinellidae	Coccinella #1		-		-		-		0.01	±0.01
			<i>Coccinella septempunctat</i>		0.07	±0.04	0.04	±0.03	-		0.08	±0.06
			<i>Asaphidion semilucidum</i>	D	0.73	±0.28	0.39	±0.20	0.01	±0.01	0.05	±0.03
	Harpalidae		<i>Pterostichus solskyi</i>		0.01	±0.01	-		0.01	±0.01	0.07	±0.04
			<i>Pterostichus raptor</i>		-		0.01	±0.01	-		-	
		Leiodiidae	<i>Agathidium curticorne</i>		0.03	±0.02	0.05	±0.02	0.28	±0.13	0.07	±0.04
		Pselaphidae	<i>Batriscenellus vicarius</i>		0.01	±0.01	0.03	±0.02	-		0.01	±0.01
	Scaphidiidae		Pselaphidae #1		0.03	±0.03	0.01	±0.01	-		-	
			Pselaphidae #2		0.07	±0.03	0.08	±0.04	0.23	±0.08	0.19	±0.06
			Pselaphidae #3		0.05	±0.03	-		0.12	±0.07	0.07	±0.04
			<i>Atheta transfuga</i>		0.01	±0.01	-		0.01	±0.01	0.03	±0.03
Diptera			Philonthus #1	B	0.61	±0.34	0.35	±0.11	0.09	±0.06	0.23	±0.10
			Staphylinidae #1	B	0.01	±0.01	0.06	±0.04	0.12	±0.06	0.04	±0.03
			Staphylinidae #2		0.74	±0.17	0.99	±0.18	1.12	±0.27	0.89	±0.24
			Staphylinidae #3		-		-		-		0.01	±0.01
			<i>Tachinus sibiricus</i>	B	0.15	±0.08	0.06	±0.03	0.08	±0.04	0.05	±0.03
			Tachyporinae #1								0.01	±0.01
		Empididae	Tasgius #1		0.01	±0.01	-		0.03	±0.02	0.01	±0.01
			Empis #1		0.11	±0.05	0.09	±0.05	0.09	±0.04	0.22	±0.07
			<i>Empis flavobasalis</i>		0.01	±0.01	-		0.03	±0.02	0.01	±0.01
		Psychodidae	Psychoda #1		0.09	±0.06	0.05	±0.03	0.04	±0.02	0.14	±0.06
		Rhagionidae	Symphoromyia #1	A	-		0.03	±0.02	0.01	±0.01	-	
	Scathophagidae		<i>Scathophaga stercoraria</i>	B	0.05	±0.03	0.01	±0.01	0.01	±0.01	0.07	±0.06
		Tipulidae	<i>Limonia margarita</i>		-		-		-		0.01	±0.01
			Nephrotoma #1		0.01	±0.01	-		0.01	±0.01	-	

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FFG / Class	Classification			Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
	Order	Family	Species		Mean	SE	Mean	SE	Mean	SE	Mean	SE
Parasitoid Insecta	Hemiptera	Reduviidae	Tipula #1	B, D	-		0.01±0.01		0.01±0.01		-	
			<i>Tipula taikan</i>		0.61±0.18		0.23±0.12		0.12±0.07		0.04±0.02	
		Unidentified	Reduviidae #1		0.01±0.01		-		0.01±0.01		-	
			Neuroptera #1		-		-		-		0.01±0.01	
	Diptera Hymenoptera	Chloropidae	<i>Apotropina japonica</i>		0.03±0.02		0.06±0.03		0.03±0.02		0.07±0.04	
			Ceraphronidae #1		-		-		-		0.03±0.02	
			Ceraphronidae #2		0.05±0.03		0.04±0.03		0.12±0.05		0.04±0.02	
			Cynipidae #1		0.19±0.07		0.13±0.07		-		0.05±0.03	
		Diapriidae	Diapriidae #1		0.03±0.02		-		-		0.03±0.02	
			Diapriidae #2		-		0.05±0.02		0.04±0.03		0.03±0.02	
			Diapriidae #3		0.03±0.02		-		-		0.07±0.04	
			Diapriidae #4		0.03±0.03		0.04±0.03		0.04±0.03		0.11±0.05	
		Diapriidae	Diapriidae #5		-		0.01±0.01		0.01±0.01		-	
			Diapriidae #6		0.15±0.09		0.18±0.08		0.12±0.05		0.07±0.04	
			Diapriidae #7		-		-		0.03±0.03		0.01±0.01	
		Eulophidae	Eulophidae #1		0.08±0.06		0.06±0.03		0.05±0.03		0.05±0.03	
			Eulophidae #1		0.03±0.02		-		-		0.01±0.01	
			Eulophidae #2		0.01±0.01		0.14±0.10		0.01±0.01		0.01±0.01	
			Eulophidae #3		0.09±0.04		0.38±0.32		0.06±0.03		0.03±0.03	
	Ichneumonidae		Eulophidae #4		0.05±0.03		0.01±0.01		0.01±0.01		-	
			Ichneumonidae #1		0.22±0.19		0.01±0.01		0.03±0.03		0.04±0.04	
			Ichneumonidae #2		0.08±0.04		-		0.03±0.02		0.04±0.03	
			Ichneumonidae #3		-		0.01±0.01		0.04±0.03		0.05±0.03	
			Ichneumonidae #4		-		0.01±0.01		-		-	
			Ichneumonidae #5		0.16±0.06		0.11±0.05		0.12±0.04		0.12±0.04	
			Ichneumonidae #6		-		0.01±0.01		0.03±0.02		0.01±0.01	

