Interagency Whitebark Pine Health Monitoring Program for the Greater Yellowstone Ecosystem

2004 Annual Report

Greater Yellowstone Whitebark Pine Monitoring Working Group

Current Working Group Participants[a]

Robert E. Bennetts
USDI National Park Service
Greater Yellowstone Network

Steve Cherry
Montana State University
Department Of Mathematics

Gregg Denitto
USDA Forest Service
Forest Health Protection

Elizabeth Davy
USDA Forest Service
Bridger-Teton National Forest

Melissa Jenkins
USDA Forest Service, Caribou-Targhee National Forest

Lisa Landenburger
USDI Geological Survey
Northern Rocky Mountain Science Center

Mary Maj
USDI National Park Service
Greater Yellowstone Coordinating Committee

Dan Reinhart
USDI National Park Service
Resource Management and Visitor Protection

Charles Schwartz
USDI Geological Survey
Interagency Grizzly Bear Study Team

Erin Shanahan
USDI National Park Service
Resource Management and Visitor Protection

[a] This project represented a collaboration in the truest sense of the word, such that distinguishing order of participants with respect to relative contribution was virtually impossible. Consequently, order of participants is alphabetical.

Recommended citation for GYWPMWG (2005):

Greater Yellowstone Whitebark Pine Monitoring Working Group. 2005. Interagency Whitebark Pine Health Monitoring Program for the Greater Yellowstone Ecosystem, 2004 Annual Report. Pages 92-125 *in* C.C. Schwartz, M.A. Haroldson, and K. West, editors. Yellowstone grizzly bear investigations: annual report of the Interagency Grizzly Bear Study Team, 2004. U.S. Geological Survey, Bozeman, Montana, USA.

ABSTRACT

Whitebark pine (*Pinus albicaulis*) is a "keystone" species throughout the Greater Yellowstone Ecosystem (GYE), the cones of which serve as a major food source for grizzly bears (*Ursus arctos*) and other wildlife species. Whitebark pine stands have been decimated in areas of the northern Rocky Mountains due to the introduction of an exotic fungus—white pine blister rust (*Cronartium ribicola*)—as well as mountain pine beetles (*Dendroctonus ponderosae*). Resource managers from eight federal land management units have worked together as the Greater Yellowstone Whitebark Pine Subcommittee of the Greater Yellowstone Coordinating Committee (GYCC) to ensure the viability and function of whitebark pine in this ecosystem. In 2003 an additional working group was established to focus on an integrated monitoring effort throughout the GYE. The objectives of our monitoring were aimed at assessing the current status of white pine blister rust, whether or not blister rust is increasing within the GYE, and whether the resulting mortality of whitebark pine is sufficient to warrant consideration of management intervention (e.g., active restoration). Our study area is the entire GYE, comprised of 6 National Forests and 2 National Parks, although during 2004 our sample was restricted to within the Grizzly Bear Primary Conservation Area (PCA) because of limitations in the mapped distribution of whitebark pine (WbP) for the entire study area. We will extend beyond the PCA beginning in 2005. In 2004, transects were established and permanently marked for long-term trend monitoring in 45 stands of whitebark pine. In six of these stands, one additional transect was surveyed to assess within stand variation in blister rust. In total, 51 transects were sampled and 1,012 live trees surveyed. The number of whitebark pine trees sampled within these transects ranged from 1 to 141. Our data indicated that blister rust was relatively widespread throughout the PCA. Thirty six of the 51 (71%) transects had some indication of blister rust. Although blister rust was widespread, the infection severity was relatively low. We estimated that the proportion of trees infected with blister rust within the PCA to be 0.189 ± 0.05 SE, and most infected trees had ≤2 cankers. Further, most of the cankers also occurred on branches, which pose considerably less risk to the tree than cankers located on the trunks. Our data also indicated a high degree of observer variability in detecting indicators of blister rust and characteristics of trees used to indicate health. The concern over observer variability from our results extend well beyond the GYE effort and suggests a general need for better training and possible refinement of the methods used to assess blister rust.

INTRODUCTION

Whitebark pine occurs in the subalpine zone of the Pacific Northwest and northern Rocky Mountains of North America, where it is adapted to a harsh environment of poor soils, steep slopes, high winds, and extreme cold temperatures. Whitebark pine is a valuable species ecologically, and is considered a "keystone" species of the subalpine zone (Tomback et al. 2001). Whitebark pine's best known role in the Yellowstone ecosystem is as a food source for a variety of wildlife, most notably, the threatened grizzly bear (Mattson et al. 2001). In fact, in the GYE, annual whitebark pine cone production is one of the major predictors of annual survival and reproduction of the bears (Mattson et al. 1992, Mattson 2000). Whitebark pine seeds are high in fat and calories and are an important pre-denning food source for the Yellowstone grizzly bear. Grizzly bears gain access to large quantities of seeds stockpiled in red squirrel

(*Tamiasciurus hudsonicus*) middens (Mattson et al. 2001). As a pioneering species, whitebark often acts as a "nurse" plant for other trees, forbs, and shrubs that otherwise are not able to establish on their own in harsh environments (Tomback et al. 1993).

Background

In the early 1900s, white pine blister rust, a pathogen lethal to many 5-needled conifers, was introduced to the west coast of North America on imported, European nursery stock (McDonald and Hoff 2001). Since its arrival, it has decimated stands of whitebark pine in areas of the Cascades and northern Rocky Mountains (Kendall and Keane 2001). Although a whitebark pine tree infected with blister rust may survive for decades, its ability to produce cones, which grow in the upper canopy, is often compromised. When active, the site of infection, or canker, is a sweet attractant for rodents. The infected area is often consumed thus cutting off the flow of vital nutrients to the section of the tree above the gnawed portion. If this area is located on the trunk of the tree and it has been girdled, "top kill" will eventually occur and cone production will cease.

A more immediate threat to whitebark pine populations in the GYE is the mountain pine beetle. The mountain pine beetle is a native insect that has coevolved with pine forests in the western United States (Logan and Powell 2001). Variations in climate are largely responsible for the success of mountain pine beetle outbreaks. Mild summers and winters favor outbreaks, while cold winters and hot summers tend to decrease beetle activity and increase brood mortality (Kipfmueller et al. 2002). Evidence has shown that mountain pine beetles prefer to attack—and are more successful when attacking—trees that are already weakened by some other process, such as moisture stress, pathogens, or mistletoe (Kipfmueller et al. 2002). Some evidence indicates that older trees, weakened by other pathogens are more susceptible to mountain pine beetle infestations (Perkins and Roberts 2003, Tomback et al. 2001). It has also been suggested (e.g., Arno 1986) that fire suppression may lead to an increase of successional replacement of whitebark by more shade tolerant species such as Engelmann spruce (*Picea engelmannii*) or subalpine fir (*Abies bifolia*) (Keane 2001, Tomback et al. 2001).

Fire is an integral part of the ecology of whitebark pine communities. Yet larger, stand-replacing fires can kill mature, seed-producing whitebark pine trees, and may increase in frequency with a warmer and drier climate (Koteen 2002). Climate change may confound all of these threats and is hypothesized to affect whitebark pine communities through three mechanisms: 1) causing a shift in pathogens, which may lead to new regions of hospitable climate for white pine blister rust and increase the potential for pine beetle infestation; 2) increasing temperatures, which can lead to decreases in range availability for whitebark pine, due to exclusion by more heat-tolerant species, such as lodgepole pine (Mattson et al. 2001, Campbell and Antos 2003); and 3) changes in the frequency of severe fires, which lead to overall decreases in whitebark pine numbers (while they are adapted to small fires, large, stand-replacing fires may be detrimental to their overall distribution and abundance [Koteen 2002]).

Rationale for the Current Efforts

The "Final Conservation Strategy for the Grizzly Bear in the Yellowstone Ecosystem" (USFWS 2003) directs the National Park Service (NPS), U.S. Forest Service (USFS), and U.S. Geological

Survey (USGS) to monitor food sources of the grizzly bear, including ungulate carcasses, cutthroat trout, army cutworm moths, and whitebark pine. Specifically mentioned in the conservation strategy is monitoring of select transects throughout the GYE for cone production and white pine blister rust occurrence. Cone transect monitoring has been led by the Interagency Grizzly Bear Study Team and consists of cone counts and some blister rust monitoring (Haroldson et al. 2004). Blister rust is an important factor in the survival and reproduction of whitebark pine stands throughout the Northwest, and it has been determined that current cone counts within the GYE is not sufficient to understand the impacts of this introduced pathogen on whitebark pine stands and cone production (see Appendix B).

Given the Grizzly Bear Conservation Strategy directives, the ecological importance of WbP in the ecosystem, and that 98% of WbP occurs on public lands, the conservation of this species depends heavily on the collaboration of all public land management units in the GYE. Established in 1998, the Greater Yellowstone Whitebark Pine Subcommittee of the Greater Yellowstone Coordinating Committee is comprised of resource managers from eight federal land management units. This committee has been working together to ensure the viability and function of WbP throughout the region. As a result of this mutual conservation interest by these agencies, an additional working group (The Greater Yellowstone Whitebark Pine Monitoring Working Group) was formed in 2003-2004 with representatives from the U.S. Forest Service, National Park Service, U.S. Geological Survey, and Montana State University (MSU) for the purpose of integrating their interest, goals and resources into one unified monitoring program for the GYE. The group's intent is to estimate current status of whitebark pine relative to infection with white pine blister rust as well as to assess the vital rates that would enable us to determine the probability of whitebark pines persisting in the GYE. This project represents the initial results of that effort.

Objectives

General Questions Being Asked

Our specific monitoring objectives are intended to answer the following question(s): Is white pine blister rust increasing within the GYE, and is the resulting mortality of whitebark pine sufficient to warrant consideration of management intervention (e.g., active restoration)?

Specific Monitoring Objectives

OBJECTIVE 1 – To estimate the proportion of individual whitebark pine trees (>1.4 m high) infected with white pine blister rust, and to estimate the rate at which infection of trees is changing over time.

Justification/Rationale for this Objective: White pine blister rust has devastated whitebark pine in other parts of the northern Rocky Mountains (Kendall and Keane 2001, Koteen 2002), and anecdotal evidence suggests that infection rates may be escalating in the GYE (Koteen 2002, D. Tomback, personal communication). Given whitebark pine's importance in the upper subalpine ecosystem, and its being a key food source for a variety of wildlife, including grizzly bears, the

loss of seed-producing trees can affect not only a multitude of species, but also the persistence of this community type within the GYE.

