# MONITORING PANDORA MOTH (*COLORADIA PANDORA*) ON THE KAIBAB NATIONAL FOREST

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# ARMILLARIA ROOT DISEASE DISTRIBUTION IN NORTHERN ARIZONA

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# Professional Paper Abstract

Pandora moth, *Coloradia pandora* Blake 1863 (Lepidoptera, Saturniidae), is the largest member of the *Coloradia* genus in the United States and one of the few that is recognized as a pest. Outbreaks of *C. pandora* occur in 20 to 30 year intervals lasting 6 to 8 years. Large areas of western coniferous pine forests are defoliated during outbreaks, however, defoliation rarely leads to tree mortality due to the moth's two year life cycle; however, defoliation can reduce the trees defenses allowing them to succumb to other agents. I monitored pandora moth population density, developed new monitoring techniques, and examined natural enemy populations, on the Kaibab National Forest, Arizona. My monitoring results from 2010 to 2012 demonstrated that the pandora moth population was distributed over several thousand hectares but larval densities were low relative to previous outbreak densities in the 1980's and no significant defoliation had occurred. Because the population density was lower than previously monitored outbreak populations, new techniques were needed to monitor larvae densities and defoliation; rather than using single tree sampling, multiple small trees were examined for larval presence and defoliation levels. Average larval density per tree was 0.5 (± 0.8) with the greatest number of larvae per tree at 4. Larval density per location did not exceed 60 larvae per ~0.4 ha plots. Defoliation was less than 1% with an average of 8 needles defoliated per tree. Mortality of late instar larvae from parasitoid and NPV infection was 1% and 1%, respectively. Parasitization rates of pupae were 2%. Other mortality factors such as climate, vertebrate predation rates, egg and early instar predation and parasitization rates were not monitored.

A second project I conducted examined the distribution and identification of *Armillaria* root disease in northern Arizona. Armillaria root disease was sampled on two national forests in northern Arizona utilizing USDA Forest Service Forest Inventory and Analysis permanent plots. Samples of *Armillaria* were identified using DNA sequences and were determined to consist of a single species, *Armillaria ostoyae* (Romagnes) Herink. Armillaria root disease was more commonly found in mixed conifer and subalpine forests and was rare in ponderosa pine forests, which was consistent with previous studies conducted in the Southwest.

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**Chapter I**

# Preface

This professional paper is presented in the form of three independent papers as follows:

Chapter 1: A review of pandora moth biology and impacts. Authors: C. W. Hoffman and R. W. Hofstetter, and R. P. Hanavan,

Chapter 2: Pest Monitoring Report: pandora moth (*Coloradia pandora davisi*, Lepidoptera: Saturniidae) in Arizona: 2010 to 2012. Authors: C. W. Hoffman, R. W. Hofstetter, R. P. Hanavan, A. Grady, and J. Anhold

Chapter 3: Armillaria Root Disease in Northern Arizona. Authors: C. W. Hoffman, R. Mathiasen, and R. W. Hofstetter

The first two chapters relate to pandora moth monitoring on the North Kaibab Ranger District, Kaibab National Forest, Arizona. The final chapter relates to *Armillaria* species distribution on two northern Arizona national forests. Samples from these two forests were identified using DNA sequences. These two projects were funded under different grants and both projects were completed as part of my Masters of Forestry.

# Professional Paper Introduction

This work incorporated two separate projects. The first documented the population dynamics, spatial distribution, and natural enemy population densities of pandora moth (*Coloradia pandora davisi* Blake) from 2010 to 2012 on the North Kaibab Ranger District, Kaibab National Forest in northern Arizona and provided baseline data for future monitoring efforts. The second project documented the presence and distribution of *Armillaria* root disease on two national forests in northern Arizona. Samples of *Armillaria* collected from infected trees were identified using DNA sequences.

Pandora moth has defoliated many pine forests in the West once it has reached outbreak density which has occurred on a semi regular basis every 20 to 30 years. Defoliation occurring during outbreaks has caused a reduction of basal area growth over the course of an outbreak (6 to 8 years) and has directly caused mortality. However, indirect impacts associated with the stress of defoliation have been more severe, particularly when pathogens or insects have attacked and killed these trees.

Because climate has been predicted to change across the range of pandora moth, monitoring this species has become more important. Historically, pandora moth has exhibited a two year life cycle and has not destroyed buds which has allowed trees to re-foliate between defoliation events. Should the predicted climate changes alter the biology of pandora moth such that development times become shorter, more severe impacts can be expected. However, climate could disrupt life stage development rates and alter synchrony in moth emergence, change predator-prey interactions, or influence host species resistance and susceptibility to pandora moth defoliation.

Pandora moth adult populations were monitored in 2010, 2011, and 2012 using light traps; larvae and defoliation were surveyed across 136 plots in 2011; and natural enemy levels were examined for late-larval and pupal stages. Given my findings, the pandora moth population has not yet reached densities found during the previous outbreak and defoliation has not yet reached moderate or severe levels. As previous research has not been conducted on non-outbreak population densities present on the North Kaibab Ranger District, this study provided insight into population development.

Armillaria root disease has been reported to affect more than 600 species of plants and has a wide range of signs, symptoms, and host responses. *Armillaria* is among the most prominent mortality and decay agents of coniferous and deciduous trees. In the western United States, *Armillaria* has been considered an aggressive primary pathogen, while in the eastern United States it has been considered to act as a secondary pathogen.

A total of 73 FIA plots were surveyed for *Armillaria* on the Coconino and Kaibab National Forests in the summers of 2011 and 2012. A total of 29 *Armillaria* samples were collected and identified using DNA-based methods. Of the 29 samples, 100% were identified as *Armillaria ostoyae.*

# Chapter I:

## A review of pandora moth biology and impacts

# A review of pandora moth biology and impacts

## Introduction

Pandora moth is a member of the family Saturniidae in the subfamily Hemileucinae. This group contains small to medium sized moths with hindwings more brightly colored than the forewings. The three genera in the subfamily Hemileucinae: *Coloradia* Blake, 1863, *Hemileuca* Walker, 1855, and *Automeris* Hubner, 1819, often have a red and black (or yellow and black) ringed abdomen, and share a behavior unique among the saturniids thought to aid in making them more cryptic. Adults rock their thorax side to side and pull their wings inward to form a tent that peaks over their body often hiding their antennae under their wings when settling down to rest. This behavior helps eliminate the moth's telltale shadow (Tuskes et al. 1996).

There are eight species and two subspecies of *Coloradia* found in North America but only four species (with one species separated into two subspecies) north of Mexico (*Coloradia doris, C. luski, C. velda, C. pandora pandora, and C. pandora davisi*). Moths in the *Coloradia* genus are cryptic in coloration, typically black, grey, white and occasionally brown to assist in concealing themselves on the pines on which they feed. *Coloradia doris*, *C. luski*, and *C. pandora* all feed primarily on ponderosa pine, *Pinus ponderosa* Douglas ex Lawson & C. Lawson while the primary host for *C. velda* is pinyon pine, *Pinus edulis* Engelmann in Wislizenus; these species all feed on other pine species in captivity (Tuskes et al. 1996) suggesting that their diet may be more extensive.

*Coloradia velda* occurs in pine forests of the San Bernardino Mountains in California (Johnson and Walter 1979, Tuskes et al. 1996). Compared to other *Coloradia* species, sexual dimorphism in *C. velda* is the most reduced (Tuskes et al. 1996) and is unique from all other

North American *Coloradia spp*. in appearance and genitalia (Johnson and Walter 1979). It is larger and more robust than both *C. doris* and *C. luski* and the intensity of scaling on the wings reduces the translucency of the wings (Johnson and Walter 1979). *Coloradia velda* flies in May to July. It occurs sympatrically with *C. pandora pandora*; however, *C. velda* is reproductively isolated by the seasonal flight periods (Tuskes et al. 1996).

*Coloradia doris* is the most widely distributed of the *Coloradia* in the United States (Tuskes et al. 1996). It has been reported to occur across the Rocky Mountain States from southern Montana to southern Arizona and eastern Wyoming to central Nevada (Tuskes et al. 1996). This species is sympatric with other *Coloradia* species across parts of its range although *C. doris* is seasonally isolated from the other species and is the earliest flier (Tuskes et al. 1996). *Coloradia doris* flies as early as April in southern Arizona; however, in the northern parts of its range it flies in mid-July. Morphologically, this species is distinguished from *C. velda* in that it has less defined forewing maculation in males and has a much less bold coloration in the hindwing. The hindwings of *C. doris* are faintly marked and are almost translucent (Tuskes et al. 1996). The North American species of *Coloradia* are shown in Figure 1.1.

*Coloradia luski* is the smallest of the *Coloradia* spp. and the most sexually dimorphic (Tuskes et al. 1996). It occurs in mid elevations (1,800-2,300 meters) in Utah, Colorado, New Mexico, and Arizona. Adult male *C. luski* are easily separated from *C. doris* by its smaller size and greater amount of black and pink on the hindwings. Adult females are harder to separate from *C. doris*, but size, a melanic ground color, and a more opaque appearance are diagnostic. *Coloradia luski* adults fly in early to mid-summer from late June to early August (Tuskes et al. 1996). *Coloradia luski* is sympatric with both *C. doris* and *C. pandora* and while they are

separated seasonally there is some overlap which suggests some differences in pheromones in order to avoid reproductive interaction (Tuskes et al. 1996).

The largest member of the *Coloradia* genus is *C. pandora* and it is one of only a few saturniids that achieves major pest status (Tuskes et al. 1996). Outbreaks occur in Oregon (Patterson 1929), California (Richers 1985, Tuskes et al. 1996), Colorado (Wygant 1941, Ciesla et al. 2010), Utah and Wyoming (Ciesla et al. 2010), Nebraska (Tuskes et al. 1996), and Arizona (Schmid and Bennet 1988). There are two recognized subspecies of *Coloradia pandora: C. pandora pandora* (Barnes and Benjamin, 1926) and *C. pandora davisi* (Barnes and Benjamin, 1926). Large size and prominent discal spots on both sets of wings are identifying characteristics of this species (Tuskes et al. 1996).

The two subspecies have three disjunct populations which are distributed across the western United States. The distribution of the two subspecies is allopatric. *Coloradia pandora davisi* is found in Arizona, southern Utah, New Mexico and West Texas. *Coloradia pandora pandora* has two disjunct populations; one in California, Oregon, and Nevada, and the other in southern Idaho, Wyoming, Nebraska, South Dakota, Colorado, and Utah (Figure 1.2) (Tuskes et al. 1996). *Coloradia pandora davisi* is 15-20% smaller on average, with males having darker forewings than *C. pandora pandora* (Ferguson 1971, Tuskes et al. 1996). Sexual dimorphism is also more pronounced in *C. pandora davisi* as males are usually darker than females (Tuskes et al. 1996). The two *pandora* subspecies have semivoltine life cycles (2 or more years) while *C. doris* and *C. luski* are univoltine (Tuskes et al. 1996). Although sometimes reported as *C. pandora pandora* (Schmid and Bennet 1988), we believe that the populations in northern Arizona are *C. pandora davisi* based on Tuskes et al. (1996) (however see Ciesla et al. 2010).

For the purposes of this review, pandora moth will include both subspecies unless otherwise indicated.

**Pandora Moth (*Coloradia pandora*)**

The life cycle and behavior are very similar between the pandora moth subspecies (Tuskes et al. 1996). Only Tuskes et al. (1996) and Ferguson (1971) make a distinction between the subspecies. The remaining literature refers to both as *C. pandora* Blake 1863 (Lepidoptera: Saturniidae) (e.g. Furniss and Carolin 1977). During outbreaks, pandora moth can completely defoliate large areas of western pine forests (Furniss and Carolin 1977). The principal hosts of pandora moth are ponderosa pine (*Pinus ponderosa*), Jeffrey pine (*Pinus jeffreyi* Greville & Balfour in A. Murray), and lodgepole pine (*Pinus contorta* Douglas ex Loudon); with Coulter pine (*Pinus coulteri* D. Don), sugar pine (*Pinus lambertiana* Douglas) and pinyon pine (*Pinus edulis*) being occasional hosts (Schmid and Bennett 1988, Ciesla et al. 2010). However, not all western pine forests are susceptible as pandora moth larvae require loose bare mineral soils to pupate (Furniss and Carolin 1977, Schmid and Bennett 1988). Defoliation over the course of an outbreak causes tree growth loss and several sociological implications including diminished visitor experience. Impacts associated with millions of moths or larvae in heavily used recreation areas include diminished visual quality with severe defoliation, increased allergens, and the smell of carcasses. Direct tree mortality due to the defoliation has been low (2%) (Speer and Holmes 2004); however, presence of inciting factors such as high dwarf mistletoe abundance can lead to higher levels of tree mortality (Wagner and Mathiasen 1985). Defoliation can contribute to direct mortality and stressed conditions within stands which can lead to subsequent outbreaks of other mortality agents such as bark beetles (Patterson 1929, Ciesla et al. 2010).

Dendrochronology indicates that the length, duration, and interval between historic outbreaks fluctuate (Speer et al. 2001); however, multiple reports state that 6 to 8 year outbreaks of pandora moth occur in 20 to 30 year intervals (Patterson 1929, Carolin and Knopf 1968, Schmid and Bennett 1988, Speer et al. 2001, Ciesla et al. 2010). While the cause of the 20 – 30 year interval between outbreaks is unknown, the decline of an outbreak is believed to be the result of an increased prevalence of a nucleopolyhedrosis virus (NPV) (Furniss and Carolin 1977, Schmid and Bennett 1988).

Since the 1920's, scientists have been examining the history, biology, growth loss, parasitism, effect of defoliation on aesthetics, and possible management strategies for pandora moth (Chamberlin 1922, Patterson 1929), yet there is still much about the pandora moth that requires attention particularly as climate and forest conditions change. The cyclic nature of outbreaks is of particular interest when dealing with changing annual temperatures. There are several hypotheses pertaining to the cyclic nature of defoliating insects (Myers 1988, Berryman 1996); however, none are more plausible than others in relation to pandora moth.

If indeed population fluctuations of forest moths are cyclic, the population fluctuations can arise from first order feedbacks involving density dependence or second order feedbacks involving climate, predators and parasitoids, disease, or combinations of all these factors (Myers 1988, Berryman 1996). Circular causality involving negative feedback mechanisms is at the forefront as a general explanation (Berryman 1996). Pathogen-caterpillar interactions are probably not the cause (Myers 1988, Berryman 1996). Viruses associated with high mortality, such as NPV, do not disrupt the basic dynamics of population fluctuations (Myers 1988), yet in

the case of pandora moth, NPV seems to be the primary cause of population decline (Patterson 1929, Schmid and Bennet 1988).

Pandora moth egg parasitoids can kill up to 55% of eggs at the peak of the population (Patterson 1929). NPV is also most prevalent at high larval densities. Together, these factors along with other biotic factors such as vertebrate predation (Patterson 1929), could reduce the fecundity and vigor of pandora moth populations sufficiently enough to sustain the population decline, although this is not yet confirmed.

In addition to parasitoids, predators, and pathogens, the interaction of pandora moth with fire is likely substantial. Fires occurring within the infested area of outbreaks impact all life stages and fires occurring between outbreaks may contribute to limiting the locations of future outbreaks. The most obvious interaction that might limit the population is a lack of host in a given area following a high severity fire. Pupation in the soil may be a way to avoid damage by fire under the natural (historic) fire regime in ponderosa pine forests (frequent low severity fire). Some pupal mortality occurs under low severity prescribed fire conditions (Schmid et al. 1981) and high severity fire conditions are likely to cause higher mortality rates. High severity fires can increase soil temperatures in excess of 100° C to depths of 100 cm (Neary 1999), well past the depth of pupae (5– 8 cm).

**Life History/ Description/ Behavior**

Pandora moth develop from egg to adult over a period of 24 months (Patterson 1929, Ciesla et al. 2010) with moths appearing in even numbered years in Arizona (Ciesla et al. 2010),

although some off-year flights do occur (Schmid 1984, Ciesla et al. 2010, see Chapter 2); asynchronous flights generally consist of significantly lower moth numbers (see Chapter 2).

**Adult.** Adult *Coloradia pandora pandora* have a wingspread of 7.6 - 11.4 cm (Carolin and Knopf 1968) with females having an average expanse of 8.6 cm and males 6.9 cm (Chamberlin 1922). Their bodies can be as long as 3.8 cm (Carolin and Knopf 1968). The average body length for females is 3.4 cm and for males is 3.1 cm (Chamberlin 1922). *Coloradia pandora davisi* is consistently 15 - 20% smaller (Tuskes et al. 1996).