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FFG / Class		Classification		Sig.	Live tree (n=74)		Early decay stage (n=79)		Middle decay stage (n=78)		Late decay stage (n=74)	
Order	Family	Species	Mean ±SE		Mean ±SE	Mean ±SE	Mean ±SE	Mean ±SE				
Detritivore Insecta	Diptera	Ichneumonidae #8	0.07±0.04	0.05±0.03	0.04±0.02	0.05±0.03	0.05±0.03	0.05±0.03	0.04±0.02	0.04±0.02	0.05±0.03	
		Ichneumonidae #9	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.04±0.04	
		Ichneumonidae #10									0.15±0.08	
		Megaspilidae #1	0.05±0.03	0.03±0.03	-	-	-	-	-	-	-	
		Proctotrupidae #1	0.01±0.01	0.03±0.02	0.03±0.03	0.03±0.03	0.03±0.03	0.03±0.03	0.03±0.03	0.03±0.03	-	
		Proctotrupidae #2	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.03±0.03	0.03±0.03	0.03±0.03	0.03±0.03	-	
		Pteromalidae #1	0.01±0.01	-	-	-	-	-	-	-	-	
		Scelionidae #1	0.03±0.03	0.03±0.02	0.05±0.03	0.05±0.03	0.05±0.03	0.05±0.03	0.05±0.03	0.05±0.03	0.09±0.06	
Uneaten group Insecta	Diptera	<i>Bibio pseudoclavipes</i>	0.03±0.02	-	-	-	-	-	-	-	-	
		Calliporidae #1	-	0.01±0.01	-	-	-	-	-	-	-	
		Bradysia #1	0.22±0.11	0.90±0.34	0.67±0.42	0.58±0.23	0.58±0.23	0.58±0.23	0.58±0.23	0.58±0.23	0.58±0.23	
		Bradysia #2	0.03±0.02	0.14±0.10	-	0.11±0.09	0.11±0.09	0.11±0.09	0.11±0.09	0.11±0.09	0.11±0.09	
		Sciara #1	0.34±0.15	0.34±0.15	0.29±0.12	1.00±0.70	1.00±0.70	1.00±0.70	1.00±0.70	1.00±0.70	1.00±0.70	
	Orthoptera	<i>Anoplophilus koreanus</i>	0.14±0.06	0.09±0.04	0.14±0.05	0.23±0.10	0.23±0.10	0.23±0.10	0.23±0.10	0.23±0.10	0.23±0.10	
Unknown Insecta	Diptera	Stenochironomus #1	-	0.03±0.03	-	-	-	-	-	-	-	
		Stenochironomus #2	B	0.69±0.16	1.05±0.32	1.03±0.35	1.50±0.64	1.50±0.64	1.50±0.64	1.50±0.64	1.50±0.64	
		Stenochironomus #3		0.39±0.21	1.13±0.66	0.41±0.16	0.36±0.15	0.36±0.15	0.36±0.15	0.36±0.15	0.36±0.15	
		Stenochironomus #4		0.04±0.03	0.06±0.03	0.05±0.03	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02	0.03±0.02	
		Stenochironomus #5		0.07±0.07	0.03±0.02	0.05±0.04	0.05±0.04	0.05±0.04	0.05±0.04	0.05±0.04	0.05±0.04	
		Stenochironomus #6		0.05±0.05	-	0.01±0.01	-	-	-	-	-	
	Diptera	Unidentified		0.01±0.01	0.03±0.02	0.01±0.01	0.03±0.03	0.03±0.03	0.03±0.03	0.03±0.03	0.03±0.03	
		224 species		117±58.26	121±46.24	62±24.46	139±88.62	139±88.62	139±88.62	139±88.62	139±88.62	
		99 family										
		22 order										
11 group / 6 class												

Abstract

Community Structure of Arthropods inside Korean Fir (*Abies koreana*) Snags on Mt. Halla National Park, Jeju Island, Korea