OBJECTIVE 2 – Within infected transects, to determine the relative severity of infection (i.e., stage and magnitude of infection, and proportion of canopy kill) of white pine blister rust in whitebark pine trees >1.4 m high.

Justification/Rationale for this Objective: Determining the proportion of trees infected with white pine blister rust can be misleading without a further understanding of the magnitude of the infection. Given that within-tree spread of blister rust occurs primarily from new infections from the source, rather than spread from existing infections, trees that are infected at low levels may persist for considerable time in the absence of new infections (Koteen 2002). If the tree is infected near the crown, then the infection is most likely to cause cessation of cone production; it has been hypothesized that these types of infections occur more often than other types of infections in the GYE (Koteen 2002). The influence of the infection on tree mortality is highly dependent on the location of the infection, the age of the tree and other factors (such as mountain pine beetle infestations, root diseases, etc.); for instance, young trees that become infected almost always die relatively quickly, as do trees weakened by other causes (Koteen 2002).

OBJECTIVE 3 – To estimate survival of individual whitebark pine trees >1.4 m high, explicitly taking into account the effect of infection with and severity of white pine blister rust, and infestation by mountain pine beetle and dwarf mistletoe, and fire.

Justification/Rationale for this Objective: There has been some debate as to whether whitebark pine in the GYE is as vulnerable to the effects of white pine blister rust as it is in other regions (Carlson 1978, Arno 1986). Basidiospores of white pine blister rust are thought to be transported primarily during high moisture events (e.g., during periods of rain and fog [Hirt 1942, Van Arsdel 1956]), and the GYE is generally drier than other regions where white pine blister rust has been devastating to whitebark pine. Estimating survival will enable us to distinguish the occurrence (and severity) of white pine blister rust from the ecological effect of infestation (i.e., loss of mature whitebark pine); thus enabling us to determine the vulnerability of whitebark pine in the GYE directly, rather than relying on potentially controversial extrapolation from other regions.

Future Objectives under Consideration

At the present time our monitoring objectives focus on the status and trends of infection by white pine blister rust, to a lesser degree on occurrence of mountain pine beetle, and the resulting effect of these on survival of whitebark pine trees. Two additional topics that are currently being considered for future objectives are recruitment of whitebark pine trees into the reproductive population and the effects of forest succession on existing whitebark pine within suitable whitebark pine habitat types. Persistence of whitebark pine within the GYE depends on not only the survival of seed-producing trees, but also the recruitment of immature trees to the seed producing segment of the population. Monitoring changes in survival could result in misleading conclusions without some knowledge of the extent to which increased mortality is offset by recruitment. From a management perspective, there is also considerable concern about potential

replacement of whitebark pine by more shade-tolerant conifers (primarily subalpine fir). Understanding if, and to what extent, this is occurring could have important implications for potential restoration management of whitebark pine.

METHODS

Study Area

Our study area is the Greater Yellowstone Ecosystem and is comprised of 6 National Forests and 2 National Parks (Fig. 1). During 2004, our sample of WbP stands were restricted to within the Grizzly Bear PCA because of limitations in the mapped distribution of WbP for the entire study area. This region is approximately 2.4 million ha (5.9 million acres) (USFWS 1993) and includes approximately 50% of the known distribution of WbP within the GYE. An ongoing mapping effort will enable expansion of our study area beyond the PCA during 2005.

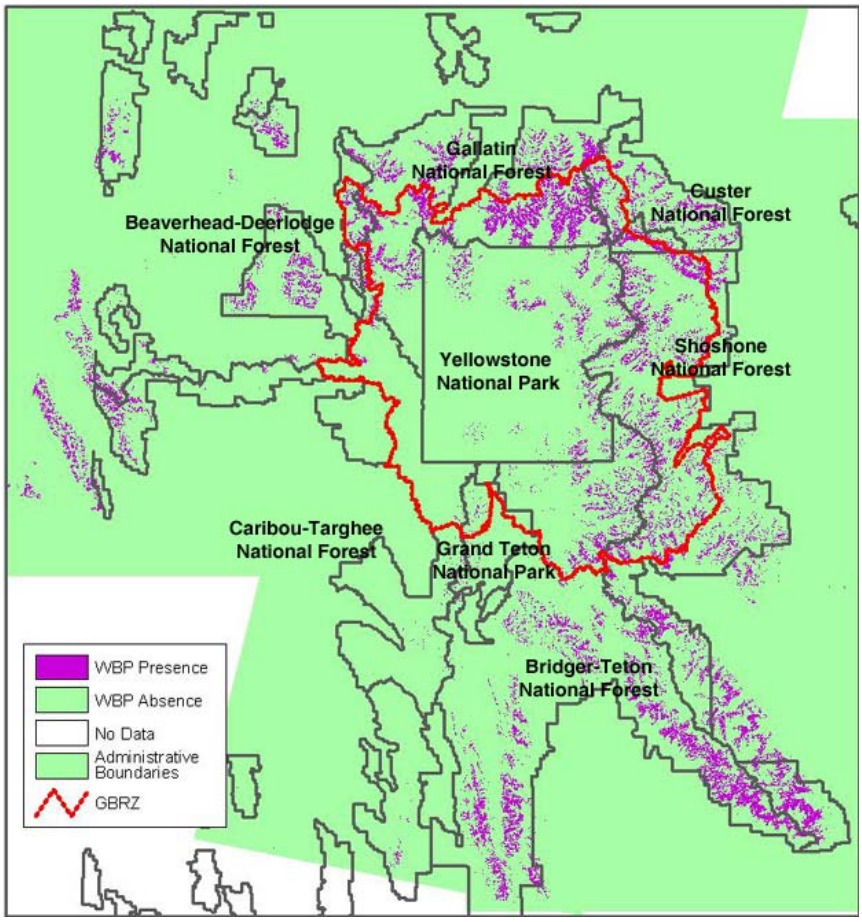

Fig. 1. Predicted occurrence of whitebark pine in the Greater Yellowstone Ecosystem. Sampling during 2004 was restricted to the Grizzly Bear Primary Conservation Area shown in red as the Grizzly Bear Recover Zone (GBRZ).

Sampling Design

Some Preliminary Assessments leading to our Design

A common problem encountered when designing studies is the balance between the number of samples (in this case transects) and the elements measured within each sample (in this case the number of trees within each transect). The Whitebark Pine Ecosystem Foundation (WPEF) Protocol (Tomback et al. 2004) initially approached this problem by using a variable transect length to ensure a minimum number of trees within each transect. We were concerned that this would produce biased estimates. To explore this concern and to evaluate the tradeoffs between the number of transects verses the number of tree per transect, we used two preliminary simulations which are described below.

Effect of Variable Transect Length for Obtaining Minimum Sample of Trees

The WPEF protocol (Tomback et al. 2004) initially suggested using variable length transects. The length of the transect is extended from 50 m if there are not at least 50 trees within the transect. Variable length transects can be a part of a valid sampling plan but varying the length of the transect to attain a minimum sample size will lead to biased estimators.

A simple simulation was used to show the effect of requiring a minimum sample size on the estimation of a proportion. We assumed a population with an infection rate of 0.20, very close to that observed in the GYE, and a random number of trees for each transect. A check was made for each transect, and if the number of trees was less than 50, an additional sample was taken to bring the minimum sample size up to 50. This was repeated 1000 times.

The result of this simulation was a mean of the empirical sampling distribution of 0.175, approximately 9% less than the actual rate of 0.200. Thus, the estimator (the sample proportion) was biased low. The statistical reason for this is may not seem intuitively obvious, but it centers on the fact that we no longer have an assumed binomial distribution; rather a new distribution which is a mixture of the binomial and another distribution with a lower mean. The practical consequences of this in the GYE whitebark pine monitoring program are not clear, but it raises concern that the earlier WPEF protocol may produce estimates that are biased low. The best way to avoid this concern is to use transects whose width and length are not determined by the number of trees in them. It should be noted that the WPEF protocol has since adapted their methods to a 10 x 50 m fixed transect length (Tomback et al. 2005).

Balancing the number of transects with the number of trees within each transect

Recognition of the potential bias resulting from variable length transects still does not resolve our concern about how to balance the number of transects with the number of trees within each transect. Thus a second simulation was used to explore these tradeoffs.

For this simulation, the mean number of trees within transects varied from 10 to 50 in increments of 10. The number of transects varied from 50 to 150 in increments of 50. Thus, there were 15 combinations of transect/tree numbers. The number of trees in each transect was determined by

drawing a random sample from a negative binomial distribution with the specified mean. The negative binomial was used because the number of trees was more variable than required for sampling from a Poisson distribution. Once the number of trees on a plot was determined, the number infected was determined by assuming each tree had a probability of 0.10 of being infected (based on infection rates observed during previous studies). The mean and standard error was computed for each trial and 1000 trials were run for each of the 15 transect/tree size combinations. The results indicated that the standard errors were fairly low in each case (Fig. 2).

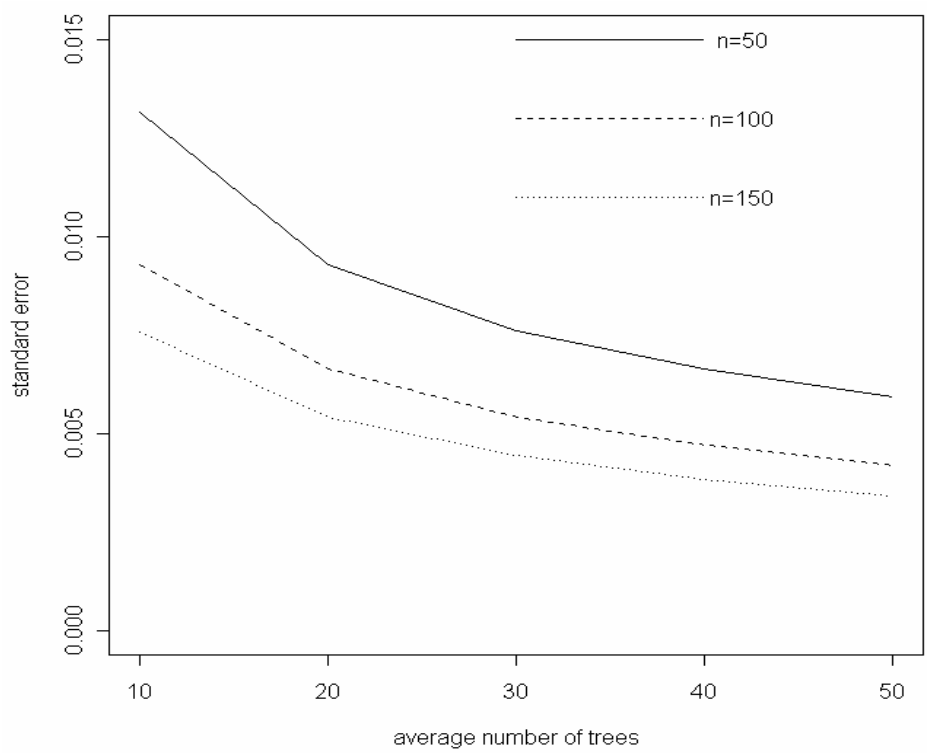

Fig. 2. The mean standard errors resulting from simulation increasing numbers of transects and increasing numbers of trees within each transect.