Adults are brownish gray; the antennae are yellow and narrow (female) or plumose (male); the biserate is a little longer than the thorax (Chamberlin 1922) (Figure 1.1). The thorax is covered in soft hairs. The abdomen is dark brown dorsally with gray sides and apex is tufted extending beyond the wings (Chamberlin 1922). Forewings are semitransparent with two indistinct wavy bands and a distinct black spot on the discal nervure (Chamberlin 1922, Ciesla et al. 2010). The hindwings have an indistinct cloudy band, are broader at the interior margin and gradually taper to the exterior and also have a pale brownish spot on the disc (Chamberlin 1922) and are more transparent than the forewing (Ciesla et al. 2010). The underside of the wings is brownish gray with a pinkish tint; the base of the hindwings has pale pinkish hairs and whitish cilia at the extremity of the veins (Chamberlin 1922). The discal spots are more apparent on the underside then on the upper surface (Chamberlin 1922).

Pandora moth adults exhibit nocturnal or crepuscular flight activity. Moths are most active between 20:00 and 23:00 (personal observation). Male moths search for female moths which are flightless until after mating (Ciesla et al. 2010) and are generally not found flying

during daylight (Schmid 1984). However, as emergence proceeds through the population, more males can be seen flying during daylight hours frequently hovering 8 – 15 cm from boles of trees seeking a mate (Schmid 1984). During the outbreak in Arizona in the early 1980's, males initially outnumbered females by a 4:1 margin, eventually approached a 1:1 margin during the peak emergence, and females outnumber males over the last 10 days of August with a ratio of 1:1.5 (Schmid and Bennett 1988). Thus, it appears that males that emerge early are less likely to find a mate.

Pandora moth adults are thought to survive for 5 – 10 days (Gerson and Kelsey 1997); Schmid (1984) indicates the lifespan of the moth to be 7 days which fits the Gerson and Kelsey (1997) estimate. Male moths typically die within one day of mating, and females die within 3 days of oviposition (Patterson 1929).

Following mating, females lay an average of 50 to 80 eggs in multiple egg clusters (Patterson 1929, Ciesla et al. 2010); this number may vary between populations as dissected females (collected as they emerged and mated in captivity) have an average of 145 eggs with a range of 108-188 (Schmid and Bennett 1988). The eggs are pale bluish-green (Figure 1.3) and semitransparent at the time of oviposition becoming opaque and duller green as the eggs age (Chamberlin 1922). Eggs are oviposited in multiple clusters of 2 - 50 eggs per cluster (Ciesla et al. 2010) or 6 - 74 (Chamberlin 1922), although more than 20 and less than 3 are rare (Schmid and Bennett 1988). Eggs are usually deposited on the needles and bark of pines (Ciesla et al. 2010), although eggs can be oviposited on anything in the forest including ground litter, brush, light posts, cars, and buildings (Schmid and Bennett 1988). Eggs hatch after an incubation period of 40 - 50 days (Schmid and Bennett 1988, Ciesla et al. 2010) typically between late September

and November (in Arizona) with most emerging in October (Schmid and Bennett 1988). Eggs are 2.5 mm long by 2.0 mm in width flattened on upper and lower surfaces (Chamberlin 1922).

**Larvae.** The larvae, when first hatched (Figure 1.4) have shiny black heads and black spiny bodies 5 mm in length (Chamberlin 1922, Ciesla et al. 2010). There are five larval instars and all have the characteristic spines (Carolin and Knopf 1968). First instar larvae initially feed on the yolk of the egg shells then begin feeding on the needles of branch tips as discrete groups moving from one area to the next in a single file line (Carolin and Knopf 1968). The gregarious feeding method (Figure 1.5) continues until late fall after which the larvae disperse and feed individually (Patterson 1929, Carolin and Knopf 1968).

Larvae overwinter at the base of the needles mostly as second instar in the Rocky Mountains (third instar if above average temperatures occur) (Schmid and Bennett 1988) or as third instar in Oregon and California (Carolin and Knopf 1968). Some feeding occurs during warmer days during the winter (Ciesla et al. 2010). Larvae consume large quantities of needles once temperatures warm up in April and May (Carolin and Knopf 1968) and quickly pass through their remaining instars (Figure 1.6). The literature does not specify temperatures nor does it address other environmental cues such as photoperiod or degree days at which larvae will resume feeding. For instance, Patterson (1929) states that when winter conditions set in, caterpillars go into hibernation, in clusters of from 4 to 30 individuals at the base of the needles, and are more or less dormant during the winter.

The second to fourth instars are characterized by two narrow white lines marking the ventral surface and progressively more brownish bodies (Carolin and Knopf 1968). The fifth

instar larvae are green (Chamberlin 1922) or olive-brown marked by transverse yellow bands and a longitudinal white stripe (Carolin and Knopf 1968). They have orange-brown heads and a pale yellow-brown collar (Carolin and Knopf 1968). The full-grown larva measures 5.7 – 7.6 cm in length (Carolin and Knopf 1968). Fifth instar caterpillars have a white stripe down their back and orange-brown heads; their bodies also have a greenish tint, especially ventrally (pers. observation).

The fifth instar remains in the tree until June when it begins decent from the canopy into the soil to pupate (Schmid and Bennett 1988, Ciesla et al. 2010). Pre-pupation commences in the soil when the larvae contract in length and thicken in width and form a hard case (Schmid and Bennett 1988). Newly formed pupae are initially light green in color, matching the color of the fifth instar larvae (Figure 1.7).

**Pupae**. Pupae are encased within hardened cases that turn dark purplish brown (or dark reddish) in color (Figure 1.7), ranging from 2.5 to 3.8 cm in length (Carolin and Knopf 1968). They are not enclosed in a cocoon of any type and all body parts are clearly discernible (Carolin and Knopf 1968). Pupae develop in loose mineral soil (Ciesla et al. 2010) around the base of trees at distances ranging from 0 – 3 meters (Schmid and Bennett 1988); however, there seems to be a preference for areas under open canopy with the low fuel loads that occur beyond the dripline (Miller and Wagner 1984). Pupae remain in the soil for 12 – 13 months with a substantial part of the population remaining in the soil for two years (Schmid and Bennett 1988), and some individuals for three or four years (Ciesla et al. 2010). Male and female pupae are distinguished by a notch on the terminal segment of

the pupal case (Figure 1.7), the notch can be present on both male and female; however, it is more developed in females.

**Defoliation.** Carolin and Knopf (1968) found that pandora larvae will eat needles of all ages during the spring feeding; however, Schmid and Bennett (1988) indicate that defoliation is limited to older needles rather than the new shoots and foliage. The first instar consumes 1.5 – 2.0 needle bundles per day and the fifth instar consumes 5 – 8 needle bundles per day (Carolin and Knopf 1968). However, needle consumption rate during early instars is strongly dependent upon the size of the group feeding on the needle (pers. observation). The buds of trees are not targeted and left undamaged (Schmid and Bennett 1988, Ciesla et al. 2010) which moderates the effect and allows the trees to recover the following year.

Defoliation severity changes over the course of the outbreak and can be quite severe over significant portions of the host's range during the peak of an outbreak. In Arizona, reports indicate that approximately 7,500 ha were moderately or severely defoliated during the 1981 defoliation event on the North Kaibab Ranger District (RD), Kaibab National Forest, AZ; in 1983, the reports indicate that total defoliation covered a total area of 11,500 ha (Figure 1.8) (Schmid and Bennett 1988). In Oregon, reports indicate that 12,400 ha were infested in 1988 and by 1994 the outbreak covered 864,000 ha (Speer et al. 2001).

Pandora moth causes little to no direct mortality (~2%) to its host (Patterson 1929, Gerson and Kelsey 1997, Speer and Holmes 2004) and long term visual quality impacts are generally limited. Visual quality due to the defoliation is typically reduced from severe conditions to moderate conditions within 2 – 3 weeks, but can remain in a reduced condition for

2 – 3 months every other year (Schmid and Bennett 1988). However, visual quality could be more lasting if mortality increases significantly due to the prevalence of other agents that stress the trees prior to the time of defoliation, such as dwarf mistletoe (Wagner and Mathiasen 1985). Defoliation acts as a predisposing factor in that it stresses trees allowing other damaging agents to establish which can create a more lasting negative quality through increased mortality (Patterson 1929). Bark beetles are perhaps the most noted damaging agent mentioned in the literature; however, no direct link exists between the defoliation and a bark beetle outbreak (Patterson 1929, Carolin and Knopf 1968).

**Pandora moth on the North Kaibab**

Reports indicate that the last outbreak of pandora moth on the North Kaibab RD occurred from 1979 to the mid 1980's. Over the course of that outbreak it is known that approximately 11,543 ha were moderately or severely defoliated with ~2% of direct mortality (Schmid and Bennett 1988). Adult pandora moth was detected on the North Kaibab RD in 2008 (USDA Forest Service 2009) and it appears that another outbreak is beginning. In Chapter 2, I examine population density, defoliation severity, methodologies that improve detection and population dynamics of this moth in northern Arizona pine forests during low densities. I monitor *C. pandora davisi* adult and larval density as well as defoliation severity from 2010 - 2012 on the North Kaibab RD to determine population density.

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**Figure 1.1.** Examples of *Coloradia* species 1. *C. doris* 2. *C. doris* 3. *C. velda* 4. *C. pandora pandora* 5. *C. pandora davisi* 6. *C. pandora pandora* 7. *C. doris* 8. *C. doris* 9. *C. velda* 10. *C. pandora pandora* 11. *C. pandora davisi* 12. *C. pandora pandora* 13. *C. luski* 14. *C. luski* 15. *C. luski* 16. *C. luski* 17. *C. velda* 18. *C. doris* (adapted from Tuskes et al. 1996). The red box highlights male and female *C. p. pandora* and *C. p. davisi*. Males are distinguished from females by plumose antennae.

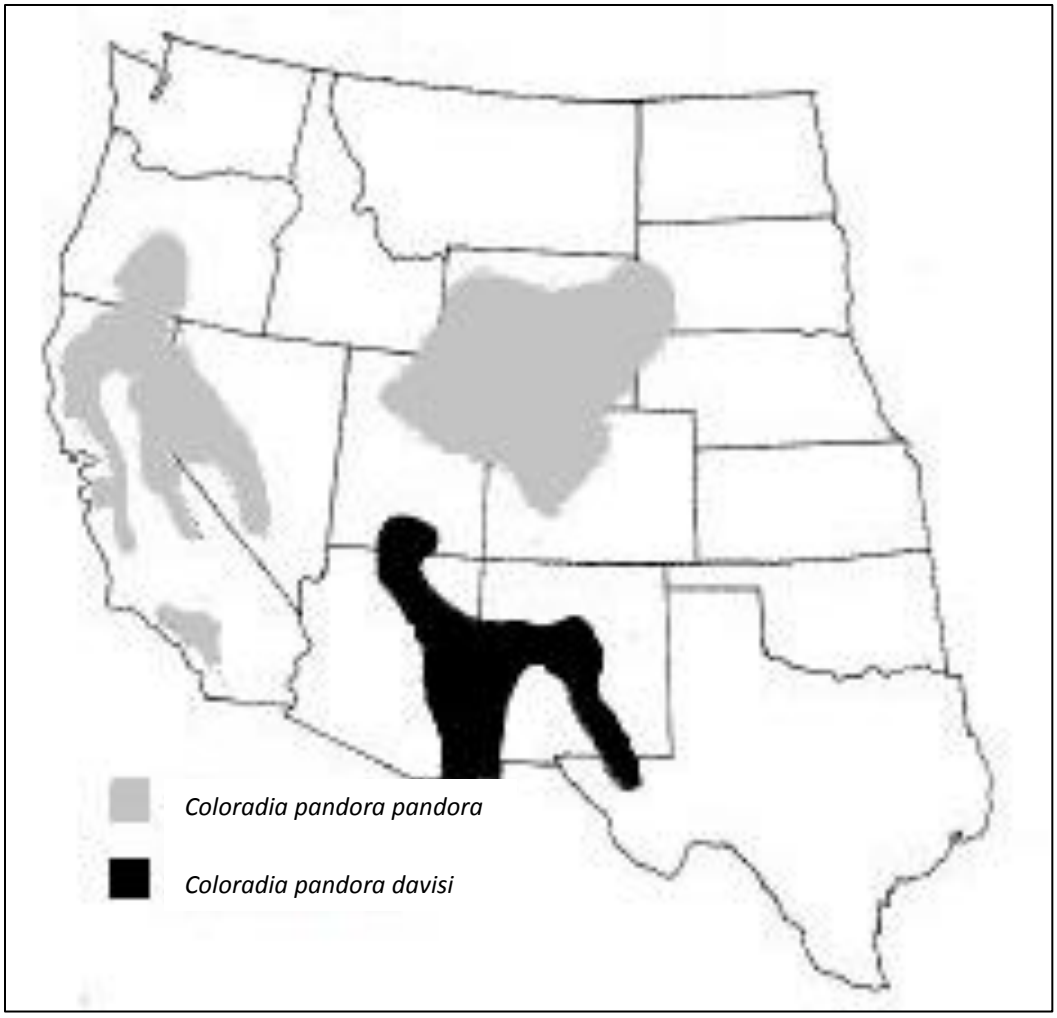


**Figure 1.2.** Pandora moth distribution adapted from Tuskes et al. (1996) for *Coloradia pandora pandora* and *C. pandora davisi*.

**Figure 1.3.** Pandora moth eggs collected on the North Kaibab RD in 2010. Eggs are 2. 5 mm long by 2. 0 mm in width flattened on upper and lower surfaces. Pictures taken by C. Hoffman (left) and R. P. Hanavan (right). August, 2010.

**Figure 1.4.** Newly emerged first instar pandora moth larvae. Picture taken by R. P. Hanavan 2010.

**Figure 1.5.** Pandora moth larvae (Second instar) feeding gregariously on ponderosa pine needles in the laboratory. Picture taken by R. P. Hanavan 2010.


**Figure 1.6.** Pandora moth third, fourth, and fifth instar larvae (from left to right). Third and fourth instars pictures taken by C. Hoffman 2011; Fifth instar (USDA Forest Service Archive, USDA Forest Service, Bugwood.org).

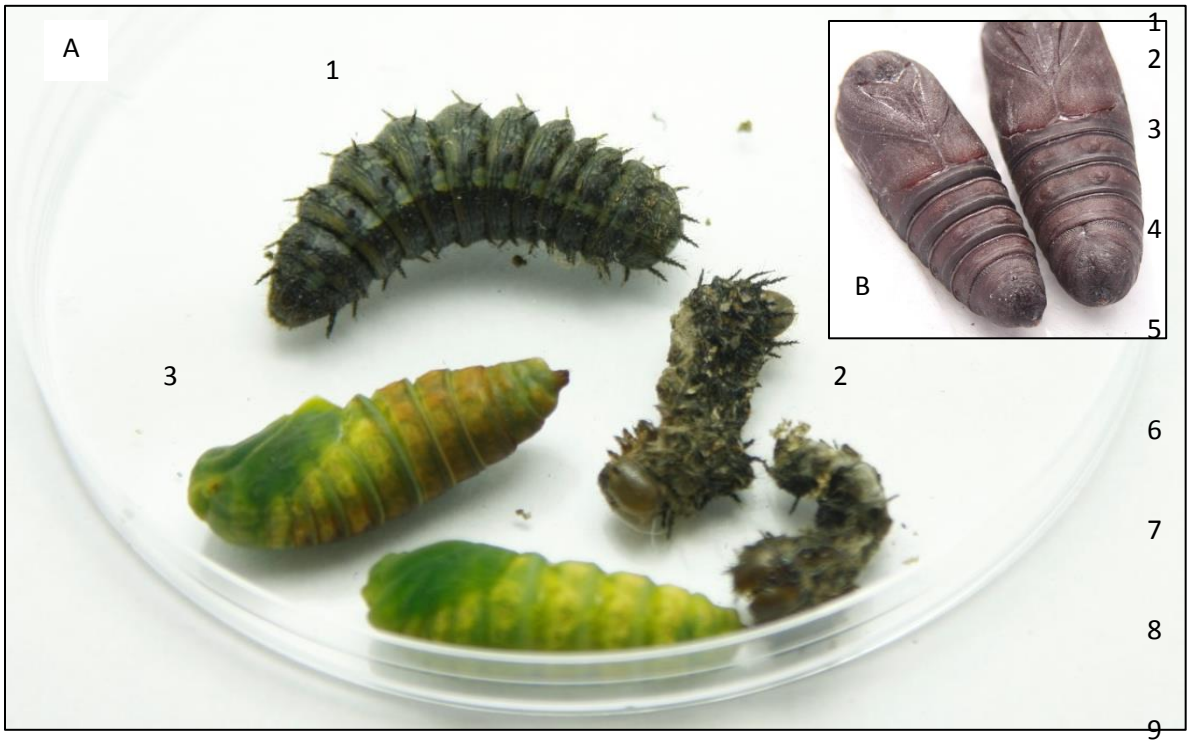


**Figure 1.7.** A) (1)Pandora moth larva (fifth instar) preparing to pupate, 2) Final molt from fifth instar larva, and 3) fresh pandora moth pupae. B) Male (left) and female (right) pandora moth pupae. Picture by Nick Aflitto 2012.