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I executed this research to understand the importance of decaying woods as the diverse arthropods' habitat in *Abies koreana* forests of Mt. Halla, Korea from 2013 April to 2014 July. I discriminated the *Abies koreana* forests into one live stage and three decay stages at the three blocks (Sungpanak, Yeongsil, Donnako) with three replicates and I collected arthropods by using an emergence trap per a tree. I also used the different slope, altitude, decay stage and characteristics of dead wood as statistical variables. I collected 6 classes 23 orders 99 families 224 species (69,674 individuals) from 71 emergence traps. I found that there was significant difference in an abundance into decay stages, study sites. I classified these arthropod individuals into 10 functional

feeding groups: predator (53 species, 23.66%), Sap-sucker (38 species, 16.96%), parasitoid (30 species, 13.39%), xylophagous (26 species, 11.61%), saprophagous (23 species, 10.27%), omnivore (15 species, 6.70%), phytophagous (15 species, 6.70%), fungivore (10 species, 4.46%), detritivore (7 species, 3.13%) and others (3.13%). Among them, total 60 species was indicator as each decay stages. Most indicators were Coleoptera and Hymenoptera, and they were more identified in the live tree stage (and late decay stage than early and middle decay stages. My research results will be relevant for developing the ecologically sustainable forest management strategies and I expect these results will be used as the basic data for the forest management plans of *Abies koreana*.

Keywords: *Abies koreana*. Arthropods, Dead wood, Mt. Halla

요약

제주도 한라산 국립공원내 구상나무(*Abies koreana*) 고사목에 서식하는 절지동물 군집 구조

김현정

생물학과

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본 연구는 구상나무 고사목의 서식지로서의 중요성과, 고사목의 부후단계에 따른 고사목에 서식하는 절지동물 군집의 변화를 알아보기 위해 2013년 4월부터 2014년 7월까지 제주도 한라산의 구상나무림 지역에서 진행되었다. 구상나무림이 분포하는 성판악, 영실, 돈내코 세 지역에서 100m x 100m의 크기의 조사구를 세 개씩 설치하였고, 조사구 별로 살아있는 나무와 초기·중기·후기의 부후단계의 고사목을 각각 두 그루씩 선택 후 우화트랩(Emergence trap)을 설치하여 두 달을 주기로 절지동물을 채집하였다. 채집된 절지동물은 80% 알코올이 든 바이알에 보관하였고, 술팅과 동정을 진행하였다. 동정이 끝난 종은 섭식하는 먹이의 종류에 따라 10개의 섭식기능군 그룹으로 구분하였다. 이후 통계프로그램을 이용하여 군집분석과 다차원척도법, 지표종분석을 진행하였으며, 트랩을 설치한 고사목의 부후단계와 고사목 특성, 조사구의 사면방향, 고도, 채집시기 등을 통계적 변수로 활용하였다. 본 연구기간동안 총 71개의 우화트랩에서 6강 23목 99과 224종 69,674개체가 채집되었다. 구상나무의 부후단계별 절지

동물 군집의 변화는 조사가 진행된 세 지역에서 각각 다른 군집 패턴을 나타내었다. 성판악 지역은 후기 고사목 단계에서 가장 많은 종수를 보였으며, 영실 지역은 살아있는 나무 단계에서 가장 높은 종수를 나타내었다. 그러나 돈내코 지역은 부후단계에 따른 종수의 통계적인 차이가 나타나지 않았다. 섭식기능군별 분류 결과, predator가 53종(23.66%)으로 가장 많은 종이 나타났으며, sap-sucker 38종(16.96%), parasitoid 30종(13.39%), xylophagous 26종(11.61%), saprophagous 23종(10.27%), omnivore와 phytophagous가 각각 15종(6.70%), fungivore 10종(4.46%), detritivore 7종(3.13%) 그밖에 기타 (3.13%) 순으로 확인되었다. 전체 확인된 종 중에서 총 60종이 고사목의 각 부후단계별 지표종으로 확인되었고, 살아있는 나무와 후기 부후단계 고사목에서 많은 수의 지표종이 확인되었다. 지표종의 섭식기능군은 구상나무의 부후단계에 따라 차이를 보였으며, 살아있는 나무에서는 predator와 herbivore, omnivore, parasitoid 그룹에 속하는 종이 지표종으로 확인되었고, 초기부후단계에서는 hervivore 그룹이, 중기부후단계에서는 predator 그룹이, 후기부후단계에서는 omnivore와 parasitoid 그룹이 지표종으로 다수 확인되었다. 본 연구 결과는 고사목과 절지동물 군집의 상호관계에 관한 첫 번째 연구로서, 본 연구 결과를 바탕으로 생태학적으로 지속가능한 산림관리 방안의 발전에 밑바탕이 되고, 특히 산림 내 구상나무 관리 방안을 위한 기초 자료로 활용되길 바란다.

핵심어: 고사목, 절지동물, 구상나무, 한라산