Another view of the tradeoffs between the number of transects and the number of trees within each transect is to examine the resulting confidence intervals (Fig. 3).

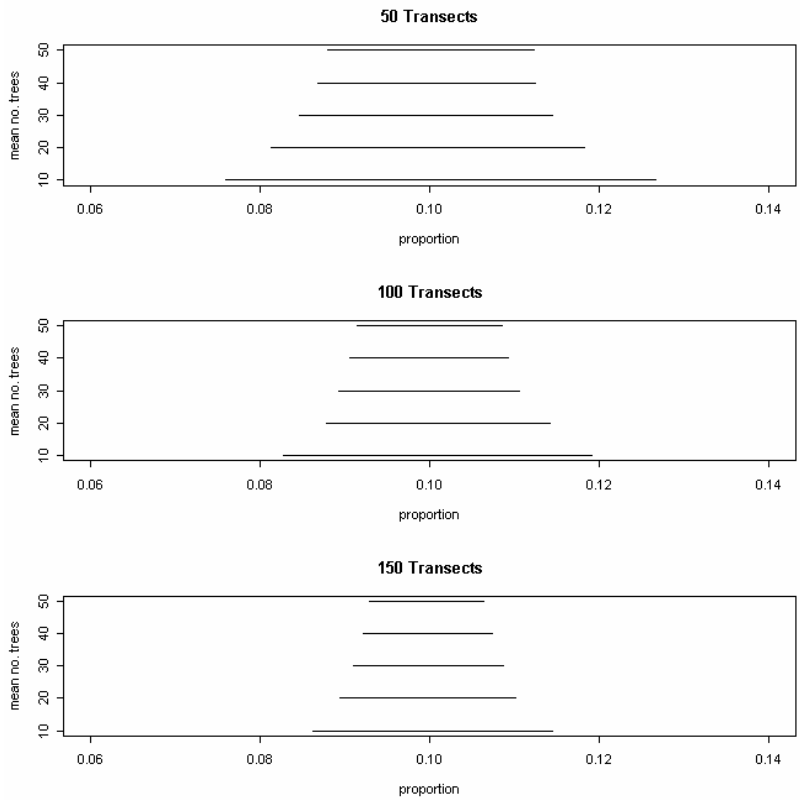

Fig. 3. The empirical 95% confidence intervals for the true mean resulting from simulations.

Obviously the more transects and the more trees within transects the better. But realistically, it appears that 100 transects with somewhere around 15 to 20 larger trees per transect on average, will be sufficient to produce reasonable estimates of status. It also appears that we gain relatively more efficiency by increasing the number of transects in our sample, as opposed to increasing the number of trees per transect. However, these results are based on an assumed simple random sampling plan with clusters as the primary sampling unit. This simulation does not take into account spatial considerations nor does it take into account stratification. We know that we will not be using this approach, relying instead on some kind of stratified sampling plan. However, the results do provide an initial indication of the precision we may expect.

Overall Design

The goal of the 2004 sampling effort was to characterize the current status of blister rust in the GYE. The sampling effort started early July and continued through late October.

The basic design was a 2-stage cluster design. Primary sampling units were stands of high-elevation whitebark pine dominated stands of approximately 2.5 hectares or larger. Secondary sampling units were 10 by 50 meter transects located within each stand. A simple random sample of primary units was selected followed by random selection of secondary units within each primary unit.

Target Population, Sampling Frame, and Sampling Units

The target population of ultimate interest is all whitebark pine trees in the GYE. It was clearly not possible to identify and map all whitebark pine trees. The sampling frame was actually defined in terms of mapped whitebark stands. The primary sampling unit was a whitebark pine polygon (stand) from the vegetation layer of the Cumulative Effects Model for grizzly bears derived from photo-interpretation (Dixon 1997). As indicated above, these were high-elevation whitebark pine dominated sites of approximately 2.5 ha or greater. A further restriction was that these stands were from areas that matched a forest layer derived from satellite imagery. Areas that were allegedly burned were omitted. The result was a sampling frame of 3,382 primary sampling units. These sampling units varied in size from approximately 2 ha to 594 ha. Each primary sampling unit was comprised of 10 by 50 m transects (secondary sampling units).

Selection of Primary and Secondary Sampling Units

We selected a simple random sample of 100 polygons from our sampled population of 3,382 such polygons. We wanted to ensure that the sample of polygons was adequately spatially distributed over the ecosystem and although we considered a stratified sampling approach we settled on the simple random sample because it did achieve the desired spatial distribution. The sampling frame is subject to inaccuracies due to mapping errors. There is the potential for the field crew to spend a great deal of time walking into an area only to find that a mapped polygon does not contain whitebark pines. Accordingly we also selected additional polygons near the initial selection. If the initial polygon is not suitable, then the crew is to choose the next nearest polygon. This seems a minor constraint on the randomization procedure that is justified by the limited time during which the crew has to collect data.

Secondary sampling units were 10 by 50 m transects located within each polygon. The number of secondary sampling units varied with polygon size. We selected a simple random sample of starting points for 6 secondary sampling units within each polygon. The first unit to visit was also chosen randomly. Details of how the transect is laid out and data are collected are described below.

Initially we planned on sampling one secondary unit per polygon. This is not an ideal sampling design because it will not be possible to estimate within polygon variability and it will not be possible to estimate standard errors of estimates of population totals and means without further assumptions. We have at least three options available for standard error estimation. First, we can take two 10 by 10 m subplots located at the end of each of the larger plots and use those to provide some information on within plot variability. This will not be ideal because the two plots will be paired, but it could still provide useful information for designing a long-term plan. Second, field crews have been instructed to attempt to read two transects per polygon whenever possible. Initial indications are that getting to a selected polygon and reading one transect takes the better part of a day but we anticipate that as the summer progresses the crew should become more proficient. Third, we can consider the resulting sample of transects to be a random sample of transects and get estimates of standard errors based on that assumption.

Field Methods

Many of our field methods were based on the protocol developed by the Whitebark Pine Ecosystem Foundation (Tomback et al. 2004). We deviated from these methods when appropriate to meet our specific objectives, or when we felt that an alternative was more biologically or statistically reliable.

Starting points for Transects

To identify potential monitoring transect locations throughout the study area, 100 primary stands of varying whitebark pine density were randomly selected from the primary units. Of these 100 stands, 45 were sampled by completing transects in as many stands as possible within a region within a 10-day sampling period and then shifting to a new region of the study area after each sampling period. Stands were grouped by geographic proximity into clusters of 3 stands, with the designations of one "Primary" stand and two associated "Alternate" stands per cluster. Within each stand, 5 random points were selected to serve as potential center points for each transect. A corresponding number between 0 and 359 was randomly chosen to define the vector for the transect. The random points were listed in rank order of selection, such that the first point in the list is the intended starting location. Should however, that location be unsuitable (i.e., misclassified as having whitebark pine when it does not), the next, closest point on the list became the starting point, and so on.

A handheld GPS was used to navigate to these coordinates with an error factor that varied from a few to several meters. If a site was suitable for sampling (i.e., had at least one whitebark pine tree), a 10 x 50 m transect was established. The start and end points of the transect were monumented by a 12" steel nail with a large washer and numbered tag driven in at ground level. Universal Transverse Mercator (UTMs) were recorded and photos were taken into the plot at both monuments. Inside the plot, 3 bearing trees were noted by species, diameter-at-breast-height (DBH) (1.4 m), and azimuth in regards to the monument. The overall habitat type (Steele et al. 1983) and forest cover type (Despain 1990) of the stand were recorded.

Inclusion of Individual Trees Within a Plot

All whitebark pine trees within the transect and >1.4 m high were marked and included as secondary sampling units. A given tree or cluster of trees (see below) was included within a plot if, and only if, the center of the trunk (or cluster of trunks) at ground level was within 5 m of the center of the transect line. This differs slightly from the criteria of the WPEF protocol, which includes trees if the center at breast height (rather than ground level) is within the plot boundary. The reason for this departure is that using a hypothetical plane 1.4 m above ground level is (1) more ambiguous than using ground level, (2) more difficult to determine than using ground level, and (3) results in a different sampling frame for trees (<1.4 m) and marked trees >1.4 m. For practical purposes the differences between these criteria should be negligible.

Tree Clusters

Tree clusters may form when multiple seeds are cached at the same location by Clark's Nutcrackers *(Nucifraga columbiana).* Although multiple branches of an individual tree are certainly possible, it is more often the case that multiple trees can sprout from the same location. Thus, to ignore that these are individual trees can be problematic and under sample the density of trees at a given location. Further, a given tree within a cluster may suffer damage and/or mortality from blister rust, while an adjacent trunk with less or no infection may remain undamaged and survive. However, we also recognize that because such trees sprouted from the same site, the canopy may be intertwined, etc., that these trees are not statistically independent. However, this may also be true for other trees within the same plot, depending on a variety of factors, including proximity. Thus, for the purposes of our sampling, we followed the guidelines of the WPEF protocol (Tomback et al. 2005) and record data for each individual tree within a cluster if the tree(s) stems are separate below ground (root level). In such cases we also identified it as being part of a cluster, allowing for analyses to take this into account when appropriate.

Dead trees

Dead whitebark pine trees >1.4 m height within the plot were not marked, but were recorded as being present. DBH (see below) was the only individual tree measurement taken. In contrast with the WPEF protocol (Tomback et al. 2004), no determination of cause of death was recorded due to the unreliability of retrospective assignment of cause of death. Evidence of insect or disease agents was noted in the comments.