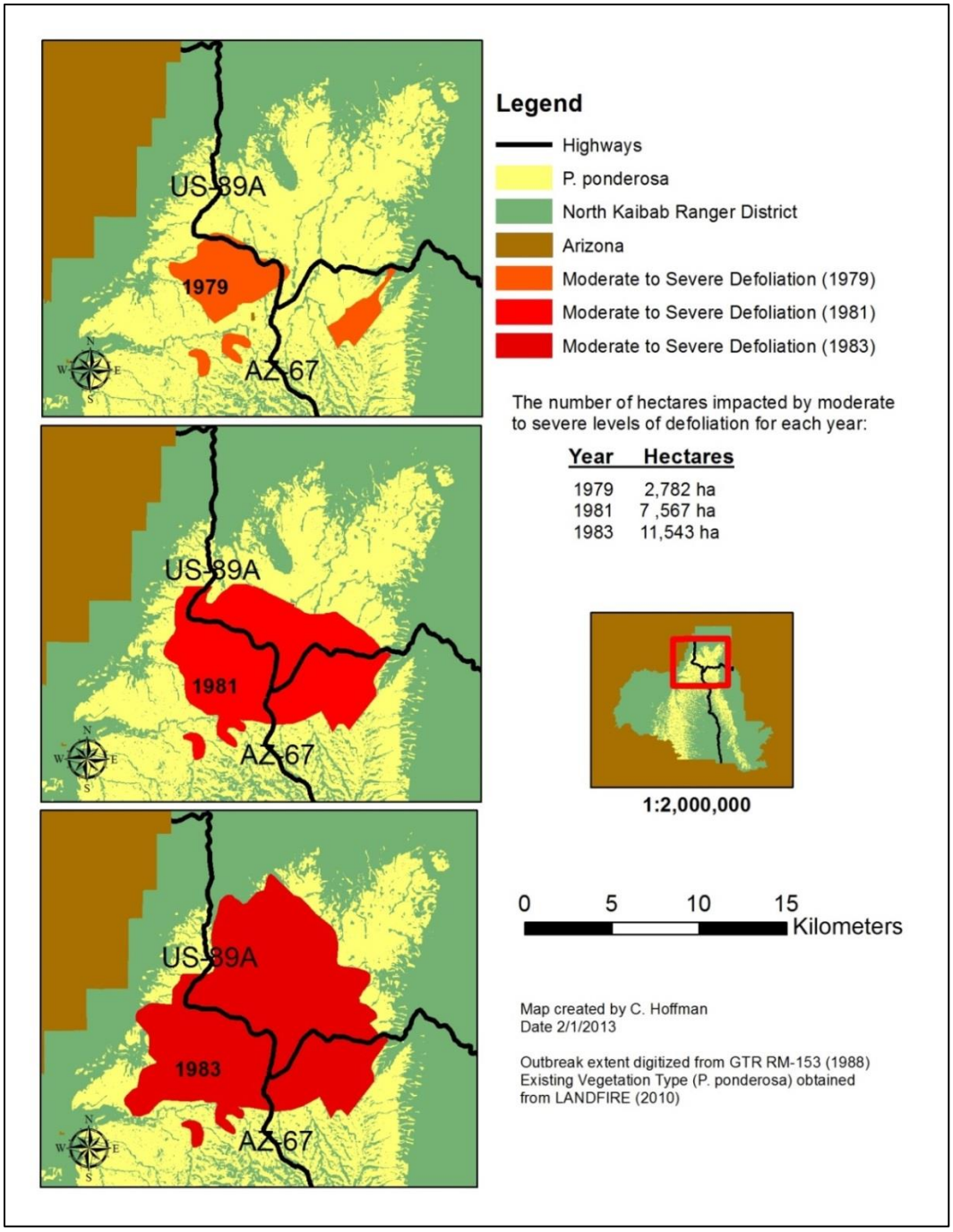


**Figure 1.8.** Extent of moderate and severe defoliation by pandora moth on the North Kaibab RD from 1979 to 1983. Adapted from Schmid and Bennett (1988)

# Chapter II:

# Pandora moth (*Coloradia pandora davisi*, Lepidoptera: Saturniidae) in Arizona: 2010 to 2012

# Pandora moth (*Coloradia pandora davisi*, Lepidoptera: Saturniidae) in Arizona: 2010 to 2012

## Introduction

Pandora moth, *Coloradia pandora* Blake 1863 (Lepidoptera, Saturniidae), is an important defoliator of pines in western forests (Patterson 1929, Furniss and Carolin 1977, Tuskes et al. 1996, Ciesla et al. 2010). Outbreaks of *C. pandora* occur in 20 to 30 year intervals lasting 6 to 8 years (Schmid and Bennett 1988, Speer et al. 2001, Ciesla et al. 2010). Large areas of western pine forests are defoliated during outbreaks (Patterson 1929). Due to the semivoltine life cycle of this insect, the effects of defoliation rarely results in tree mortality (Patterson 1929) and outbreak populations are believed to crash after several generations due to increased prevalence of parasitoids and of a nucleopolyhedrosis virus (NPV) (Patterson 1929, Schmid and Bennett 1988). For instance, low levels of mortality (~2%) were reported in Oregon, during the 1988 to 1994 outbreak which covered 864,000 ha (Speer et al. 2001) and in Arizona during the 1979 to 1985 outbreak which covered 11,500 ha (Schmid and Bennett 1988).

*Coloradia pandora* requires two years to complete its life cycle (Patterson 1929, Furniss and Carolin 1977, Ciesla et al. 2010) with adults appearing during the summer after a year-long pupation period. Larvae occur from early fall to the following summer, remaining on the foliage though the winter (Patterson 1929). Larvae feed on pine needles of ponderosa pine, *Pinus ponderosa* Douglas ex Lawson & C. Lawson, lodgepole pine, *Pinus contorta* Douglas ex Loudon, and Jeffrey pine, *P. jeffreyi* Greville & Balfour in A. Murray (Furniss and Carolin 1977, Cielsa et al. 2011). New and old needles are consumed, but the buds are not damaged. When

fully grown, larvae crawl down tree trunks and enter loose soil or duff to pupate (Ciesla et al. 2010). The pupal stage typically lasts one year, but some pupae may remain in diapause for up to 5 years (Carolin 1971).

There are two recognized subspecies of *Coloradia pandora: C. p. pandora* (Barnes and Benjamin, 1926) and *C. pandora davisi* (Barnes and Benjamin, 1926) although they are not always recognized in the literature (e. g. Furniss and Carolin 1977). The two subspecies have three disjunct populations which are distributed across the western United States. The distribution of the two subspecies vary considerably; *C. pandora davisi* is found in Arizona, southern Utah, New Mexico and West Texas and *C. pandora pandora* has two disjunct populations one in California, Oregon, and Nevada, and the other in southern Idaho, Wyoming, Nebraska, South Dakota, Colorado, and Utah (Figure 2.2) (Tuskes et al. 1996).

An outbreak of *Coloradia pandora davisi* on the North Kaibab Ranger District, Arizona occurred from 1979 to the mid 1980's. Over the course of that outbreak approximately 11,500 ha were moderately or severely defoliated (Schmid and Bennett 1988). Adult pandora moths were again detected on the Kaibab National Forest in 2008 (USDA Forest Service 2009). I monitored *C. pandora davisi* adult and larval density as well as defoliation severity from 2010 - 2012 on the Kaibab National Forest to determine whether the population was beginning to build up. I tracked population density, defoliation severity, and parasitoid and pathogen infection levels of pandora moth in northern Arizona pine forests to test several hypotheses. The first hypothesis was that pandora moth population would occur in the same location(s) as found in the beginning of the 1980's outbreak. The second was that natural enemy levels (i.e. parasitoid and NPV) would be

low at the start of the outbreak. And lastly that pandora moth population density would increase from 2010 to 2012.

**Methods**

The North Kaibab Ranger District, Kaibab National Forest resides to the north of the Grand Canyon in Arizona USA. Ponderosa pine makes up 25% (or ~68,500 hectares) of the North Kaibab Ranger District (RD) (Figure 2.3) (LANDFIRE 2010). The elevation of ponderosa pine ranges between 900 meters and 2,800 meters on the North Kaibab Plateau. The North Kaibab RD receives an average of 52 cm of precipitation per year; average low temperatures range from -17° C in January to 10.6° C in July, average high temperatures range from 4.5° C in January to 26.6° C in July; average annual snowfall is 268 cm (Western Regional Climate Center). The soil types present within the ponderosa pine cover type are primarily Typic Eutroboralfs and Typic Haplustalfs.

To address whether pandora moth populations occurred in the same locations as that found in the 1980's outbreak, I measured pandora moth late larval densities and defoliation intensity on plots established at ~0.8 km (half mile) intervals along Forest Service roads throughout the range of ponderosa pine on the North Kaibab RD. Each plot consisted of 20 randomly selected ponderosa pine between 1.5 and 6.1 m tall (Figure 2.4). The tree sizes used allowed for the measurement of larval and defoliation intensity during low larval densities that occurred during the study period. In June 2011, each tree was examined for the presence of larvae and signs of defoliation before larvae vacated trees to pupate. Larvae were counted on a per tree basis and larvae within reach were collected and reared to examine for pathogen (particularly the NPV) and parasitoid infection. Defoliation was measured by counting the

number of needles eaten per tree as well as the number of branches that had defoliation. Counts of defoliated needles were limited at 100 eaten needles per tree. In 2011, a total of 136 plots were examined. Previous defoliation estimate methods (Schmid and Bennett 1988) were not practical given low defoliation levels during the study period. Given only one year of sampling, no statistical tests were performed on larval densities or defoliation estimates. Data collected will provide a baseline and additional data for changes in population densities and defoliation over time.

ARCGIS 10.1 was used to create a prediction map and prediction standard error map of larval density and defoliation severity using geospatial analyst universal kriging with a constant trend removal. The model was optimized to produce an 8.5 goodness of fit. The semivariogram utilized 12 lags at a lag size of 266.8 m. The output regression function was 0.36 * x + 2.13. As no mask can be applied to a geostatistical layer, two extraneous data points were added to the dataset and assigned 0 larvae (outside the northwest and southeast corners of the range of ponderosa pine) to extend the rectangular extent of the kriging analysis to encompass the range of ponderosa pine. The visible extent was modified in the data frame to limit the kriging output to the actual extent of ponderosa pine. The surface utilized 10 classes to classify the various levels of the larval data to create a surface that replicated field observations.

To measure parasitoid densities of late-larvae and pupae, larvae collected in June (2011) were reared in the lab in containers and monitored for parasitoid emergence. The remaining pandora moth pupae (400 individuals) were placed back into the field at 20 locations within the outbreak area in August (2011). Two sets of 10 pupae were placed at each location (Figure 2.6). All pupae were buried 2.5 – 5 cm deep in soil contained within a 30.5 cm x 45.7 cm wooden

frame 15.24 cm tall screened with chicken wire on top and window screening on bottom to prevent predation and allow water drainage. Two hundred pupae were collected in October (2011) and the remaining 200 pupae were collected in May (2012) and monitored in the laboratory for parasitoid emergence or evidence of prior parasitoid emergence. Late instar larvae both in the field and laboratory were monitored for the presence of NPV infection.

To test whether adult pandora moth densities increased from 2010 to 2012, I determined relative moth abundances using light traps set up at 3 sites near Jacob Lake, Arizona (Figure 2.5). Differences in adult moth densities across years was tested using a *z*-test. Trap construction consisted of a piece of clear flexible plexiglass (GE Polymershapes, Salt Lake City, UT, USA) fashioned into a cone with a 10 cm opening at the base secured to a 5 gallon bucket with a black light suspended a few centimeters above the base of the funnel (switched to a 20 gallon trashcan 7 August 2010 due to high capture rates). Black lights were automated with an electric timer and were operational for 9 hours (8pm-5am) at each location during the flight period. Light traps were operated daily in 2010, 2011, and 2012; from 17 July 2010 to 20 August 2010 and during the weekends in September until no moths were captured, from 16 August 2011 to 14 September 2011 and from 14 July 2012 to 10 September 2012. Moths were collected, counted, and sorted by sex for each trap.

In 2012, an additional light trap was set up on the Tusayan RD (south of the Grand Canyon) to determine if adult moths were present and if that population had similar characteristics as the North Kaibab RD population. The trap was operated from 1 August 2012 to 1 October 2012. Moths were collected two or three times a week.

## Results

A total of 594 larvae were observed and collected from trees in 2011. Thirty six percent (50 plots) of the 136 plots contained larvae. Eleven percent (16 plots) had more than 10 larvae and 5% (8 plots) had more than 25 larvae (Figure 2.7). From the 36% of plots with larvae, larvae were only on 24% of the trees sampled. The greatest density of larvae occurred on the north east side of the North Kaibab RD as shown on the prediction surface (Figure 2.8a). The mean number of larvae across all plots containing larvae was 11 ± 16 (standard deviation) per plot (or 0.5 ± 0.8 larvae per tree); a histogram of the larval frequency across plots is shown in Figure 2.8b. The location of the highest larval density varied from where the previous outbreak started by several kilometers; however, since no moderate or severe defoliation was present in 2011 location, comparisons for the start of the outbreak are still premature.

Ocular estimates of defoliation in 2011 indicated that even on the most heavily defoliated trees, defoliation was less than 1%. There were a total of 364 trees with defoliation on 63 plots. The number of needles eaten on these plots ranged from 4 to 809 (averaging 154 needles per plot or 8 needles per tree) (Figure 2.8b); however, 19 trees across 11 of the 63 plots had more than 100 needles defoliated and 8 trees across 6 plots were too tall to accurately measure defoliation.

Late larval mortality due to the NPV and parasitoids was 2%. There were 3 larvae (0.4%) infected with NPV and 11 parasitoids (1%) (4 diptera, 7 ichneumonid wasps) emerged from larvae while in the lab. Two additional larvae were found dead while sampling due to unknown causes. Pupae collected in October 2011contained 7 parasitoids (3.5%). Pupae collected in May 2012 had 2 parasitoids (1%). Pupal parasitoids collected during both periods were Ichneumonidae and Diptera.

A total of 24,239 adult moths (28% female) were captured in light traps in 2010 (Figure 2. 9a); the average total number of moths was 8,069 ± 1,908 (standard deviation) total per trap. The first female was captured on 28 July and females reached their highest peak on 16 August (daily mean 56 ± 4 females per trap); the first male was captured on 21 July and males reached a peak on 11 August (daily mean 203 ± 65 males per trap). Males outnumbered females until 16 August. The number of females in the population exceeded the number of males (sex factor) starting August 14, 2010 (Figure 2.9b) until August 20, 2010 (when trapping periodically ended). The last adult was captured between September 12 and 17.

The total number of adults captured in 2011 was much lower at 156 total moths (15% female); the total mean number of moths per trap was 52 ± 15 (standard deviation). The first female was captured during the second week of trapping (24 August 2011) and peaked during the same week (daily mean 1 ± 1 females per trap); the first male was captured during the first week (16 August 2011) and peaked during the third week (daily mean 2 ± 2 males per trap) on (31 August 2011) (Figure 2.9a). At no date during 2011 did female densities outnumber male densities (Figure 2.9b). The last adult was captured the week of 14 September.

In 2012, a total of 8,006 adults (29% female) were captured in light traps; the average total number of moths per trap was 2,681 ± 274 (standard deviation). The first female was captured during the first week of trapping (14 to 21 July 2012) and peaked 9 August (daily mean 17 ± 25 females per trap); the first male was also captured during the first week and peaked 6 August (daily mean 39 ± 53 males per trap) (Figure 2.9a). The males outnumbered females until 11 August; females only outnumbered males for 4 days during the last weeks of trapping (Figure 2.9b). The last adult was captured the week of 3 September. Testing the difference in adult

abundances between 2010 and 2012 using a z-test, gives us a z-score of 4.8 for a p-value < 0.001 (thus rejecting the hypothesis that the population would increase; and in fact it significantly decreased).

The light trap on the Tusayan RD (located south of Grand Canyon National Park; 2012 only) captured 1,218 total moths; 907 females and 311 males (Figure 2.10). The first female was captured between 11-13 August 2012, and the first male was captured between 13-15 August 2012. Females made up 74% of the population sampled and females outnumbered males prior to 24 August and after 1 September (Figure 2.10b). The last adult was captured between 5 and 10 September.

**Discussion**

Given the population density in 2010 to 2012, it is unlikely that pandora moth on the North Kaibab RD had entered the outbreak phase. This is supported by the low number of both larvae and adults (M. Wagner, pers. comm.) as well as the lack of detectable defoliation in comparison to the previous outbreak (Schmid and Bennett 1988). The 66% decline in adults from 2010 to 2012 may indicate that the current population will not outbreak in 2014; however, such fluctuations are not uncommon and may be due in part to low winter temperatures (Leather 1984, Battisti et al. 2005). Record low temperatures were recorded on the North Kaibab Plateau on 1 January 2011 (-1.67°C) and on 13 January 2013 (-6.67°C) (National Weather Service, Grand Canyon National Park Airport, AZ). Parasitization and NPV infection resulted in less than 3% larval and pupal mortality and thus contributed little to the 66% total reduction in adult capture rates. The level of parasitoids and NPV can be expected to increase if pandora moth

population densities increase (Briggs and Godfray 1995), but is unlikely to regulate the population at current levels unless egg parasitization rates (not sampled) or other mortality factors were considerable. If lower winter temperatures increase, pandora moth will most likely increase; however, the effects of winter temperatures on pandora moth have not been well studied or documented (Patterson 1929). Studies are needed to determine if cold winter can collapse the population or further delay potential population growth.

The population does not appear to have reached outbreak density as indicated by the lack of defoliation (Schmid and Bennett 1988), adult density (M. Wagner, pers. comm.), and larval density (Schmid 1984). Parasitoid and pathogen densities are low and may increase with an increasing host density however little information is known about parasitoid and NPV dynamics in pandora moth populations.

Interestingly the current population center occurred several miles northeast of where the last outbreak initiated in 1979 (Schmid and Bennett 1988); however, this alone is not enough to reject my hypothesis that the outbreak will begin at the same location as the previous outbreak. Also, the 2011 larval densities are extremely low compared to densities in the previous outbreak. High levels of defoliation in 1979 occurred south of Highway 89A the progressed north and south in progressive years (1981 and 1983) (Schmid and Bennett 1988). Whether high levels of defoliation will occur in similar locations is yet to be determined.

The hypothesis that pandora moth densities increased from 2010 to 2012 was rejected because adult pandora moth populations significantly decreased. However, the low number of adults captured in 2010 (compared to previous outbreak years, M. Wagner pers. comm.) and even lower numbers in 2012 could (at least in part) be an artifact of trapping in the same location

over several years and may not reflect the true population. The placement of the traps southwest of the population center and the presence of artificial lights between the population center and the traps could have affected adult population densities and reproductive success in 2010 (Frank 1988).

**Future Work**

There are many aspects of the pandora moth that remain unknown, in part due to the cyclic nature of outbreaks. As changing climatic conditions have the potential to alter pandora moth development rates, survival and defoliation severity, the interaction between climate, host, and insect should be monitored closely. Under predicted climate conditions, such interactions are poorly understood and deserve further examination to understand the cyclic nature of outbreaks or identify changes in the insect host interaction.

Under current conditions, pandora moth outbreaks are frequently left unmanaged (Furness and Carolin 1977), yet there might come a time when direct or indirect tree mortality is high and active management is necessary. While the utility and application aspects of the NPV as a biological control has not been thoroughly vetted for pandora moth it has considerable potential for pandora moth management (Patterson 1929) and seems like the next logical step.

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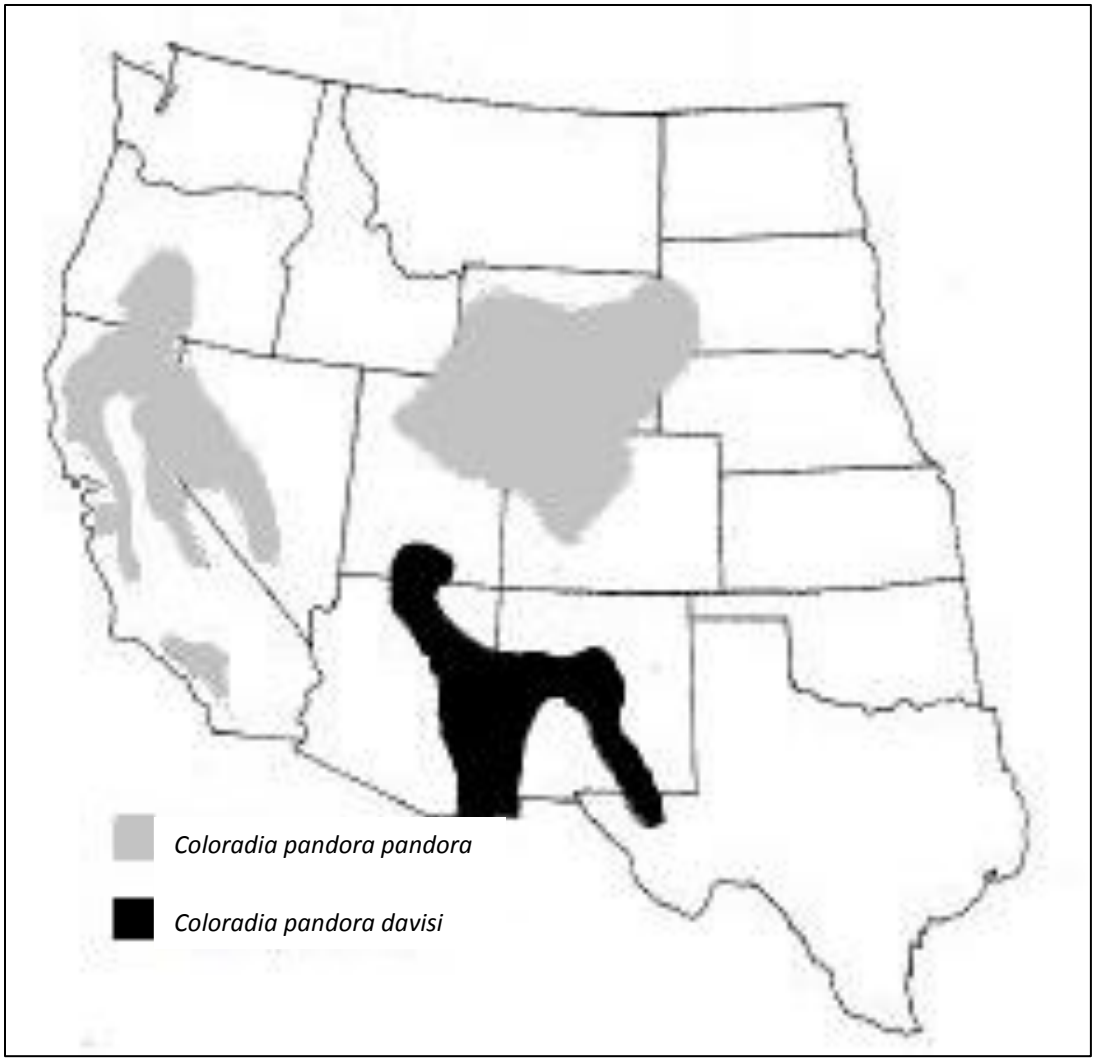



**Figure 2.1**. Pandora moth distribution adapted from Tuskes et al. (1996) for pandora moth species.

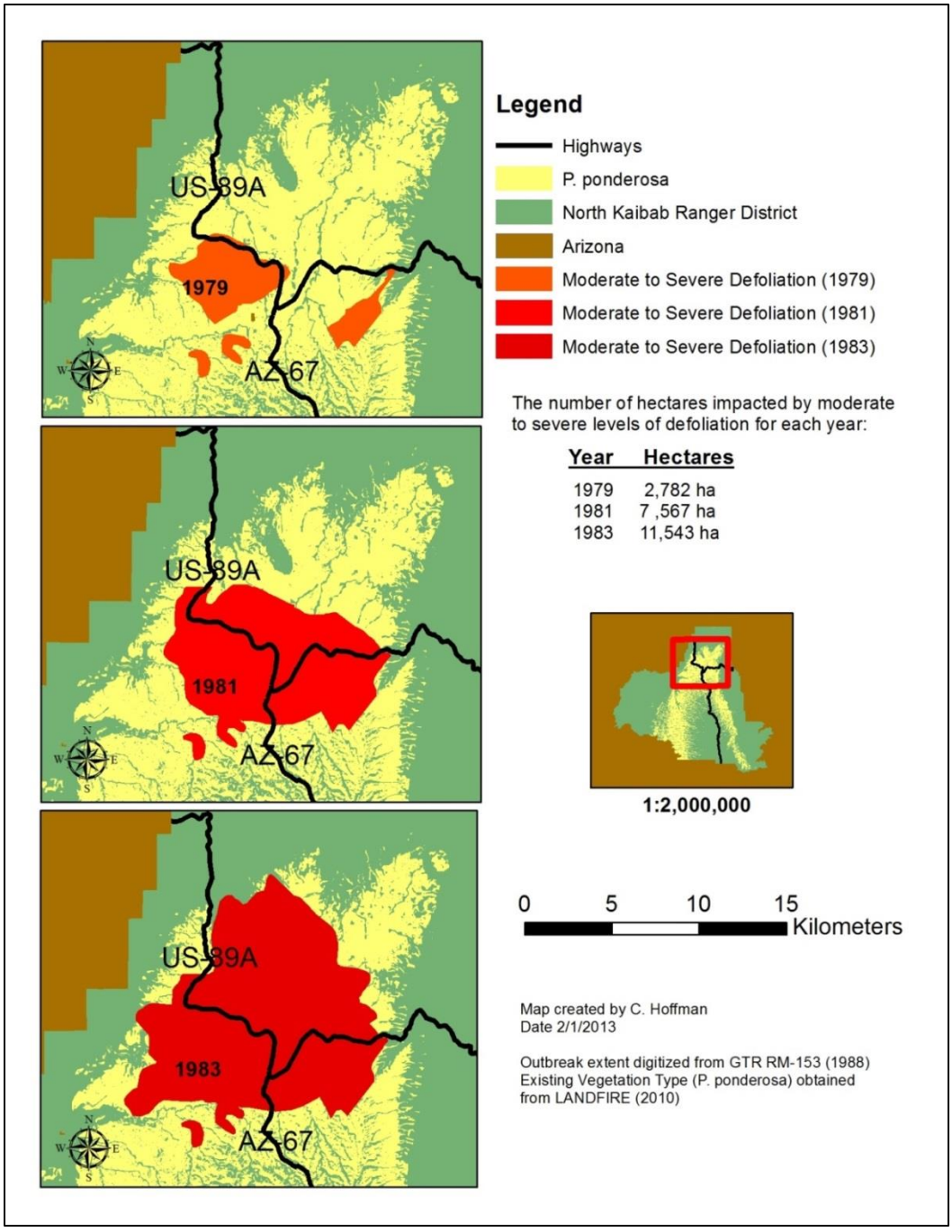



**Figure 2.2.** Moderate to severe defoliation by pandora moth on the North Kaibab RD from 1979 to1983. Adapted from Schmid and Bennett (1988).