Individual Tree Measurements

All live whitebark pine trees >1.4 m height within the transect were individually marked at 1.4 m breast height (BH) on the downside slope of the tree with a numbered metal tag (in federally-designated Wilderness Areas, tags were placed on the downside slope at the base of the tree). As per WPEF protocol, if stems are separate below BH (4.5 ft or 1.4 m), each bole stem is tagged and receives a letter designation to indicate clump membership. For live trees, we recorded DBH and crown ratio (i.e., the percentage of live canopy for the entire tree from top to bottom)(USFS 2002). The tree was surveyed for blister rust cankers and aecia (the active, fruiting body of the canker) in the upper, middle, and bottom thirds of the branches and on the upper, middle, and bottom third of the trunk (Fig. 4). Five auxiliary signs of blister rust infection: rodent chewing, branch flagging, swelling, roughened bark and oozing sap were also recorded. If three of the five auxiliary signs occurred in the same spot on a tree, that location was noted as having a canker. The number of branch and trunk cankers was recorded for each of these tree sections. A tally of the regenerating whitebark less than 1.4 m in height was taken and noted for the presence, absence, or uncertainty of blister rust.

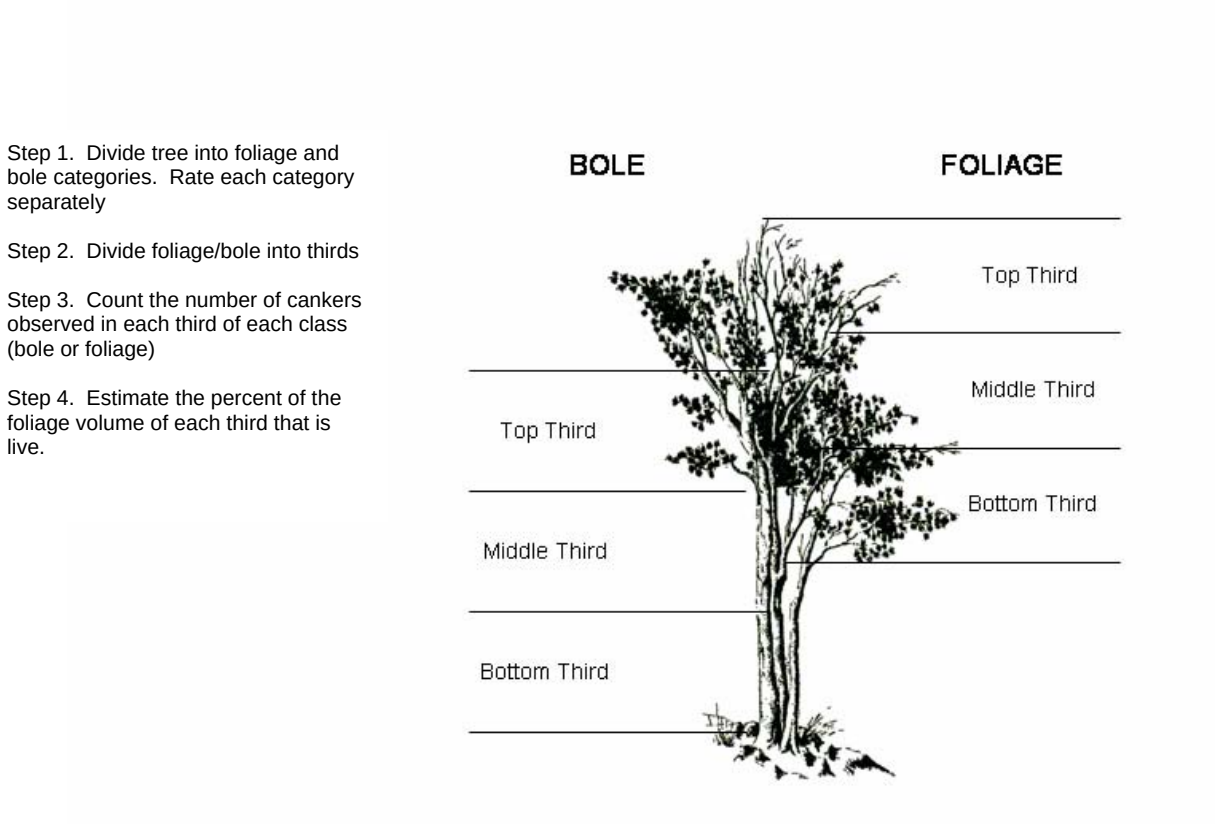

Fig. 4. Conceptual diagram of severity rating adapted from Six and Newcomb (in preparation).

In order to assess the extent of observer variability on this monitoring effort, 6 of the 45 transects were independently surveyed on the same day by three different observers. The variability amongst the observers was assessed out of the field (no discussion while at the plot between the crew). The focus of these additional six was on blister rust identification (cankers and aecia) and canopy percentage estimation.

Mountain pine beetle is also a major source of mortality for whitebark pine. Although this source of mortality is native to the GYE, there may also be an interaction between blister rust and pine beetle and there may be changes in the patterns and extent of beetle outbreaks resulting from climate change (Kipfmueller et al. 2002). Thus, as per the WPEF protocol, we recorded presence/absence of mountain pine beetle.

Statistical Analyses

Proportion of Infected Trees

Estimation of the proportion of infected trees requires estimation of the population total of infected trees and total trees. Most sampling texts present two alternative methods of doing this

for two-stage cluster designs. We assume below that we have a simple random sample of primary units followed by a simple random sample of secondary units within each primary unit.

Let M_i be the number of secondary units in the *i*th primary unit. Let m_i be the number of secondary units sampled from the *i*th primary unit. The total number of primary units will be denoted by *N* and the sample size of primary units by *n*. The total number of trees observed in the *j*th transect of the *i*th polygon is y_{ij}. Then

$$\hat{t}_i = \sum_{j=1}^{m_i} \frac{M_i y_{ij}}{m_i} = M_i \bar{y}_i$$

is the estimated total number of trees in the *i*th primary unit. This simply says that the estimated total number of trees in the *i*th polygon is the sample mean number per transect times the number of transects in that polygon. A similar equation holds for the total number of infected trees. Denoting the total number of trees observed in the *j*th transect of the *i*th polygon is x_{ij}. Then

$$\hat{u}_i = \sum_{j=1}^{m_i} \frac{M_i x_{ij}}{m_i} = M_i \bar{x}_i$$

is the estimated total number of infected trees in the *i*th primary unit. An unbiased estimator of the population total number of trees is

$$\hat{t}_{unb} = \frac{N}{n} \sum_{i=1}^{n} \hat{t}_i \ .$$

This just says that the estimated total number of trees in the population of polygons is equal to the average number per polygon times the total population size. Similarly an unbiased estimator of the population total number of infected trees is

$$\hat{u}_{unb} = \frac{N}{n} \sum_{i=1}^{n} \hat{u}_i \ .$$

These estimators tend to be highly variable.

A second estimator of the total number of trees is

$$\hat{t}_r = M_o \frac{\sum_{i=1}^{n} \hat{t}_i}{\sum_{i=1}^{n} M_i}$$

where M_o is the total number of transects. The corresponding estimator of the total number of infected trees is

$$\hat{u}_r = M_o \frac{\sum_{i=1}^{n} \hat{u}_i}{\sum_{i=1}^{n} M_i}.$$

This ratio estimator is biased but less variable and is generally preferred because the bias tends to be small. The number of polygons is $N = 3382$. The polygon sample size is $n = 3382$. There are approximately $M_o = 3717433$ transects in the population.

If we were simply interested in these totals then we would probably choose the ratio estimators because they tend to be less variable. However, we are interested in the proportion of infected trees in the population. A ratio estimator of this quantity can be obtained using either of the estimation procedures above,

$$\hat{p} = \frac{\hat{u}_{unb}}{\hat{t}_{unb}} = \frac{\hat{u}_r}{\hat{t}_r} = \frac{\sum_{i=1}^{n} \hat{u}_i}{\sum_{i=1}^{n} \hat{t}_i}.$$

The variance estimator is somewhat complicated. It has two components; one measuring the between polygon variability and one measuring the within polygon component. Let

$$d_{ij} = x_{ij} - \hat{p} y_{ij} \text{ and } \bar{d}_i = (1/m_i) \sum_{j=1}^{m_i} d_{ij}.$$

The estimator is

$$\hat{v}(\hat{p}) = \left(\frac{1}{\sum_{i=1}^{n} (\hat{t}_i / n)} \right)^2 \left[\left(1 - \frac{n}{N}\right) \frac{s_r^2}{n} + \left(\frac{1}{nN}\right) \sum_{i=1}^{n} M_i^2 \left(1 - \frac{m_i}{M_i}\right) \frac{s_i^2}{m_i} \right],$$

where

$$s_r^2 = \frac{\sum_{i=1}^{n} \left(M_i^2 (\bar{x}_i - \hat{p}\bar{y}_i)^2 \right)}{n-1}$$

and

$$s_i^2 = \frac{\sum_{j=1}^{m_i} \left(d_{ij} - \bar{d}_i\right)^2}{m_i - 1}.$$

The term in the square brackets containing s_r^2 is the between polygon component and the term containing s_i^2 is the within polygon component. If there is only one sampling unit in the *i*th polygon (i.e. $m_i = 1$), then the within polygon component for that polygon cannot be determined and the total variance will be underestimated. Note however that the within polygon component will tend to be smaller than the between polygon component because of the $\frac{1}{nN}$ term. The standard error of $\hat{p}$ is of course the square root of the estimated variance.

RESULTS AND DISCUSSION

A total of 45 polygons (stands) were visited with 51 transects being sampled. A total of 1,012 live trees were examined. The number of live trees per transect ranged from 1 to 141 with an average of 19.84 trees per transect.

Proportion of Trees Infected

The estimators described above produced the following estimated numbers of trees and number of infected trees in the population (Table 1). Note that these are estimates of the overall population totals, not the totals from our samples.

Table 1. Intermediate results of the estimated population totals of the number of trees and number of infected trees using unbiased and ratio estimators.