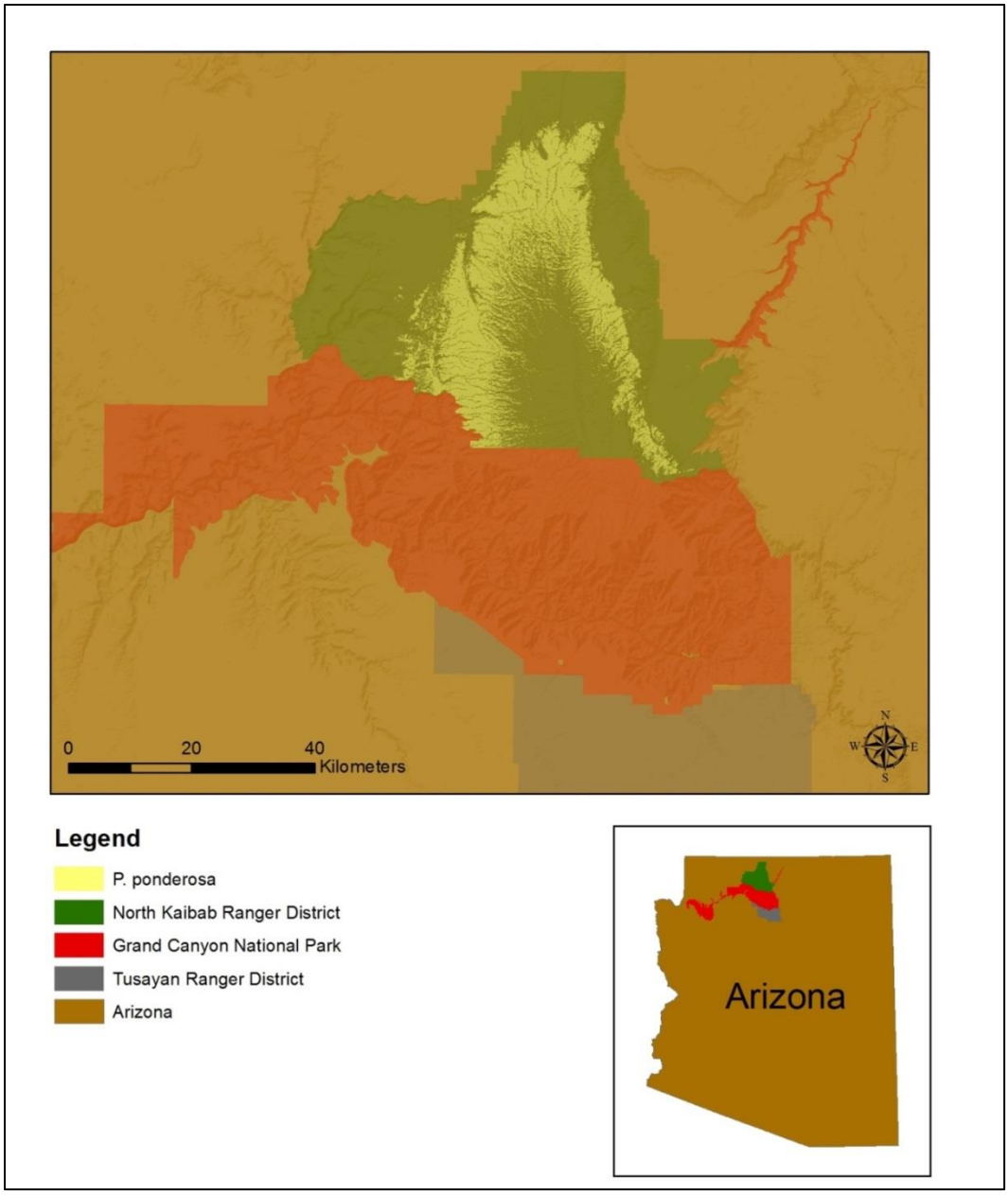



**Figure 2.3**. Ponderosa pine range on the North Kaibab RD.

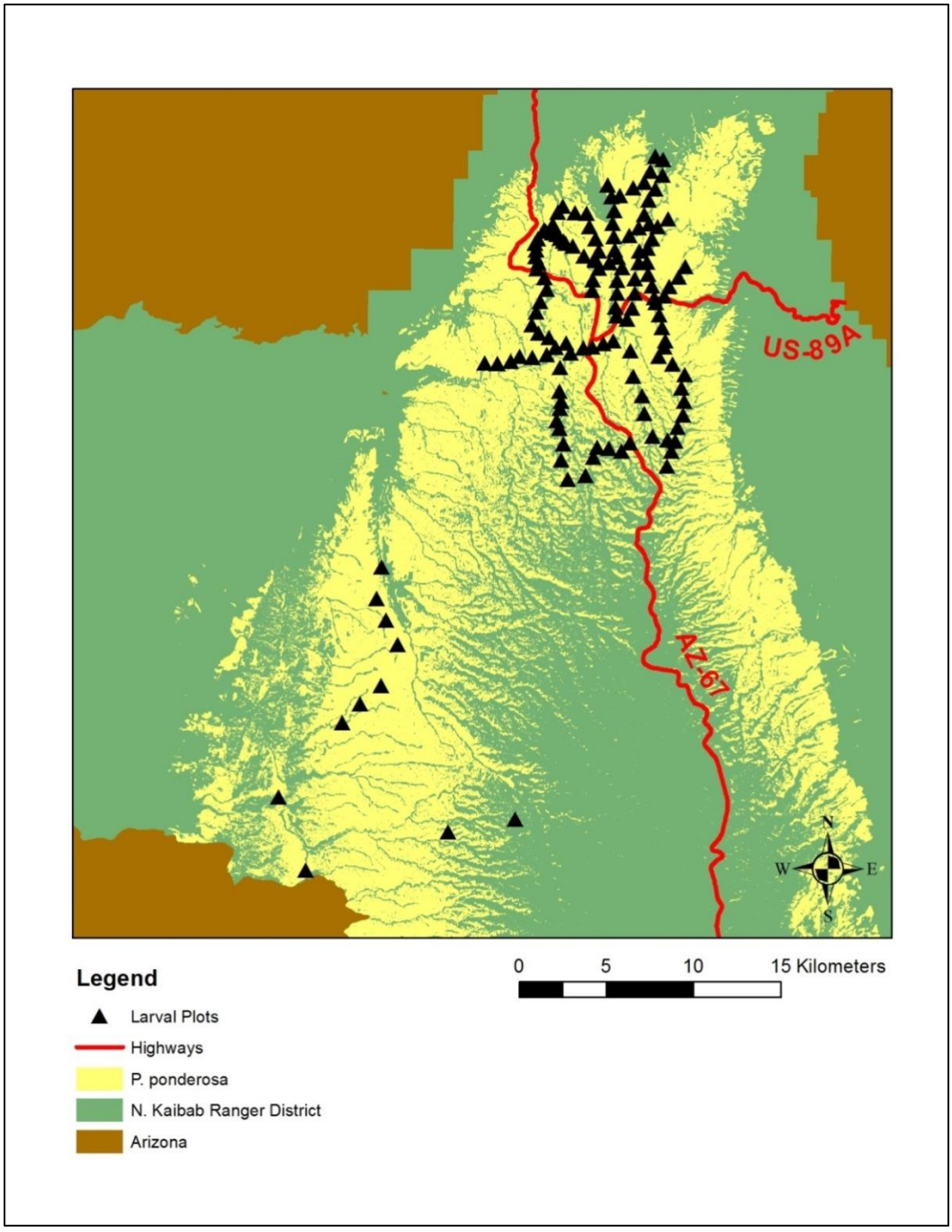



**Figure 2.4**. Pandora moth larval plot locations sampled in 2011 on the North Kaibab RD. 136 plots were sampled.

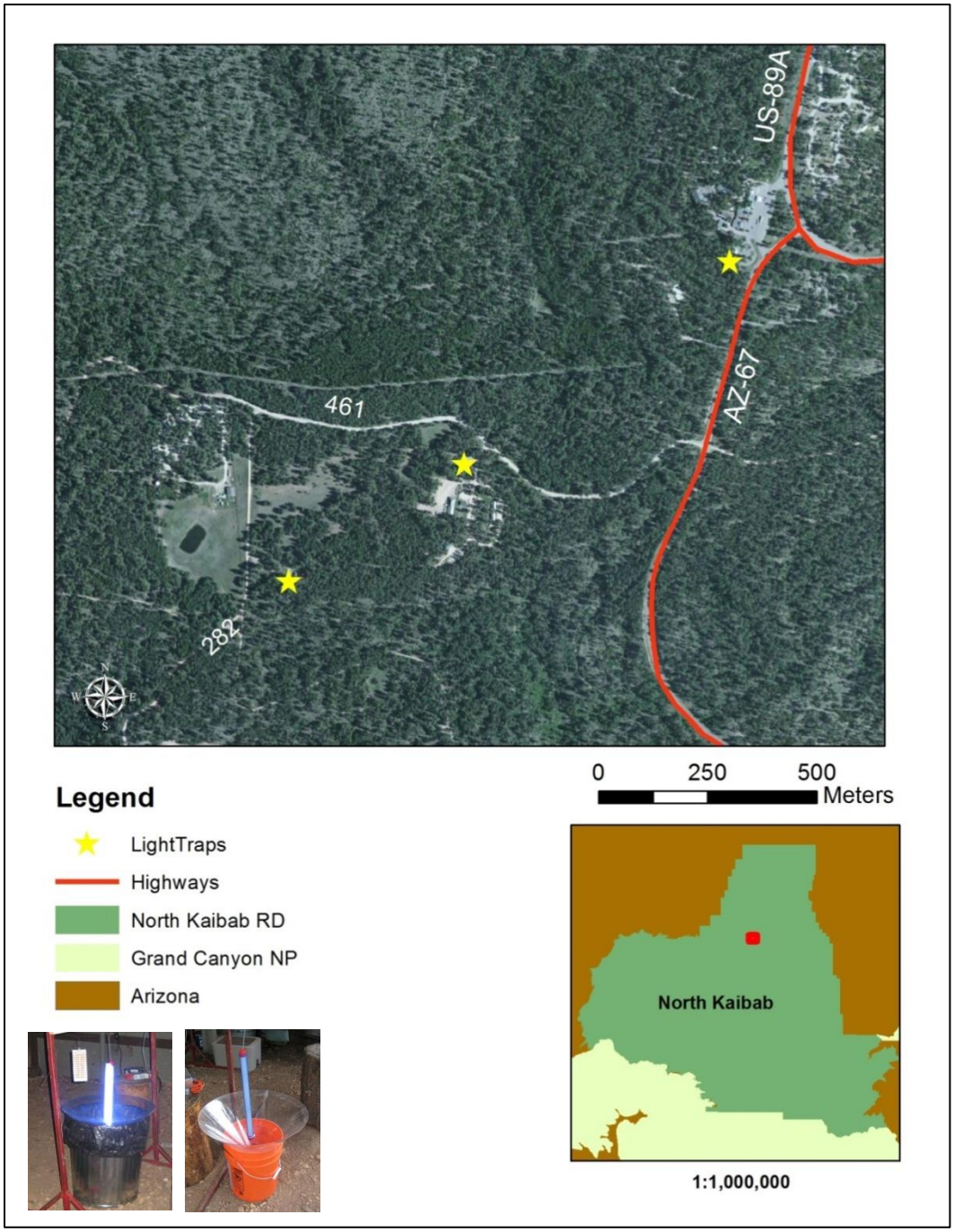



**Figure 2.5.** Location of light traps set up near Jacob Lake, AZ in 2010, 2011, and 2012.

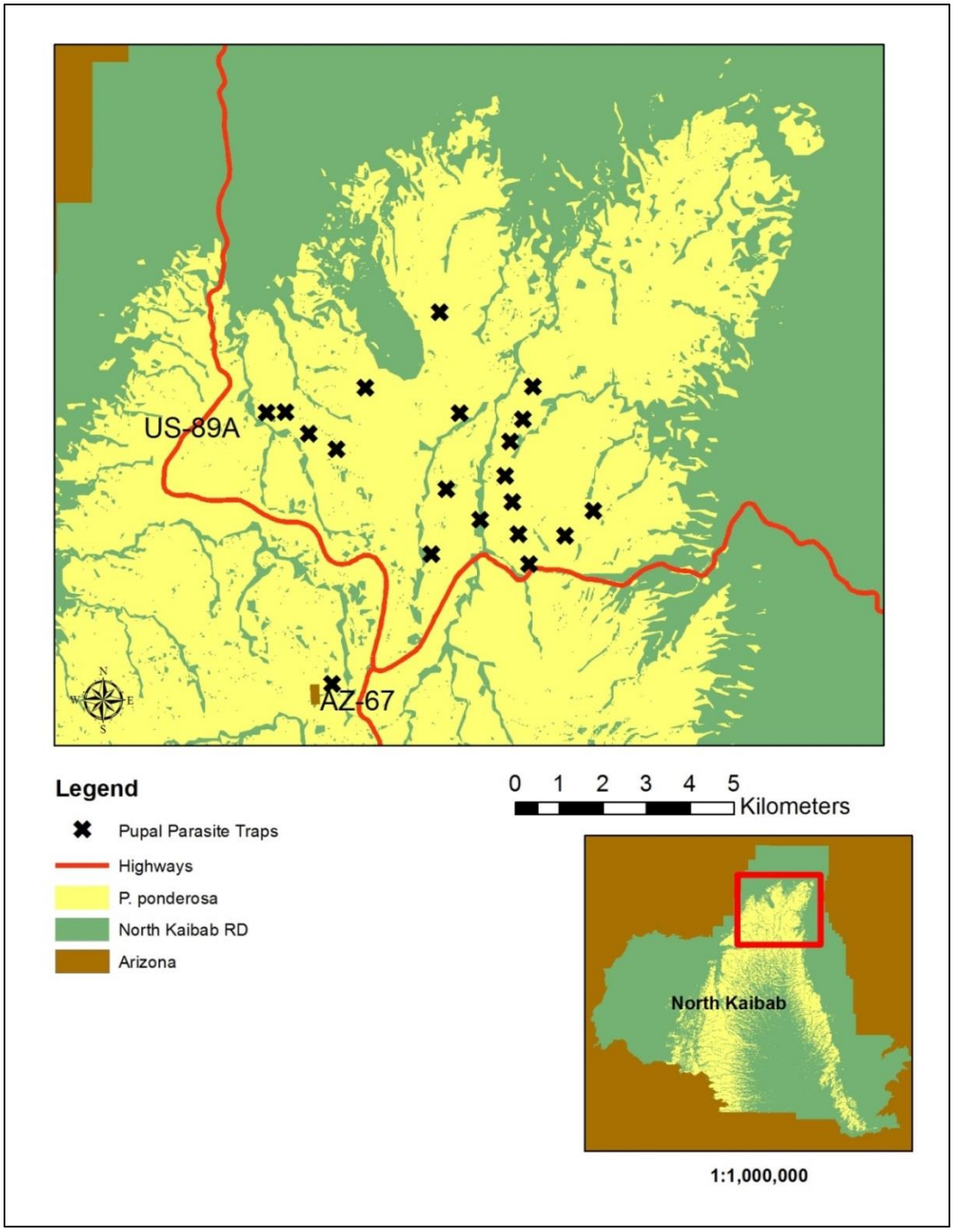



**Figure 2.6**. Pupal parasitoid trap locations on North Kaibab RD. One set of 200 pupae from 20 locations was collected in May and the remaining set of 200 pupae was collected in October 2011.

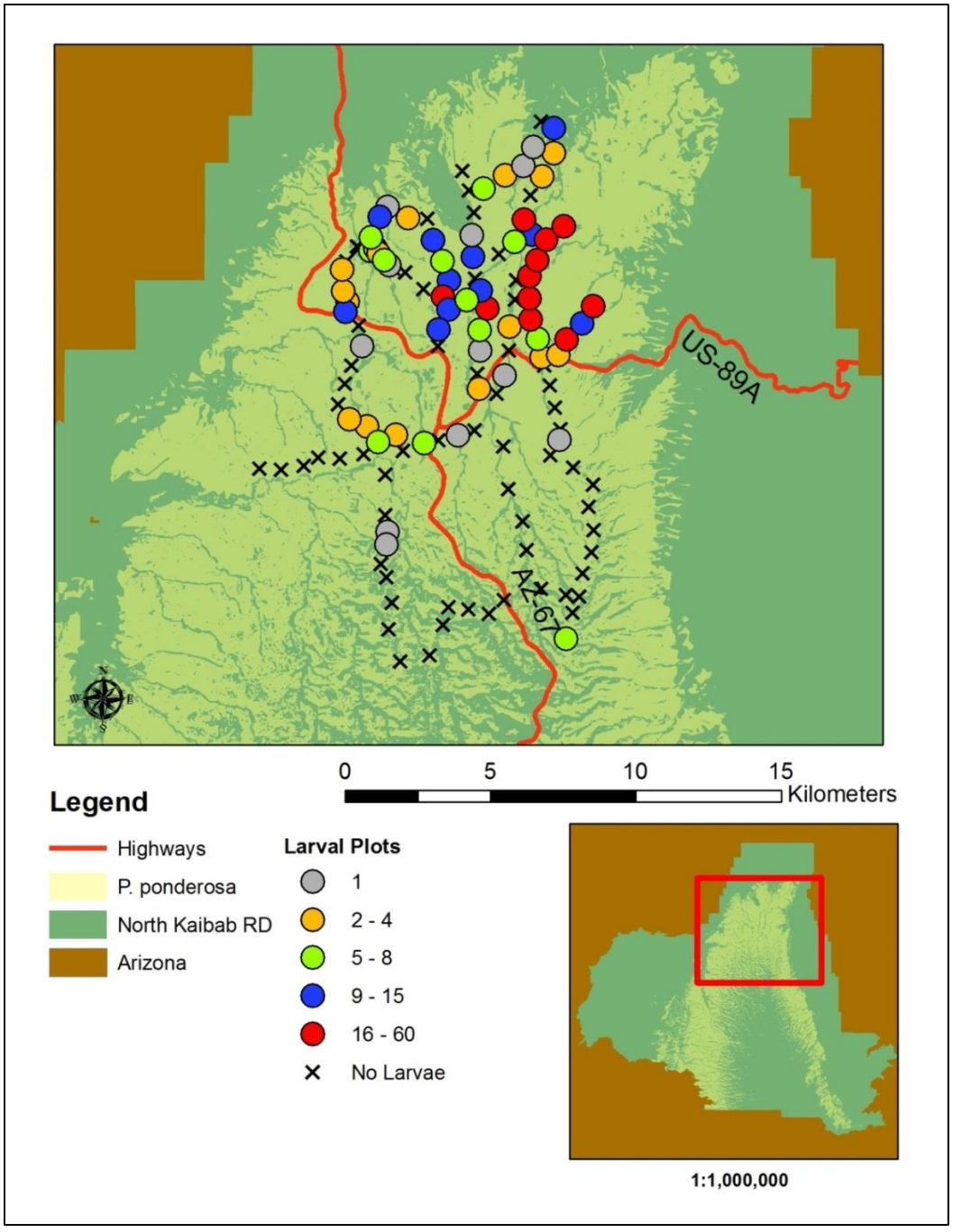



**Figure 2.7**. Pandora moth plots sampled on the North Kaibab RD in 2011 shown in relation to the maximum extent from 1979 - 1983 outbreak. Plot color depicts the quartile abundance of larvae collected per plot (20 trees).

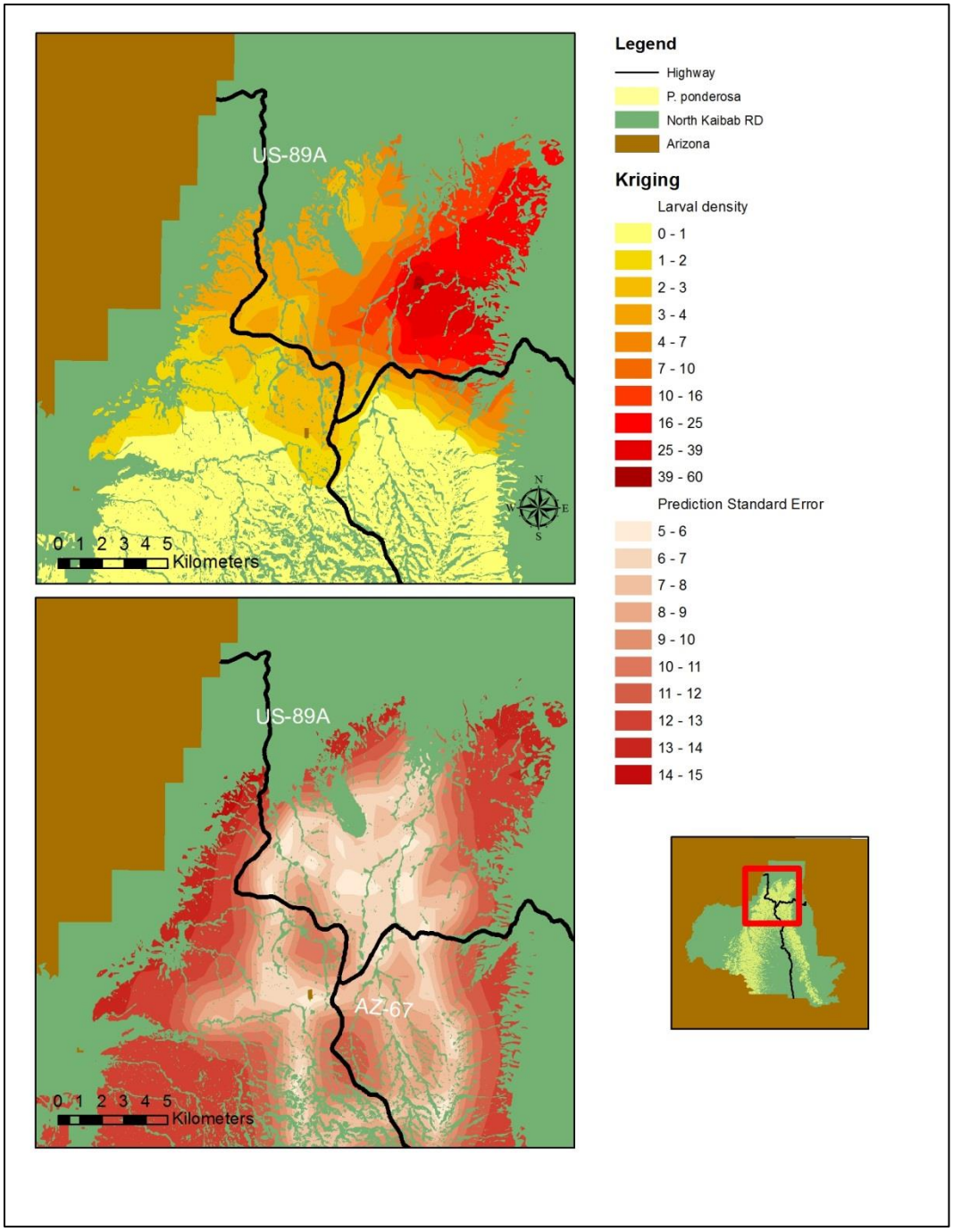
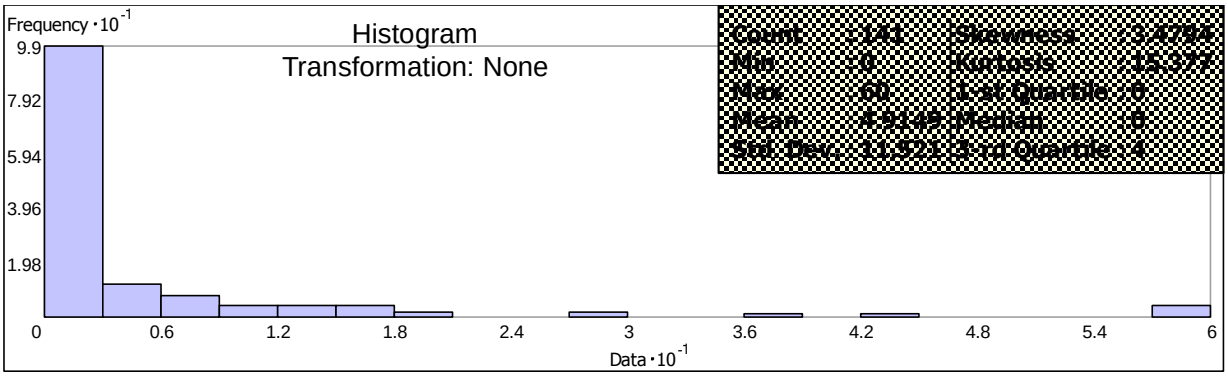
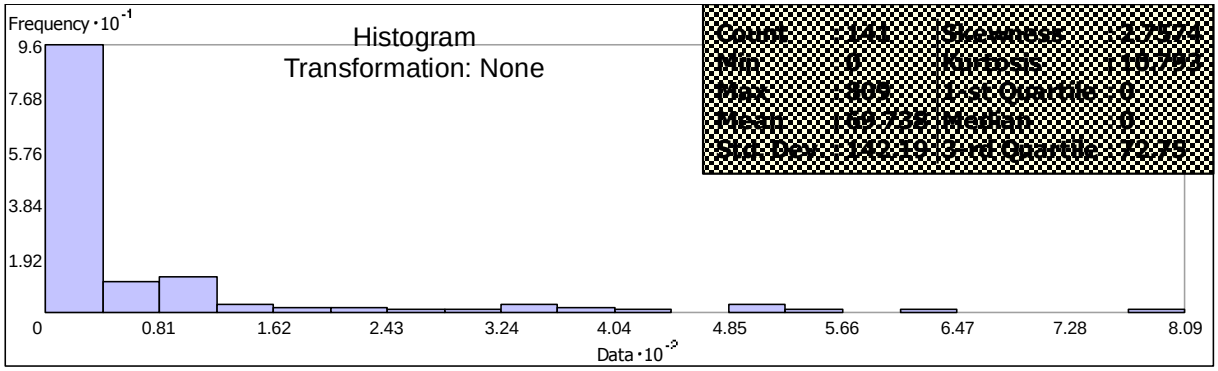



**Figure 2.8a.** Prediction surface and prediction standard error produced for 2011 North Kaibab RD pandora moth larval density distribution using ARCGIS 10.1 geostatistical analyst universal kriging (regression function (0.36 * x + 2.13)) using 143 of 143 larvae density data points.




1 Data Source: Larvae 2011 Attribute: Larva




2 Data Source: Larvae 2011 Attribute: Defoliated

3 **Figure 2.8b.** Frequency distribution of larval plot data relating to the number of larvae per plot

4 and number of needles eaten.

5

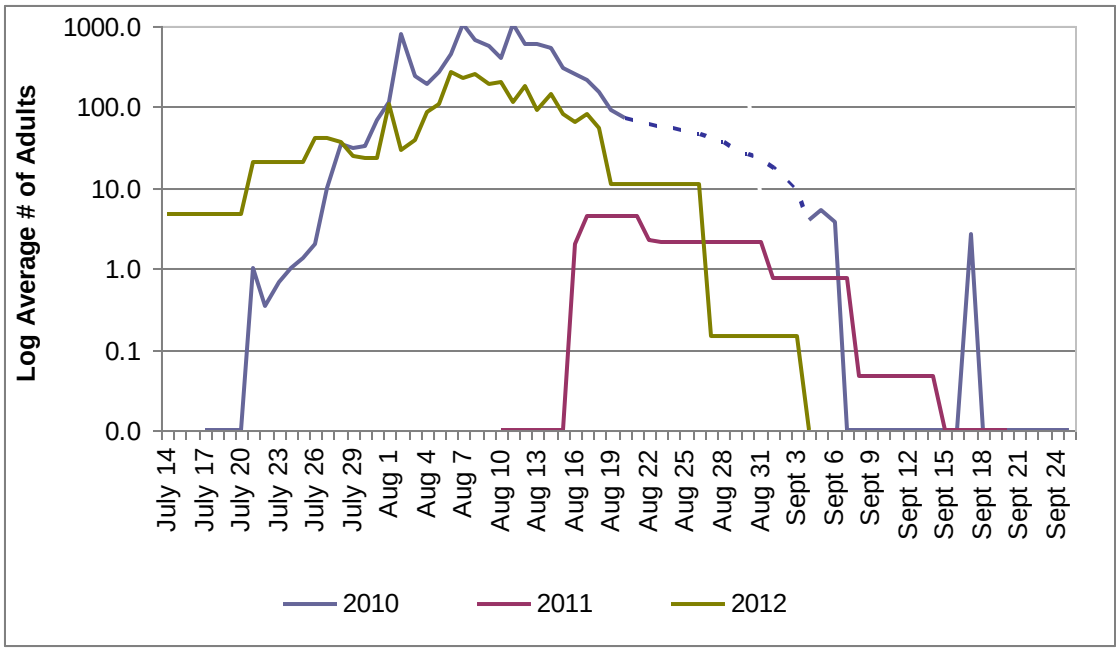



**Figure 2.9a.** Average daily population for 2010, 2011, and 2012. North Kaibab RD. A total of 24,254 moths were captured in 2010, 156 moths were captured in 2011, and 8,006 moths were captured in 2012. For each year, the first adult was captured on: 21 July 2010, 16 August 2011, and 14 July 2012.

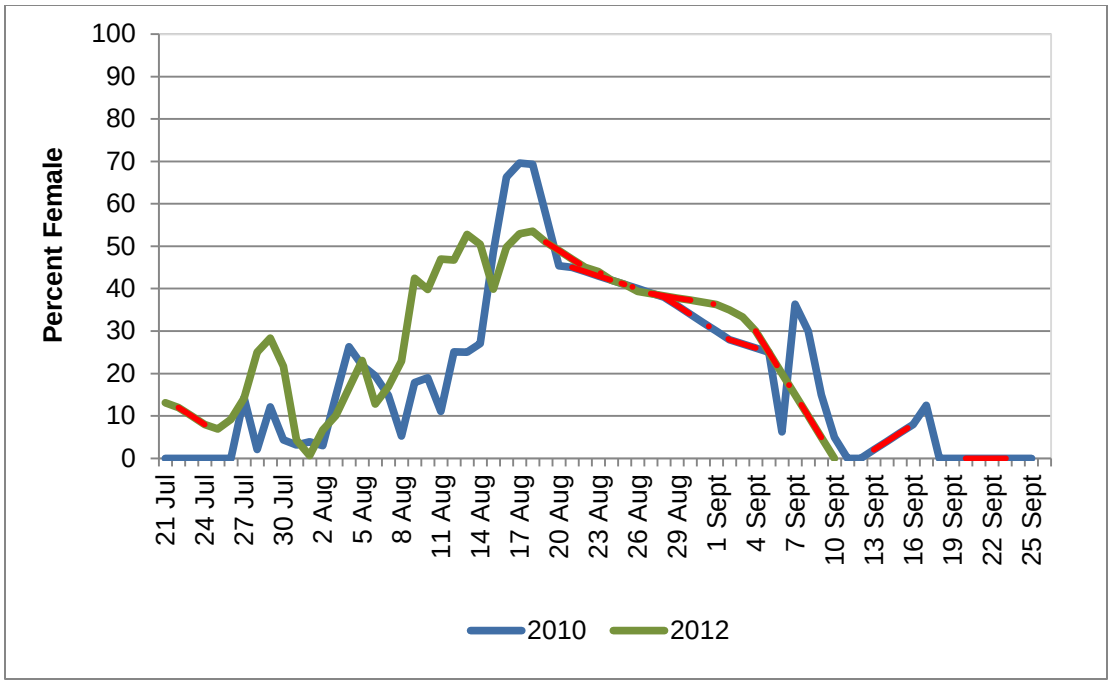



**Figure 2.9b**. The percentage of females in the 2010 and 2012 pandora moth populations captured in light traps in from the North Kaibab RD. Red dash lines are predicted values used to complete curves

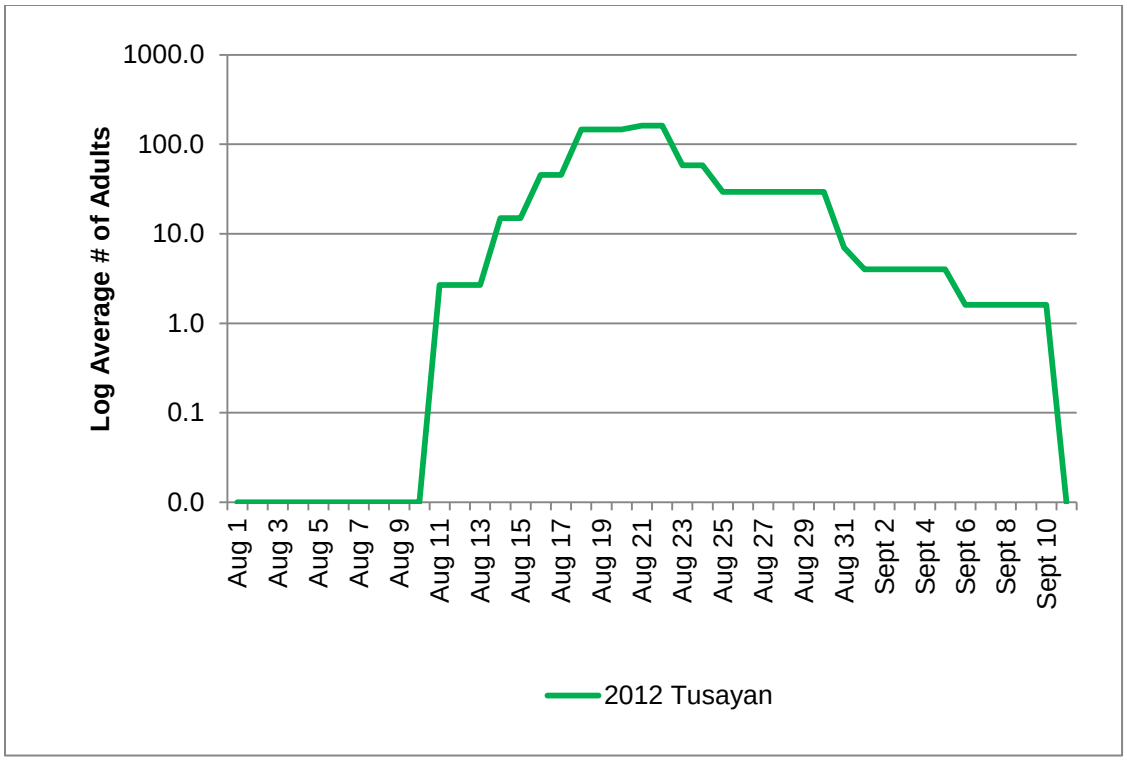



**Figure 2.10**. Average daily population for 2012, Tusayan Ranger District, Kaibab National Forest. A total of 1,218 moths were captured. The first adult was captured on 11 August 2012.

# Chapter III:

# Armillaria Root Disease in Northern Arizona

# Armillaria Root Disease in Northern Arizona

## Introduction

Armillaria root disease has been commonly associated with root decay and mortality of deciduous and coniferous trees and shrubs (Garraway et al. 1991) and has been reported to affect more than 600 species of woody plants (Morrison et al. 1991). This damaging root disease has been found in most forests of the world but it has been reported to be more common and abundant in temperate and boreal forests than in tropical regions (Kile et al. 1991). It has been reported to occur in nearly every state of the continental United States and also reported widely in Canada and Mexico (Williams et al. 1989). This economically important tree disease has been consistently associated with fungi in the genus *Armillaria* (Fr.:Fr) Staude, (Tricholomataceae), hence the common name.

The classification of the genus *Armillaria* has undergone a great deal of modification, but has now been reported to contain 40 species, ten of which have been documented in North America (Watling et al. 1991, Ross-Davis 2012, Volk 2013)(Table 3.1). Some species of *Armillaria* reportedly survive as saprophytes in woody substrates in soil or in standing dead material, while others have been demonstrated to be aggressive parasites of living trees. The parasitic species can kill living roots, eventually killing the infected tree, and then have been shown to continue living in dead material as saprophytes for several years (Kile et al. 1991). Species of *Armillaria* have been reported to spread by basidiospores, vegetatively by rhizomorphs, and via transfer from infected roots to healthy roots by contacts and/or graphs (Kile et al. 1991, Redfern and Filip 1991). Often trees infected with Armillaria root disease have

experienced stress to the extent that other agents, such as bark beetles, attack them and have caused the death of the tree. Therefore, it is common to observe mortality caused by a complex of factors in forests infested with this disease in northern Arizona (Wood 1983). Due to differences in pathogenicity and host preferences among the different species of *Armillaria* found in North America forest managers have required precise information on which species are present in different regions and when possible, information on the probability that Armillaria root disease has become established in different forest types and stands (McDonald et al. 1987, Kile et al. 1991).

The use of habitat types (Daubenmire 1952) has been demonstrated to be a useful forest vegetation classification system for predicting the environmental conditions in which Armillaria root disease may be consistently present or absent (Williams and Marsden 1982, McDonald et al. 1987, Byler et al. 1990, McDonald 1990). Habitat types have been shown to be particularly useful in predicting the presence or absence of *Armillaria* in the Northern Rocky Mountains (McDonald et al. 1987). The overall climatic conditions influencing forest habitat types were correlated with predicting the occurrence of *Armillaria*. In the Northern Rocky Mountains, habitat types characterized as cold-dry or hot-dry environments were found to be outside the ecological range of *Armillaria* and excessively cold or moist sites may also limit the growth and development of *Armillaria* and hence have little of the fungus present (McDonald et al. 1987). In the Southwest, where many of the forests are characterized by dry-hot or warm-dry climatic conditions, Armillaria root disease has historically been considered as a disease of little importance (Wood 1983). As a consequence of this perspective, few studies have been

conducted to examine the distribution of Armillaria root disease in northern Arizona or identify the species of *Armillaria* present using the currently recognized classification of the genus.

Historically, Armillaria root disease was thought to be caused by *Armillaria mellea* (Vahl:Fr.) Kummer and this nomenclature was applied to the disease in the southwestern United States (Wood 1983). Although Wood (1983) applied the concept of using *Armillariella* in place of *Armillaria*, the use of the previous genus was invalidated by Watling et al. (1982) and is no longer used as an obligate synonym for *Armillaria* (Volk 2013). Under the current classification system for *Armillaria*, *A. mellea* has been considered a week pathogen whose distribution is confined to the eastern and mid-western United States and although it has evidently been found in California, *A. mellea* has not been reported from other areas of the West (Volk 2013). The species of *Armillaria* associated with a root disease of conifers throughout the western United States has now been designated as *A. ostoyae* (Romagnes) Herink, but the appropriateness of this nomenclature for the species of *Armillaria* in the Southwest has not been confirmed (Watling et al. 1991, Volk 2013). Therefore, the identification of which species of *Armillaria* occur in Arizona using modern molecular techniques has been needed as well as additional information on the distribution and abundance of the disease and which hosts were commonly infected.

Today it is possible to identify species of *Armillaria* using DNA sequencing techniques (Kim et al. 2006, Ross-Davis et al. 2012). Kim et al. (2006) examined rDNA sequences for three regions and used amplified fragment length polymorphisms (AFLPs) to assess the phylogenetic relationships of several species of *Armillaria*. They concluded that ribosomal DNA intergenic spacer sequences (IGS-1) and AFLP genetic markers could be used to potentially distinguish between the North American species of *Armillaria*. In addition, the phylogenetic relationships

among 15 globally diverse *Armillaria* species and eight Japanese species were examined and separated using partial sequences of the translation elongation factor-1 alpha (EF-1α) gene (Maphosa et al. 2006, Hasegawa et al. 2010). DNA based identification of *Armillaria* has also been used in North America and can now confidently differentiate species (Ross-Davis et al. 2012). Five clades have been identified using the EF-1α gene which clearly separated the North American species of *Armillaria*. Therefore, current molecular methods have been shown to be effective at correctly identifying nearly all of the species of *Armillaria* (Ross-Davis et al. 2012).