Parameter	Parameter description	Estimator type	Estimate
$\hat{t}_{unb}$	Total number of trees in population	Unbiased	73,910,491
$\hat{u}_{unb}$	Total number of infected trees in population	Unbiased	14,031,505
$\hat{t}_r$	Total number of trees in population	Ratio	65,673,532
$\hat{u}_r$	Total number of infected trees in population	Ratio	12,467,763

From these intermediate results, the estimated proportion of infected trees in the population is:

$$\hat{p} = \frac{14031505}{73910491} = \frac{12467763}{65673532} = 0.189.$$

Ignoring the between polygon component we get an estimate of the standard error of 0.0616. This is the minimum the standard error can be. Adding within polygon variance will only increase this quantity. This standard error is much larger than the standard error computed assuming a simple random sample of transects, and larger than that seen in our simulations.

We can get an idea of the amount of within polygon variance relative to between polygon variance by considering the 6 polygons in which two transects were sampled. Ignoring the within polygon variance the standard error of the proportion of infected trees on these 6 transects is 0.0499. The standard error computed by considering the within polygon variance is 0.0502. This suggests that within polygon variance may be negligible.

There are some encouraging and discouraging parts of this analysis. The encouraging part is the minor role played by the within polygon variability. This is a preliminary assessment based on a sample of size 6 so more data are needed to confirm this. The discouraging part is how large the overall standard error is just considering between polygon variability. This suggests that a lot of polygons will have to be visited to have a reasonable chance to detect meaningful changes in infection rates in a reasonable length of time.

Of the 51 transects, 36 were infected with white pine blister rust and the proportion of infected trees on a given transect ranged from 0 to 1.0 (Fig. 5).

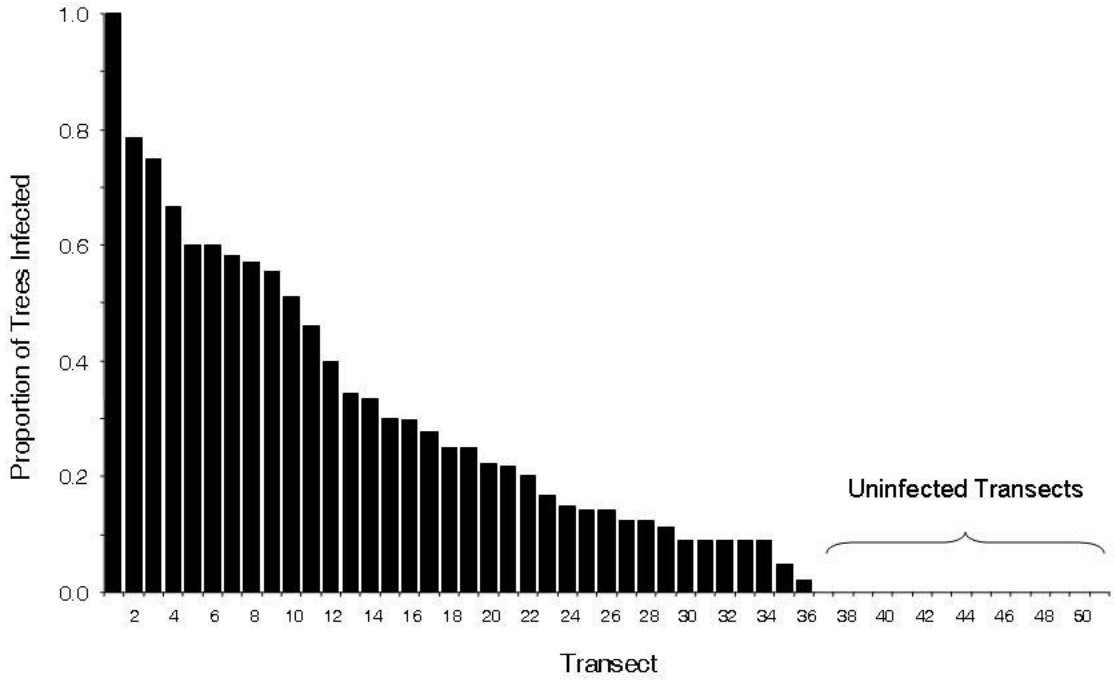

Fig. 5. The proportion of whitebark pine trees infected on each of the 51 transects sampled during 2004 arranged in rank order from most infected to least infected.

Although a formal spatial analysis has not yet been conducted, our preliminary data indicate that infection rates were highest in the northwest portion of our study area (Fig. 6). It should be noted, however, that our 2004 sampling effort was restricted to the Grizzly Bear Recovery Zone, and that the spatial distribution of infection may change substantially as we expand our effort beyond this zone starting in 2005.

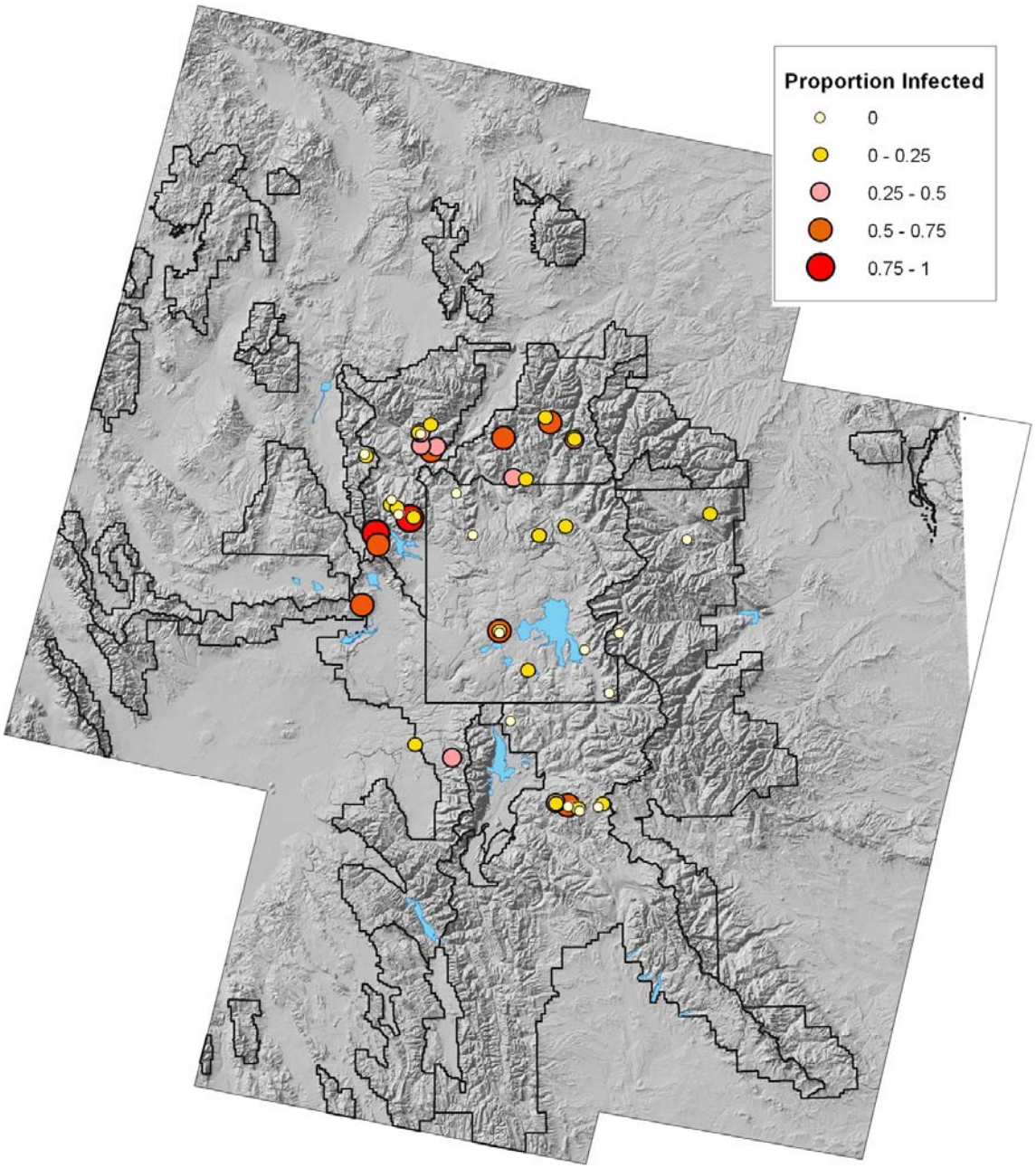

Fig. 6. Distribution of transects sampled during 2004, and class of proportion of trees infected.

Severity of Infection

Of 230 whitebark pine trees reported as infected, 128 (56%) were reported as having aecia. This is considered the gold standard for determining the presence of whitebark infection (Tomback et al. 2005). If we limit our analysis to those 128 trees where identification of blister rust cankers is virtually certain, the proportion of trees having branch cankers is substantially greater than those with cankers on the trunk (Fig. 7).

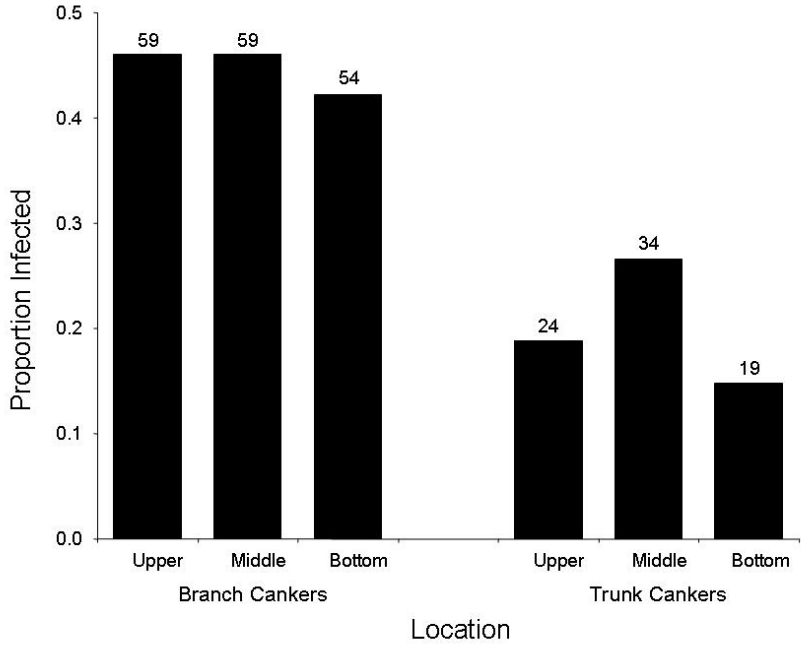

Fig. 7. The proportion of 128 trees infected with branch or trunk cankers, as determined by the presence of aecia, in each of three height classes.

This result is somewhat encouraging since cankers on the trunk are generally considered lethal to the tree, or may reduce the potential for cone production. In contrast, branch cankers, unless close to the trunk, may kill individual branches, but pose substantially less threat (Koteen 2002).

A similar conclusion is evidenced by the number of cankers within infected trees. This assessment was based on 230 trees that exhibited either aecia, and/or the presence of at least three of the other indicators; this was perhaps less conservative than the analysis above that was restricted to those trees with aecia present, but more conservative than if we had considered cankers based on the presence of any of the indicators.

This result indicated that most trees infected with blister rust had few cankers, particularly for trunk cankers. The number of branch cankers on infected trees ranged from 0 (i.e., when a tree had only trunk cankers) to 32 with approximately 90% of the trees having ≤5 branch cankers

(Fig. 8). The number of trunk cankers on infected trees ranged from 0 (i.e., when a tree had only branch cankers) to 4 with approximately 90% of the trees having ≤1 trunk canker.

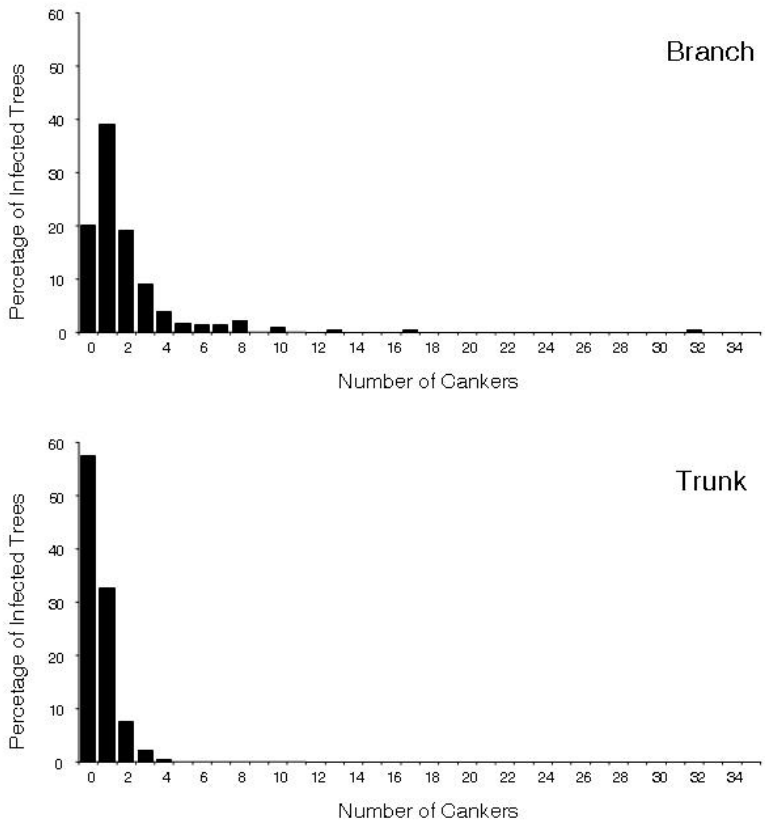

Fig. 8. The number of branch and trunk cankers on infected trees.

Mountain Pine Beetle and Mistletoe

The total number of live and dead trees for the 51 transects was 1,360. Of the live trees, 8 of 1,012 (<1%) had evidence of mountain pine beetle infestation, while 94 of 348 (27%) dead trees had evidence (galleries) of successful mountain pine beetle attack.

Dwarf mistletoe was found on one tree.

Indicators of Blister Rust Infection

A total of 128 trees were reported as having aecia, although information was also recorded on 5 other indicators of infection: rodent chewing, flagging, swelled bark, roughened bark, and oozing sap. The proportion of 128 trees with one or more cankers in each of the height and position classes along with an analogous assessment from 230 trees if a different standard is used (i.e., aecia and/or at least 3 other indicators) is given below (Table 2).

Table 2. The proportion of trees with one or more cankers in each of the height and position classes based on two criteria for identifying cankers. One assessment is based on 128 tress where aecia were present. The second assessment was based on 230 trees where aecia and/or at least 3 other indicators were present.

Height Class	Position in tree	Based on cankers with aecia present	Based on cankers with aecia and/or at least 3 other indicators
Upper	Branch	0.461 (59/128)	0.457 (105/230)
Middle	Branch	0.461 (59/128)	0.387 (89/230)
Lower	Branch	0.422 (54/128)	0.296 (68/230)
Upper	Trunk	0.188 (24/128)	0.217 (50/230)
Middle	Trunk	0.266 (34/128)	0.209 (48/230)
Lower	Trunk	0.148 (19/128)	0.104 (24/230)

These results initially appear to indicate that the more restrictive criteria of using aecia only to confirm the presence of infection did not produce substantially more conservative estimates of the proportion of trees infected in each height and position class as might have been expected. In fact only one height/position group (Upper/Trunk) had higher estimates from the more inclusive criteria. However, there are some confounding influences on this result. We included the additional indicators after the field season had started. Consequently, some transects included in the analysis based on aecia only were not included in the other analysis. Because the indicators were added after the season started, the observers also had gained additional experience in identifying cankers by the time these other indicators were included. These results should be interpreted with caution. We have no evidence that the criteria we established for using three of five indicators, in the absence of aecia, to confirm an infection does not produce substantially higher estimates.

Part of our initial effort is to assess the relationship among the various indicators and methods. By doing so, we have a better understanding of what these indicators and methods are telling us about blister rust infections. One aspect of this assessment is to understand the association, if any, of infections on different parts of the tree (i.e., height and position). The correlation matrix below shows the pairwise correlations between the numbers of cankers at the 6 locations on the trees (Table 3).

These results indicate a generally low correlation among infection on different parts of the tree. This implies that knowing something about the infection level in one part of the tree would tell us very little about infections in other parts. This reaffirms our existing protocol for recording

cankers in different parts of each tree. Where cankers occur on a given tree can have a dramatic effect on survival and reproduction for that tree, and trying to simplify our methods to ignore the height and position classes where cankers occur could result in a substantial loss of information.

Table 3. Correlation matrix showing correlations between locations of white pine blister rust cankers on trees. Data was presence/absence of cankers.

Location of cankers	Upper branch	Middle branch	Bottom branch	Upper trunk	Middle trunk	Bottom trunk
Upper branch	1	0.26	0.19	0.05	0.04	-0.05
Middle branch		1	0.74	0.19	0.40	0.02
Bottom branch			1	0.18	0.38	0.07
Upper trunk				1	0.20	0.14
Middle trunk					1	0.11
Bottom trunk						1

To further evaluate the relationship among different indicators, we also looked at what proportion of trees had indicators in addition to aecia (Fig. 9) and of those, whether they had 1, 2, 3, etc. of these other indicators (Fig. 10). For this assessment, we used 82 of the 128 trees with aecia (i.e., with confirmed blister rust), for which the other 5 indicators were also recorded.

These results indicate that the proportion of trees exhibiting at least one of the other indicators ranged from approximately 51-83%. Rodent chewing was the least frequent indicator and flagging was the most frequent. About 85% of the 82 trees with aecia (i.e., definitely infected with blister rust) had 3 or more of the indicators. We next examined the co-occurrence of individual indicators. Table 4 shows the proportion of trees with an indicator present that has another indicator. For example, 42 trees had evidence of rodent chewing and 33 (0.786) of those also had flagging.

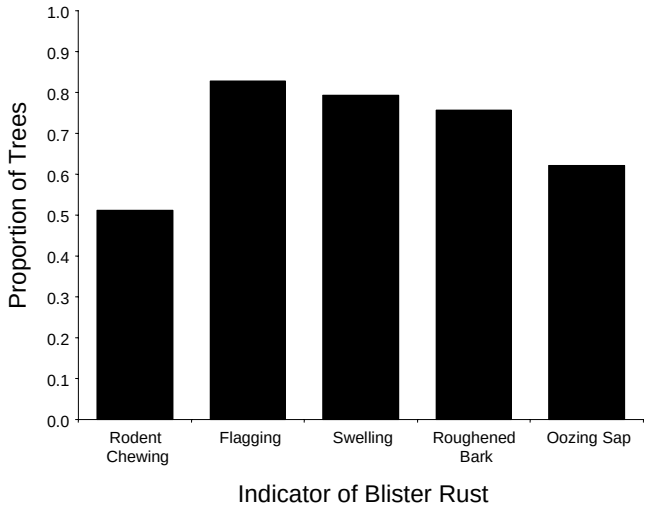

Fig. 9. Proportion of 82 trees with one or more incidences of each indicator of white pine blister rust.

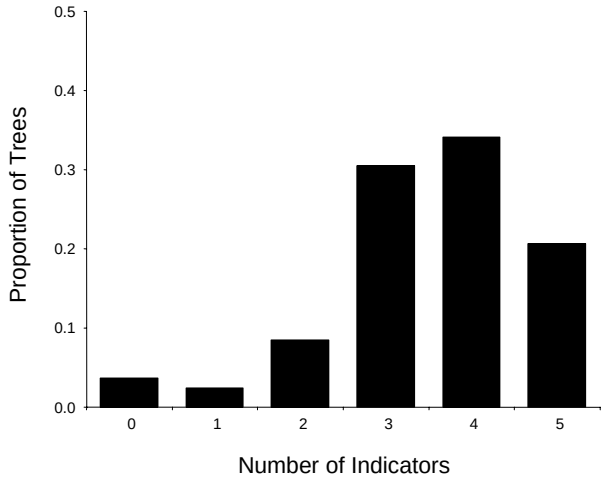

Fig. 10. The proportion of 82 trees exhibiting different numbers of indicators.

Table 4 provides information on the conditional relationships among the variables. This may provide an incomplete picture of the associations among the variables however. There are a number of ways to measure the similarity (dissimilarity) among such variables.

Table 4. The co-occurrence (proportion of trees [number of trees]) of indicators with each of the other indicators.