Because little information was available on the species of *Armillaria* that occur in northern Arizona, the hosts affected, or the distribution of the disease by forest type or habitat type, this study was initiated in 2011 in cooperation with the Rocky Mountain Research Station (RMRS) and the Interior West Forest Inventory and Analysis program (IW-FIA), USDA Forest Service. Permanent plots established by IW-FIA on the Kaibab and Coconino National Forests, Arizona were used as sampling points. Plots representing 16 habitat types on three Ranger Districts were sampled and dead trees or living trees with root disease symptoms near each plot were examined for the presence of *Armillaria*. Samples of *Armillaria* were collected when observed and sent to the RMRS Forestry Sciences Laboratory in Moscow, ID for positive identification using DNA sequencing technology. Here I report my results which support previous reports that Armillaria root disease is not common in northern Arizona and that the disease is probably associated with only one species of *Armillaria*.

## Methods

This study used permanent plots established by the Interior West Forest Inventory and Analysis program on the Kaibab and Coconino National Forests in northern Arizona. Plots on the North Kaibab, Williams, and Flagstaff Ranger Districts were selected based on ownership, accessibility, and habitat type (Figure 3.1). A total of 73 plots were sampled that represented 16 forest habitat types (Table 3.2). Rather than splitting habitat types into phases, plots representing a phase were grouped under each major habitat type sampled. Plots were located using FIA data and visited during the summer of 2011 and 2012.

Interior West Forest Inventory and Analysis (FIA) sampling units consisted of four circular subplots (radius 7.3 m, 0.02 ha) (USDA Forest Service 2011). Each unit has a central subplot with three additional subplots established 36.6 m from its center at azimuths of 360°, 240°, and 120°. Each sampling unit was classified by elevation, aspect, forest type, soil type, and habitat type. Standard forest inventory data collected from the four subplots included trees species, diameter breast height (dbh, 1.8 m above the ground), a subsample of heights, and information on downed-woody material. In order to avoid sampling within the IW-FIA subplots I established a supplemental 0.04 ha plot 36.6 m at an azimuth of 300° from the center of the central IW-FIA subplot.

In each supplemental subplot I examined one live or dead tree of each species present for the presence of *Armillaria* by the following dbh classes: < 20, 20 – 40, and > 40 cm when possible. Recently dead trees or live trees with symptoms of root disease were given priority for sampling over live trees with no root disease symptoms. Only the species and diameter (dbh, nearest cm) of trees sampled for the presence of *Armillaria* were recorded for each supplemental

plot. Examination of trees for the presence of *Armillaria* was conducted by excavating at least one main root to a radial distance of 0.8 m from the bole. When fans were present on roots, samples were collected by carefully removing a section of the infected root so the integrity of the bark remained intact. If resinosis or other symptoms of infection were present on the main bole, the root collar was also examined for mycelial fans under the bark. When mycelia fans were detected above the roots near the base of an infected trees, bark with fans attached to it were carefully removed. The size of sampled root sections or bark varied depending on the size of the infected root or bole. Up to three samples were collected from an infected tree. Each *Armillaria* sample was placed in a paper bag and all the bags collected for a tree were placed in a Ziploc bag and kept in a cooler while in the field and then refrigerated. Within two weeks samples were mailed overnight on ice to the RMRS Forestry Sciences Laboratory, Moscow, ID. Upon arrival samples were cultured on 3% malt-agar and incubated at $22^{o}$ C in the dark. Template DNA was collected from scrapings of actively growing mycelia from 1-2 week old cultures. Extracted DNA samples were used for sequencing of the ribosomal DNA intergenic spacer (IGS-1) regions (Kim et al. 2006) and/or the EF-1α gene (Ross-Davis et al. 2012) to positively identify which species of *Armillaria* each sample represented. DNA sequences yielded definitive identifications for all samples of *Armillaria* sent to the Forestry Sciences Laboratory.

**Results**

A total of 73 plots were inspected for Armillaria root disease representing 16 habitat types (Table 3.2); root disease was found in five of the habitat types sampled. It was most often found in habitat types that represented warm-dry climatic conditions of the subalpine or mixed

conifer forest types; the ABLA/JUCO, ABCO/MARE, and PSME/QUGA habitat types (Table 3.3). Armillaria root disease was also detected in one habitat type that represented cold-wet climatic conditions of the mixed conifer forest type; the PIEN/CAFO habitat type. Although 14 plots were sampled that represented three additional subalpine (PIEN/ACGL, PIEN/EREX, and ABLA/LAAR) and three mixed conifer forest habitat types (PIPU/EREX, ABCO/FEAR, and ABCO/CAFO), *Armillaria* was not detected in any of them. Armillaria root disease was only found in one ponderosa pine habitat type (PIPO/FEAR), and although 18 plots were sampled for this habitat type, the disease was only found in two plots; one each on the Kaibab and Coconino National Forests (Table 3.4). Although 25 plots representing three other ponderosa pine habitat types (PIPO/BOGR, PIPO/MUMO, and PIPO/QUGA) were sampled, *Armillaria* was not detected.

A total of 325 conifers and 62 quaking aspen (*Populus tremuloides* Michenaux) were sampled in the 70 plots that were examined for Armillaria root disease (Table 3.4). Of these, only 18 conifers (5%) and five aspen (8%) had evidence of *Armillaria* (mycelia fans) on their roots or main boles that were detected by the sampling method used. No rhizomorphs were detected on any of the trees examined. *Armillaria* was detected primarily on recently dead trees; 19 of the 23 trees (83%). The two most commonly sampled trees were ponderosa pine (*Pinus ponderosa* Douglas ex Larson & C. Larson) (180 trees) and aspen which also had the most trees detected with *Armillaria*; eight ponderosa pines (4%) and five aspen (8%). Four other conifers that were sampled in the subalpine and mixed conifer habitat types were Douglas-fir (*Pseudotsuga menziesii* (Mirbel) Franco) (44 trees), white fir (*Abies concolor* Gordon & Glendinning Hilldebrand) (43 trees), Engelmann spruce (*Picea engelmannii* Parry ex

Engelmann) (27 trees), and blue spruce (*Picea pungens* Engelmann) (20 trees). *Armillaria* was also detected on these trees and the incidence of infection was again very low: Douglas-fir (7%), white fir (5%), Engelmann spruce (11%), and blue spruce (10%). Only a few trees of the following species were examined for *Armillaria* within the sample plots and the disease was not detected: Gambel oak (*Quercus gambelii* Nuttall), Utah juniper (*Juniperus osteosperma* (Torrey) Little), Colorado pinyon pine (*Pinus edulis* Engelmann in Wislizenus), New Mexican locust (*Robinia neomexicana* Gray), and subalpine fir (*Abies lasiocarpa* (Hooker) Nuttall).

*Armillaria* was found on 18% and 9% of the plots sampled on the Kaibab and Flagstaff Ranger Districts, respectively. However, it was not detected on any of the 12 plots sampled on the Williams Ranger District of the Kaibab National Forest. All 12 plots were in ponderosa pine habitat types and only 35 ponderosa pines and three Douglas-firs were sampled on the Williams District.

The distribution of the 411 trees examined for Armillaria root disease by diameter classes was: < 20 cm – 234 trees; 20 – 40 cm – 111 trees; > 40 cm – 66 trees. Of the 23 trees in which the disease was detected, 11 were in the < 20 cm class, 10 were in the 20-40 cm class, and 2 were in the > 40 cm class. The distribution of infected trees indicates 5% small, 9% medium, and 3% large trees were affected by Armillaria root disease. The distribution of *Armillaria* infection across species by size class is provided in Figure 3.2.

A total of 34 samples were collected from the 23 trees detected with Armillaria root disease. DNA extracted from isolates of each of the samples was sequenced at the Forestry Sciences Laboratory and were positively identified using rDNA IGS-1 sequences or the EF-1α

gene as *A. ostoyae*. No isolates yielded DNA sequences for the IGS-1 region or the EF-1α gene that could have represented another species of *Armillaria*.

**Discussion**

My results indicated that the only species of *Armillaria* distributed in northern Arizona is probably *A. ostoyae*. Although some investigators classify the fungus associated with the root disease of conifers in the West as *A. solidipes* Peck, Hunt et al. (2011) believe *A. solidipes* is an ambiguous species which is probably not conspecific with *A. ostoyae* and as a result have argued that *A. ostoyae* be conserved over *A. solidipes*. This has now been formally proposed by Redhead et al. (2011) and may be adopted. Therefore, I have used *A. ostoyae* as the fungus associated with Armillaria root disease in northern Arizona. Other species of *Armillaria* that could still be reported in Arizona include *A. mellea* and *A. sinapina* Bérubé & Dessureault (Table 3.1). However, it is improbable that these taxa occur in northern Arizona based on my results, but further sampling of the fungi associated with *Armillaria* root disease may discover one or both of those species are present elsewhere in the state. *Armillaria ostoyae* has been reported to be a ubiquitous fungus found in a wide variety of forest types and it is often "triggered" by management practices that stress trees (McDonald 2011). The expression of *Armillaria* root disease has been frequently correlated with moisture and temperature gradients in addition to species composition of infested stands (McDonald et al. 1987, McDonald 2011). Because forests in the Southwest have been intensively managed for at least 100 years, *Armillaria* root disease has probably increased across the landscape, but the historical levels of the disease that existed before European settlement are unknown.

*Armillaria ostoyae* has been shown to be highly pathogenic on conifers throughout the western United States, but I also found it infecting aspen in subalpine forests on the North Kaibab Plateau and in mixed conifer forests on the San Francisco Peaks. Because I primarily found *Armillaria* root disease on recently dead conifers and aspen, it was probably associated with mortality of the infected trees, but insects that attack weakened trees (particularly bark beetles) may have also contributed to their death (Wood 1983). In addition, mortality of ponderosa pine in northern Arizona has been shown to sometimes involve a complex of *Armillaria* root disease and Annosus root diseased caused by *Heterobasidion irregulare* Garbelotto and Ostrosina (Wood 1983). Annosus root disease associated with *H. occidentale* Ostrosina and Garbelotto may also contribute to the death of other conifers in the Southwest, particularly true firs. However, I did not examine the *Armillaria*-infected trees I sampled for the presence of insect activity or other root diseases. *Armillaria ostoyae* is generally pathogenic, but can exist in a nonpathogenic state in some forests (Klopfenstein et al. 2012), however, since I primarily found it associated with dead trees, the *Armillaria* populations I sampled in northern Arizona are probably pathogens, but this needs to be confirmed.

In comparison to the northern Rocky Mountains, northern Arizona has very little *Armillaria*. McDonald et al. (1987) reported they found *Armillaria* rhizomorphs associated with over 30% of each tree species they sampled in Washington, Idaho, and Montana. In northern Arizona, it appears the distribution of *Armillaria* is limited to warm-dry climatic conditions and possibly also the cold-wet conditions where blue spruce is distributed. Additionally, when compared to forests of the northern Rockies that have high levels of infection, northern Arizona forests had relatively low incidences of Armillaria root disease. Wood (1983) also found a

relatively low incidence of Armillaria root disease in Arizona. The highest incidence of the disease he reported for Arizona was for mixed conifer/spruce-fir forests on the Apache-Sitgreaves National Forest where 24 percent of the dead trees he examined were infected with *Armillaria*.

Wood (1983) only reported that one, seven, and twelve percent of the dead ponderosa pines he examined on the Kaibab, Apache-Sitgreaves, and Coconino National Forests, respectively, had Armillaria root disease. In New Mexico, he only found Armillaria root disease on eight percent of the dead ponderosa pines he sampled on the Carson and Santa Fe National Forests. My results also demonstrated that there is a relatively low incidence of Armillaria root disease on ponderosa pine in northern Arizona. This was particularly evident in the ponderosa pine habitat types sampled where *Armillaria ostoyae* was only found on three pines in the PIPO/FEAR habitat type. Two of the pines were on the Coconino National Forest and the other one was on the Kaibab National Forest. Most of the infected ponderosa pines (62%) I observed were in mixed conifer forests. McDonald et al. (1987) hypothesized that *Armillaria* was probably completely absent from the ponderosa pine and limber pine (*Pinus flexilis* James) habitat types in the northern Rocky Mountains. My results indicated that Armillaria root disease may also be absent from or at least rare in other ponderosa pine habitat types in northern Arizona, but additional sampling is needed in these habitat types because my sample sizes were not large enough for reaching a more definitive conclusion.

Wood (1983) reported that 38% of the dead trees he examined in the subalpine forests and 15% of the dead trees in the mixed conifer forests of New Mexico were infected with Armillaria root disease. Although I did not sample a large number of habitat types (4) or plots

(10) in the subalpine forests of northern Arizona, the incidence of *Armillaria* in one of the habitat types (ABLA/JUCO) was the highest (16% of the trees examined) that I found for any of the habitat types I sampled. I also found Armillaria root disease in four mixed conifer forest habitat types. This suggests that additional sampling should be completed in the subalpine and mixed conifer forests of northern Arizona, particularly on the Kaibab Plateau where Armillaria root disease has been observed to be more common in those forest types than in the ponderosa pine type (Wood 1983). In addition, I found that 11% of the Engelmann spruce I examined was infected with Armillaria root disease, which was the highest incidence of infection for a tree species sampled. Therefore, it would be worthwhile to sample additional habitat types dominated by Engelmann spruce, and possibly blue spruce, to better determine the incidence of Armillaria root disease in subalpine and mixed conifer forests elsewhere in Arizona. My results and those reported by Wood (1983) and McDonald et al. (1987) have all indicated that Armillaria root disease is evidently more prevalent in mixed conifer and subalpine forests than it is in the ponderosa pine type and this relationship should be investigated in other regions of the West also.

This study was part of a larger collaborative project involving the USDA Forest Service, Forest Science Laboratory, Moscow, ID, USDA Forest Health Protection, Flagstaff, AZ, and the School of Forestry, Northern Arizona University, Flagstaff, AZ. The objectives of this project have been described as: 1) determine the climatic conditions where *Armillaria ostoyae* occurs in Arizona; 2) predict what forest types are at risk to Armillaria root disease; 3) develop habitat-specific management recommendations to mitigate the impacts of Armillaria root disease; and 4) develop a bioclimatic model with new information that can predict potential changes in the

distribution and activity of *A. ostoyae* (Klopfenstien et al. 2012). Although my part of the larger project is completed, other investigators with the USDA Forest Service and School of Forestry have been continuing investigations on the distribution of Armillaria root disease in Arizona. Their results will continually be incorporated into a data base describing the climatic habitat types where *A. ostoyae* has been reported to occur in Arizona and this will eventually be used in the development of management recommendations and predictions of how the distribution and risks for Armillaria root disease may be different under possible scenarios associated with future climate change in Arizona.