Indicator	Chewing	Flagging	Swelling	Roughness	Oozing sap
Chewing (42)	–	0.786 (33)	0.714 (30)	0.619 (26)	0.714 (30)
Flagging (68)	0.485 (33)	–	0.838 (57)	0.794 (54)	0.561 (46)
Swelling (65)	0.462 (30)	0.876 (57)	–	0.892 (58)	0.661 (43)
Roughness (62)	0.419 (26)	0.871 (54)	0.935 (58)	–	0.694 (43)
Oozing sap (51)	0.588 (30)	0.902 (46)	0.843 (43)	0.843 (43)	–

Table 5 is an extension of the previous analysis which contains chi-square test statistics and associated p-values of tests of independence of the occurrence of pairs of these indicators. The data were transformed from count data (number of incidences of rodent chewing for each tree) to presence/absence data (rodent chewing present or not). The 10 pairwise 2 by 2 contingency tables of matches and mismatches were constructed followed by the tests of independence. A low p-value indicates an association among the pairs. For example, the combination of swelling and roughened bark had a p-value of <0.001, indicating a strong association, in this case positive, among these two indicators (i.e., the occurrence of one indicated that the other was also likely to be present).

Table 5. Chi-square statistics and associated p-values (in parenthesis) for pairwise tests of independence among indicators of blister rust. The matrix is symmetric so only the upper diagonal is shown.

Indicator	Chewing	Flagging	Swelling	Roughness	Oozing sap
Rodent chewing	–	1.15 (0.28)	3.22 (0.073)	8.77 (0.0031)	3.12 (0.077)
Flagging		–	5.03 (0.025)	3.12 (0.077)	5.03 (0.025)
Swelling			–	31.54 (0.000)	2.09 (0.14)
Roughened bark				–	5.54 (0.018)
Oozing sap					–

These results need to be interpreted with caution due to the fact that we have evidence of considerable observer variability in the assessment of these indicators (see below). If we had data from another observer the results could conceivably change, perhaps quite dramatically. We have refined how we will record this information during our 2005 field season and should be able to provide a better assessment of the relationship among indicators and the implications of those relationships following our 2005 field season.

Observer Variability

Six transects were read independently by 3 different observers to evaluate the extent of observer variability. We plan to continue this evaluation program during the 2005 field season. Data were collected on: (1) crown ratio (%), (2) number cankers at each height/position class, (3) the presence/absence of aecia, rodent chewing, swelling, roughened bark, oozing sap, and flagging, (4) the percent of live canopy volume at each height/position class, (5) middle, and lower thirds of a tree, and the presence/absence of mistletoe and mountain pine beetle. Results for each variable are summarized below.

Crown Ratio

The crown ratio was visually estimated for 59 trees by the 3 observers. Pairwise correlations between observers was low (Table 6). A pairwise scatter plot of the estimates is also shown (Fig. 11).

Table 6. Pairwise correlations between crown ratio estimates (%) for 3 possible observer pairs.

Observer pairs	Correlation
Observer 1 and 2	0.675
Observer 1 and 3	0.533
Observer 2 and 3	0.766

These correlations are not as high as we would have liked. It is interesting to note that even though this is presumably a continuous variable, out of 177 possible ratings 176 ended in either a 0 or a 5.

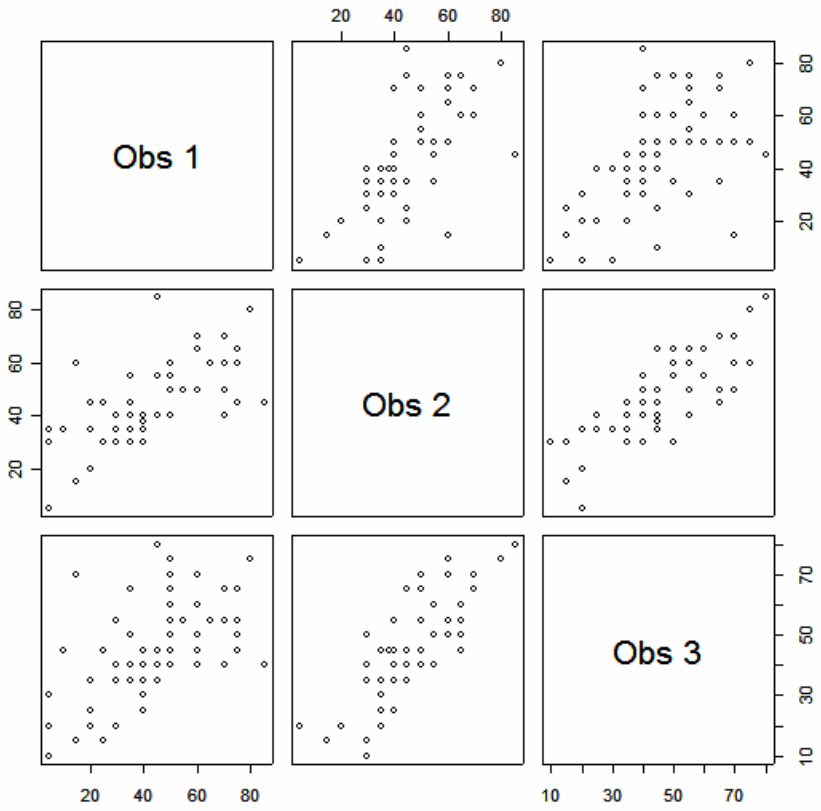

Fig. 11. Pairwise scatter plots of crown ratio estimates (%) for observer pairs.

Proportion of Trees Infected with Blister Rust

The proportion of infected trees was determined using canker counts and aecia presence/absence from each of the 3 observers (Table 7).

The final estimate, based on 60 trees, is identical for 2 of the observers. However, it is obvious that they did not identify the same 9 trees. The data suggest that there was no or little bias in how cankers were counted, i.e., one observer was not always counting more or less than another. However, even though the totals tend to be close to one another, estimates of variability are affected by the variability among transects. Further, these errors will tend to complicate any analysis requiring information from individual trees, e.g., building models examining the relationship of environmental covariates and infection status.

Aecia were noted on 9 of the 60 trees in the 6 transects but in only 2 of those cases did all 3 observers note aecia on the same tree.

Table 7. Proportion of infected trees as determined by canker counts for 3 different observers on 6 transects. Bold faced transects indicate transects where differences were recorded.

Transect ID	Observer 1	Observer 2	Observer 3
4280	0/5 (0)	0/5 (0)	0/5 (0)
2602	1/4 (0.25)	1/4 (0.25)	1/4 (0.25)
4119	**2/11 (0.182)**	**1/11 (0.091)**	**4/11 (0.364)**
1830	1/7 (0.143)	1/7 (0.143)	1/7 (0.143)
531A	**1/13 (0.077)**	**2/13 (0.154)**	**0/13 (0)**
4299A	**2/20 (0.10)**	**3/20 (0.15)**	**3/20 (0.15)**
Total	7/ 60 (0.117)	9/60 (0.15)	9/60 (0.15)

Canker Counts

All 3 observers recorded no cankers on trunks of the 63 trees. There was some variability among branch counts (Table 8).

Table 8. Counts of cankers in branches of 63 trees recorded by 3 different observers.

Observer	Upper branch cankers	Middle branch cankers	Bottom branch cankers	Total canker count
1	3	3	3	9
2	6	5	3	14
3	5	5	2	10

It was rare for observers to identify cankers on the same tree. Upper branch cankers were recorded on 8 different trees but in only 3 cases did 2 or more observers record upper branch cankers on the same tree. Middle branch cankers were recorded on 7 different trees with 5 cases of 2 or more observers recording cankers on the same tree. Lower branch cankers were recorded on 4 trees but in only 1 case did more than 1 observer note cankers on the same tree. There were 4 cases where all the 3 observers noted cankers on upper, middle, or lower branches of the same tree. In all other cases where cankers were recorded at least one observer did not see any.

Live Canopy Volume

Correlations between estimated live canopy volume (%) for 3 different areas of a tree are shown below (Table 9). Pairwise scatter plots are shown in Figures 12, 13, and 14.

Table 9. Pairwise correlations between estimated live canopy volume (%) for upper, middle, and lower sections of the canopy.

Observer pairs	Upper live canopy volume	Middle live canopy volume	Bottom live canopy volume
1 and 2	0.587	0.404	0.368
1 and 3	0.771	0.512	0.028
2 and 3	0.747	0.459	0.292

With the exception of observers 1 and 3 on upper live canopy volume, these correlations are quite low, indicating a general lack of consistency among observers. This result raises serious concern regarding the validity of this measurement. Either additional training is required to ensure better consistency among observers or this measure may need to be discarded in the future for lack of reliability.

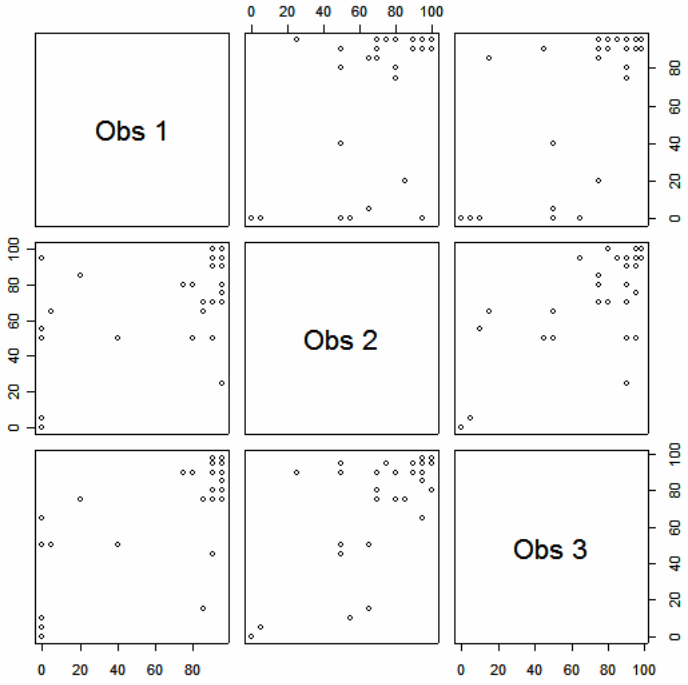

Fig. 12. Pairwise scatter plots of estimates of upper live canopy volume.