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**Table 3.1.** Species of *Armillaria* found in North America (Volk 2013).

| Species | Distribution |
|---|---|
| *Armillaria ostoyae* (Romagn. ) Herink | Northern conifer zone, occasionally on hardwoods. |
| *Armillaria gemina* Bérubé& Dessureault | Northeastern US, eastern Canada. |
| *Armillaria calvescens* Bérubé & Dessureault | Eastern Canada to MI and WI |
| *Armillaria sinapina* Bérubé& Dessureault | Northern conifer zone, but typically on hardwoods in the East and conifers in the West. |
| *Armillaria mellea* (Vahl:Fr) Kummer | Hardwood zone, mostly southeastern USA north to IA and WI and west to OK and TX. Eastern distribution from FL to the Appalachians to Québec. Known from CA, but not other areas of the West. |
| *Armillaria gallica* Marxműller & Romagn. | Hardwoods in South, Northeast, and Midwest; rare in Pacific Northwest. |
| *Armillaria nabsnona* Volk & Burdsall | ID, WA, OR, AK, and British Columbia |
| *Armillaria cepistipes* Velenovsky | WA and British Columbia |
| *Armillaria tabescens* (Scop. ) Emel | Southeastern USA into the Northeast, west to OH, also further west and north on shores of Great Lakes. |
| North America Biological Species X | ID and British Columbia |

**Table 3.2.** Number of plots sampled by habitat type on the Flagstaff Ranger District, Coconino National Forest and the North Kaibab and Williams Ranger Districts, Kaibab National Forest.

| Ranger District | Habitat Type | No. plots |
|---|---|---|
| **Flagstaff** | Douglas-fir/Arizona fescue (PSME/FEAR) | 1 |
| | Douglas-fir/creeping barberry (PSME/MARE11) | 1 |
| | Douglas-fir/Gambel oak (PSME/QUGA) | 1 |
| | ponderosa pine/Arizona fescue (PIPO/FEAR) | 6 |
| | ponderosa pine/blue grama (PIPO/BOGR2) | 7 |
| | ponderosa pine/mountain muhly (PIPO/MUMO) | 5 |
| | subalpine fir/Nevada pea (ABLA/LALAL3) | 1 |
| | white fir/creeping barberry (ABCO/MARE11) | 1 |
| **North Kaibab** | blue spruce/dryspike sedge (PIPU/CAFO3) | 4 |
| | blue spruce/sprucefir fleabane (PIPU/EREX4) | 1 |
| | Douglas-fir/Arizona fescue (PSME/FEAR) | 1 |
| | Douglas-fir/Gambel oak (PSME/QUGA) | 1 |
| | Engelmann spruce/Rocky Mountain maple (PIEN/ACGL) | 1 |
| | Engelmann spruce/sprucefir fleabane (PIEN/EREX4) | 3 |
| | ponderosa pine/Arizona fescue (PIPO/FEAR) | 4 |
| | ponderosa pine/blue grama (PIPO/BOGR2) | 2 |
| | ponderosa pine/Gambel oak (PIPO/QUGA) | 4 |
| | ponderosa pine/mountain muhly (PIPO/MUMO) | 3 |
| | subalpine fir/common juniper (ABLA/JUCO6) | 5 |
| | white fir/Arizona fescue (ABCO/FEAR) | 2 |
| | white fir/creeping barberry (ABCO/MARE11) | 4 |
| | white fir/dryspike sedge (ABCO/CAFO3) | 3 |
| **Williams** | ponderosa pine/Arizona fescue (PIPO/FEAR) | 8 |
| | ponderosa pine/blue grama (PIPO/BOGR2) | 2 |
| | ponderosa pine/mountain muhly (PIPO/MUMO) | 2 |

**Table 3.3.** Composition of plots by climate characterization associated with each habitat type as well as the proportion of plots identified as containing Armillaria infection.

| Climate Characterization | Habitat Type | No. Plots | No. Plots with *Armillaria* | % Plots with *Armillaria* |
|---|---|---|---|---|
| cold wet | Engelmann spruce/Rocky Mountain maple | 1 | 0 | 0 |
| | white fir/dryspike sedge | 3 | 0 | 0 |
| cool wet to warm dry | ponderosa pine/Gambel oak | 4 | 0 | 0 |
| typical, warm dry | blue spruce/sprucefir fleabane | 1 | 0 | 0 |
| typical | subalpine fir/Nevada pea | 1 | 0 | 0 |
| typical warm dry | blue spruce/dryspike sedge | 4 | 2 | 50 |
| | Engelmann spruce/spruce-fir fleabane | 3 | 0 | 0 |
| | ponderosa pine/Arizona fescue | 18 | 2 | 11 |
| | white fir/Arizona fescue | 2 | 0 | 0 |
| | white fir/creeping barberry | 5 | 2 | 40 |
| warm dry | Douglas-fir/Arizona fescue | 2 | 0 | 0 |
| | Douglas-fir/creeping barberry | 1 | 0 | 0 |
| | Douglas-fir/Gambel oak | 2 | 1 | 50 |
| | ponderosa pine/blue grama | 11 | 0 | 0 |
| | ponderosa pine/mountain muhly | 10 | 0 | 0 |
| | subalpine fir/common juniper | 5 | 1 | 20 |
| | Total | 73 | 8 | 11 |

**Table 3.4a.** The number of trees sampled, number of trees found with Armillaria root disease, and the number of *Armillaria* samples collected by habitat type on Flagstaff Ranger District, Coconino National Forest[1]

| Ranger District | Habitat Type | Tree Species | No. Trees | No. trees with Armillaria | No. Armillaria samples |
|---|---|---|---|---|---|
| Flagstaff | Douglas-fir/Arizona fescue | | | | |
| | | Pifl | 1 | | |
| | | Potr | 3 | | |
| | | Psme | 3 | | |
| | Douglas-fir/creeping barberry | | | | |
| | | Pipo | 3 | | |
| | | Psme | 3 | | |
| | Douglas-fir/Gambel oak | | | | |
| | | Pipo | 3 | 1 | 1 |
| | | Potr | 3 | 3 | 4 |
| | | Psme | 2 | | |
| | ponderosa pine/Arizona fescue | | | | |
| | | Pipo | 15 | 2 | 3 |
| | ponderosa pine/blue grama | | | | |
| | | Pipo | 21 | | |
| | ponderosa pine/mountain muhly | | | | |
| | | Pipo | 15 | | |
| | subalpine fir/Nevada pea | | | | |
| | | Abla | 1 | | |
| | | Pist | 3 | | |
| | | Potr | 3 | | |
| | | Psme | 3 | | |
| | white fir/creeping barberry | | | | |
| | | Pipo | 2 | | |
| | | Pipu | 3 | | |

[1] Abla - *Abies lasiocarpa*; Abco - *Abies concolor*; Pien - *Picea engelmannii*; Pipu – *Picea pungens*; Psme – *Pseudotsuga menziesii*; Potr - *Populus tremuloides*; Pist - *Pinus strobiformis*; Pifl - *Pinus flexilis*; Pipo - *Pinus ponderosa*; Quga - *Quercus gambelii*; Rone - *Robinia neomexicana*; Juut - *Juniperus utahensis*; Pied - *Pinus edulis*

**Table 3.4b.** The number of trees sampled, number of trees found with Armillaria root disease, and the number of *Armillaria* samples collected by habitat type on South Kaibab Ranger District, Kaibab National Forest [1]

| Ranger District | Habitat Type | Tree Species | No. Trees | No. trees with Armillaria | No. Armillaria samples |
|---|---|---|---|---|---|
| South Kaibab | ponderosa pine/Arizona fescue | | | | |
| | | Pipo | 17 | | |
| | ponderosa pine/blue grama | | | | |
| | | Pipo | 6 | | |
| | ponderosa pine/mountain muhly | | | | |
| | | Pipo | 6 | | |

**Table 3.4c.** The number of trees sampled, number of trees found with Armillaria root disease, and the number of *Armillaria* samples collected by habitat type on North Kaibab Ranger District, Kaibab National Forest [1]

| Ranger District | Habitat Type | Tree Species | No. Trees | No. trees with Armillaria | No. Armillaria samples |
|---|---|---|---|---|---|
| North Kaibab | blue spruce/dryspike sedge | | | | |
| | | Abco | 3 | | |
| | | pien | 3 | 1 | 2 |
| | | Pipo | 7 | 2 | 2 |
| | | Pipu | 3 | 1 | 1 |
| | | Potr | 6 | | |
| | blue spruce/sprucefir fleabane/ponderosa pine | | | | |
| | | Abco | 1 | | |
| | | Pien | 3 | | |
| | | Pipo | 2 | | |
| | | Potr | 3 | | |
| | Douglas-fir/Arizona fescue | | | | |
| | | Pipo | 3 | | |
| | Douglas-fir/Gambel oak | | | | |
| | | Ouga | 3 | | |
| | | Rone | 3 | | |
| | Engelmann spruce/Rocky Mountain maple | | | | |
| | | Abco | 3 | | |
| | | Pipo | 3 | | |
| | | Pipu | 3 | | |
| | | Potr | 3 | | |
| | | Psme | 3 | | |
| | Engelmann spruce/sprucefir fleabane | | | | |
| | | Abco | 8 | | |
| | | Pien | 6 | | |
| | | Pipo | 4 | | |
| | | Pipu | 6 | | |
| | | Potr | 9 | | |
| | | Psme | 7 | | |
| | ponderosa pine/Arizona fescue | | | | |
| | | Pipo | 12 | 1 | 1 |
| | | Potr | 3 | | |

**Table 3.4c.** Cont.

| Ranger District | Habitat Type | Tree Species | No. Trees | No. trees with Armillaria | No. Armillaria samples |
|---|---|---|---|---|---|
| North Kaibab | ponderosa pine/blue grama | | | | |
| | | Pipo | 6 | | |
| | ponderosa pine/Gambel oak | | | | |
| | | Juut | 6 | | |
| | | Pied | 6 | | |
| | | Pipo | 9 | | |
| | | Quga | 8 | | |
| | | Rone | 3 | | |
| | ponderosa pine/mountain muhly | | | | |
| | | Juut | 1 | | |
| | | Pipo | 9 | | |
| | subalpine fir/common juniper | | | | |
| | | Abco | 7 | | |
| | | Pien | 12 | 2 | 3 |
| | | Pipo | 11 | 1 | 1 |
| | | Potr | 14 | 2 | 3 |
| | | Psme | 10 | 2 | 2 |
| | white fir/Arizona fescue | | | | |
| | | Abco | 6 | | |
| | | Pipo | 6 | | |
| | | Psme | 1 | | |
| | white fir/creeping barberry | | | | |
| | | Abco | 6 | 2 | 2 |
| | | Pipo | 11 | 1 | 2 |
| | | Pipu | 2 | 1 | 1 |
| | | Potr | 9 | | |
| | | Psme | 9 | 1 | 1 |
| | white fir/dryspike sedge | | | | |
| | | Abco | 9 | | |
| | | Pien | 3 | | |
| | | Pipo | 9 | | |
| | | Pipu | 3 | | |
| | | Potr | 6 | | |
| | | Psme | 3 | | |

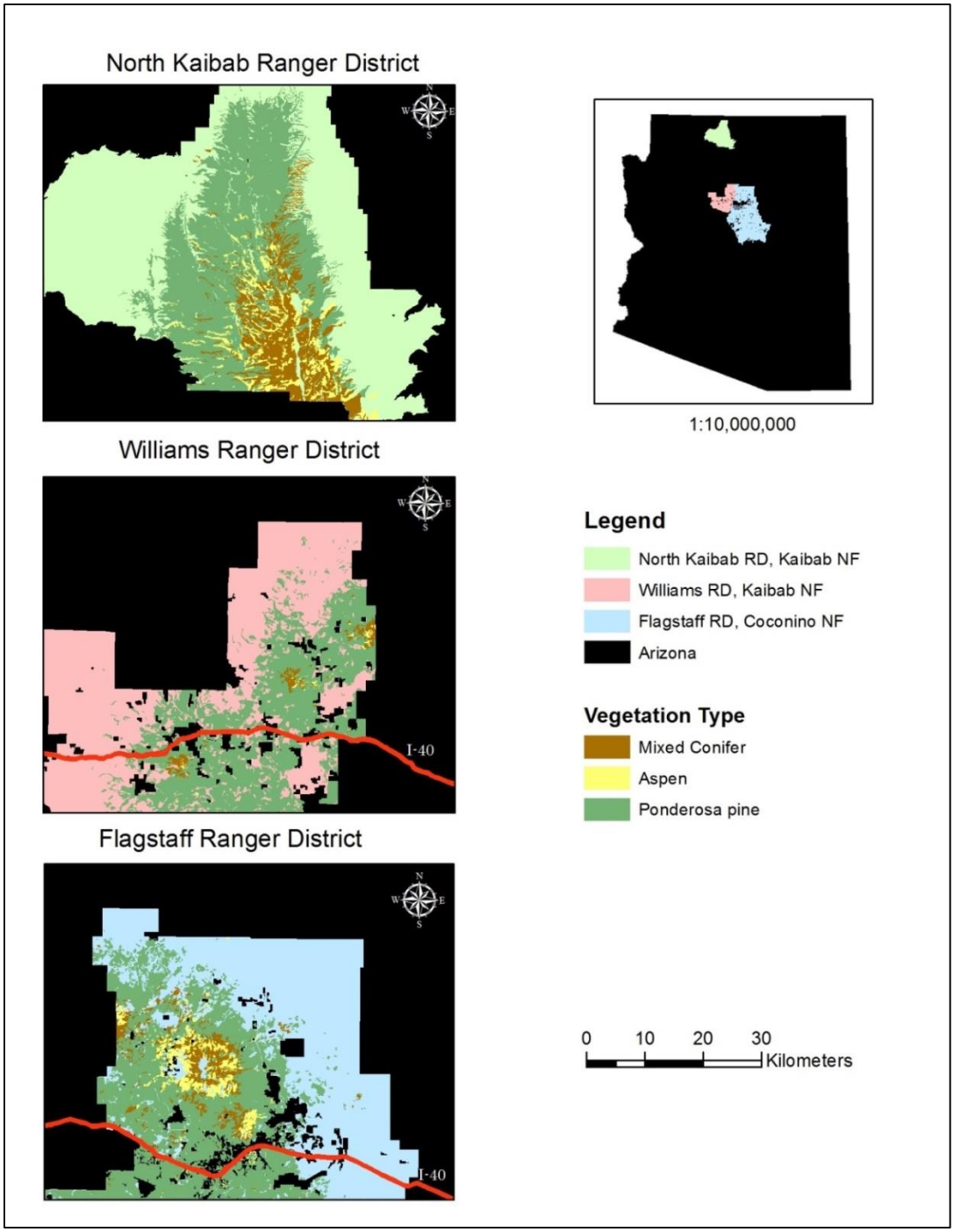


**Figure 3.1.** Location of the North Kaibab, Williams, and Flagstaff Ranger Districts in northern Arizona and the general vegetation types found in each Ranger District.

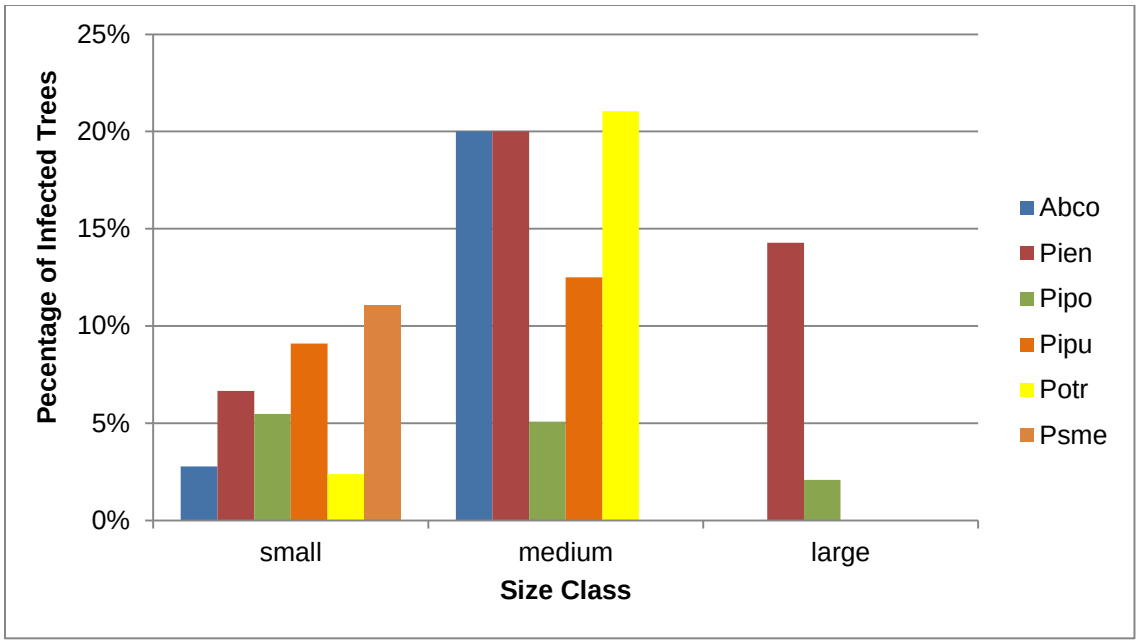


**Figure 3.2.** Percentage of trees by species infected with Armillaria root disease by diameter class: small (<20 cm), medium (20 – 40 cm), and large (> 40 cm).

# Professional Paper Conclusions

This paper contributed to our understanding of the dynamics and spatial extent of the pandora moth and Armillaria root disease in northern Arizona. In the first chapter I reviewed the current state of knowledge regarding the pandora moth. This review may be used to guide future studies of pandora moth ecology as it highlighted the diversity of pandora moth, as well as the biology and impacts to pine forests.

In chapter two, I focused on the spatial distribution and density of pandora moth from 2010-2012, and the level of defoliation and parasitization of larvae and pupae on the North Kaibab Ranger District (RD). I determined the extent of the current population using a new larval sampling method. I found that locations of larvae (i.e. local populations) during our sampling years occurred at a slightly different location from the initial 1980's outbreak location. I determined that defoliation levels, parasitoid and NPV infection levels, and adult densities are low and that adult densities surprisingly decreased during our sampling period. I also found that the pandora moth population is on the Tusayan Ranger District and that the isolated southern population emerged several weeks later than the population on the North Kaibab RD and while still at low densities the Tusayan RD population contained considerably more females than the North Kaibab RD population. Further examination is needed to compare population sizes and development rates between these populations. The low adult trap counts could be an artifact of distance to the center of the Tusayan population and a larval survey will need to be conducted.

The third and final chapter was a general survey for Armillaria root disease. The chapter described the results of a survey for Armillaria root disease by habitat types in northern Arizona.

The only species of *Armillaria* found in northern Arizona was *A. ostoyae*. I determined that the ponderosa pine habitat types were not conducive to *Armillaria* infection as much as the mixed conifer habitat types and that infection rates in northern Arizona were consistently low.