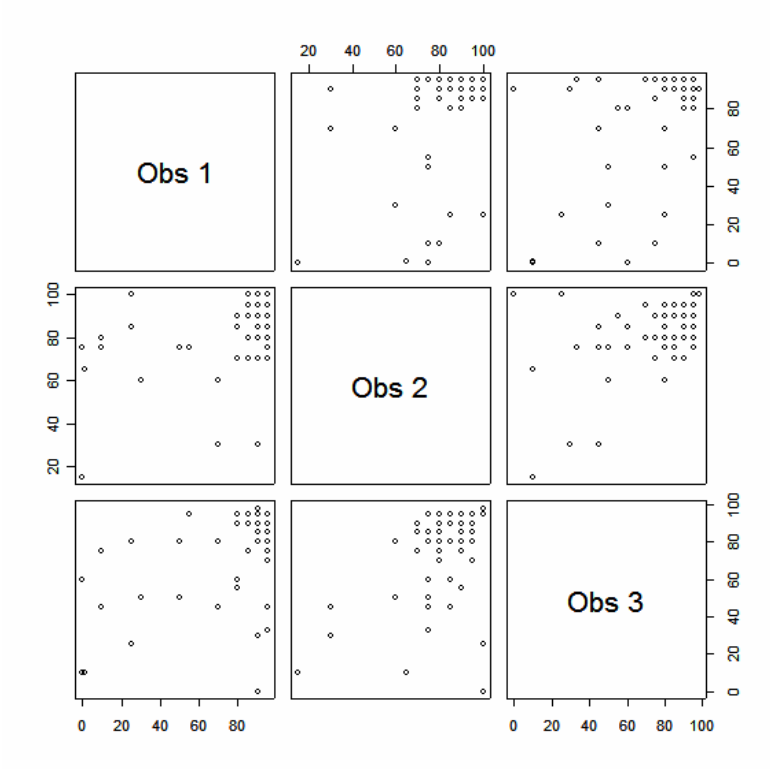

Fig. 13. Pairwise scatter plots of estimates of middle live canopy volume.

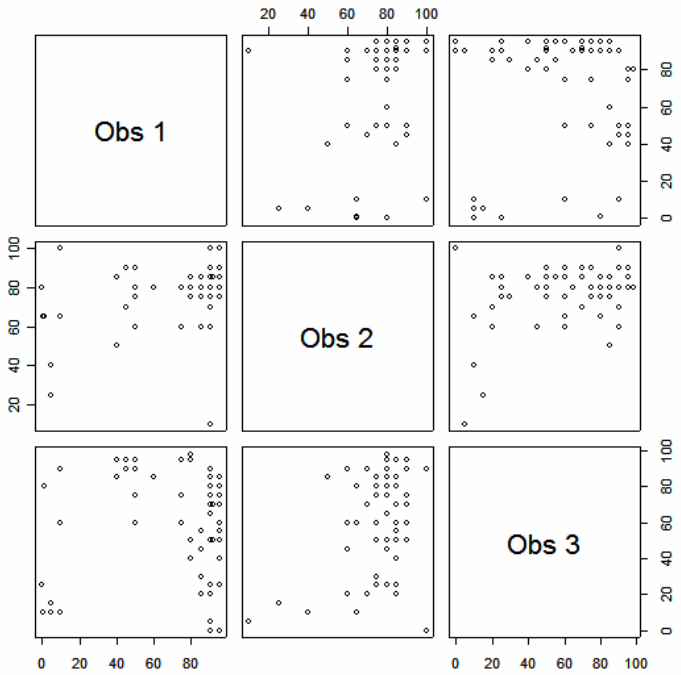

Fig. 14. Pairwise scatterplots of estimates of lower live canopy volume.

Mountain Pine Beetle and Mistletoe

There was no observer variability for the presence/absence of these 2 pests of whitebark pine.

Other Indicators

Five additional indicators of tree health were added after the start of the summer field season. These were instances of rodent chewing, flagging, bark swelling, roughened bark, and oozing sap. These were recorded for 43 trees on 5 transects. Results are summarized below (Table 10). Oozing sap was noted on 7 trees but in only 2 cases did more than one observer note an instance of this on a single tree. Roughened bark was noted on 15 different trees but in only 2 cases did more than one observer record rodent chewing on the same tree. Swelling was noted on 5 trees and in each case only one observer recorded swelling. Flagging was noted on 20 trees but in only 9 cases did 2 or more observers note flagging on the same tree. Rodent chewing was noted on 10 trees and on 7 by 2 or more observers.

Table 10. Instances of 5 potential diagnostics recorded on 43 trees by 3 different observers.

Observer	Oozing sap	Rodent chewing	Flagging	Swelling	Roughened bark
1	3	6	11	2	8
2	5	7	18	2	3
3	3	12	24	1	9

Future Considerations

Stratification

The sampling design for long-term monitoring will almost certainly involve stratified sampling. We have not decided on appropriate strata and indeed one of the goals of this summer's effort is to potentially identify relevant stratifying variables. Some sort of post-stratification may be necessary for analysis of the data collected this summer depending on how many transects are ultimately run. We have given some thought to potential strata, however. One potential pitfall to avoid is to not use strata that will change over time.

Preliminary data on blister rust infection rates is available from data collected over the past 10 years by field crews working for Gardiner District Wildlife Biologist Dan Tyers. Data have been collected on several hundred transects located primarily in the Absaroka-Beartooth Wilderness Area north of Yellowstone National Park. Data were also collected on more than 100 transects

located within the GYE by field crews supervised by USGS Research Biologist Katherine Kendall. Although these transects were not collected using a probability based sampling design they do indicate that infection rates tended to increase with elevation. However, the relationship is not particularly strong.

It may also be logical to stratify based on access with units far from roads, trails, and overnight facilities being assigned sampling weights smaller than more accessible units. Although field crews could certainly camp out during visits to inaccessible units, we need to minimize the need for camping due to safety concerns. Preliminary inquiries have indicated that elevation and access are likely strongly associated, with roads being located disproportionately at lower elevations. Thus, stratification based on access may also serve as a stratification of elevation. A final determination of strata will be made at the end of the 2005 effort.

Observer Variability

While other studies have recognized that field identification of blister rust can be difficult, we know of no other monitoring programs that have explicitly estimated the effects of variability among observers. Our results have indicated substantial variability among observers in several measurements. For certain measurements (e.g., crown ratio), this extensive variability may cause us to reconsider whether the measurement is reliable or contains any value for this program. For other measurements (e.g., primary blister rust severity measures), the variability may imply a need to refine our methods and/or to develop a more effective training program. If training is not sufficient to reduce observer variability to reasonable levels, then we may need to consider incorporating observer variation in our future analyses by incorporating that source of variation in our statistical models.

Temporal Design

Because it is infeasible to obtain a sufficient sample of transects in any one season, our monitoring effort will likely entail a repeating panel design, where the total sample is accumulated over several years and then each panel (i.e., the sample from a given year) is sampled again after several years (probably on the order of 5-10 years). This temporal design works well for whitebark pine because white pine blister rust (the primary focus of our monitoring objective) is a slow acting pathogen that has relatively little inter-annual variation. Thus, sampling a given panel every year would be extremely inefficient. Sampling panels at longer intervals allows us to develop a sufficient sample size over several years while maintaining a reasonable ability for potential changes to be detected. The final panel design will be determined and documented within our monitoring protocol.

Within Stand Variation

Preliminary analysis from our 2004 efforts have indicated that within stand variation may be a minor component of the overall population variance. However, this assessment was based on only six polygons (stands) that had replicate transects within the stand. During 2005 we will attempt to obtain a substantially great sample of within stand replicates and use these data to assess the need for within stand replication in our overall sampling design.

Additional Objectives

Since this project was initiated, additional objectives (discussed above) have been introduced that may be necessary to fully understand the viability and health of whitebark pine in the GYE. Over the next year, we will continue to evaluate and refine these objectives so as to make a determination as to their potential to be incorporated into our monitoring effort.

Acknowledgments

We thank our biological technicians Justin Hof and Amy Jesswein for their perseverance in the field, Maria Newcomb for field training, Veronika Klukas for project administration, Rob Daley, Liz Davy, Dale Dawson, Rachael Feigley, Melissa Jenkins, Bill Oliver, Andy Pils, Jim Robertson, Steve Schadt, Anne Schrag, and John Schwandt for their advice, field support and use of Forest Service and Park Service cabins, and the Royal Teton, B-Bar, and T.E. ranches for access through their properties. We are grateful to Dan Tyers (USFS) and Kate Kendall (USGS) for allowing us access to their data for some preliminary assessments relating to our design. Funding for the field work portion of this project was provided by USFS Forest Health Monitoring. Additional funding and support for preliminary analysis of data, mapping, additional field gear, and vehicle support was provided by NPS (Greater Yellowstone Network), USGS (Interagency Grizzly Bear Study Team) and the Greater Yellowstone Coordinating Committee.

Literature Cited

Arno, S.F. 1986. Whitebark pine cone crops--a diminishing source of wildlife food? Western Journal of Applied Forestry 3:92-94.

Campbell, E.M., and J.A. Antos. 2003. Postfire succession in *Pinus albicaulis – Abies lasiocarpa* forests of southern British Columbia. Canadian Journal of Botany 81:383-397.

Carlson, C.E. 1978. Noneffectiveness of Ribes eradication as a control of white pine blister rust in Yellowstone National Park. Report No. 78-18. Missoula, Montana, USA.

Despain, D.G. 1990. Yellowstone vegetation: consequences of environment and history in a natural setting. Roberts Rinehart, Boulder, Colorado, USA.

Dixon, B.G. 1997. Cumulative effects modeling for grizzly bears in the Greater Yellowstone Ecosystem. M.S. Thesis. Montana State University, Bozeman, Montana, USA. 192pp.

Haroldson, M.A., S. Podruzny, and R. Renkin. 2004.00Whitebark pine cone production. Pages 45-46 *in* C.C. Schwartz and M.A. Haroldson, editors. Yellowstone grizzly bear investigations: annual report of the Interagency Grizzly Bear Study Team, 2003. U.S. Geological Survey, Bozeman, Montana, USA.

Hirt, R.R. 1942. The relation of certain meteorological factors to the infection of eastern white pine by the blister-rust fungus. New York State College of Forestry, Syracuse University, Syracuse, New York. Technical Publication 59. 65pp.

Keane, R.E. 2001. Successional dynamics: modeling an anthropogenic threat. Pages 159-192 *in* D.F. Tomback, S.F. Arno, and R.E. Keane, editors. Whitebark pine communities. Island Press, Washington, D.C., USA.

Kendall, K.C., and R.E. Keane. 2001. Whitebark pine decline: infection, mortality, and population trends. Pages 221–242 *in* D.F. Tomback, S.F. Arno, and R.E. Keane, editors. Whitebark pine communities. Island Press, Washington, D.C., USA.

Kipfmueller K.F., T.W. Swetnam, and P. Morgan. 2002. Climate and mountain pine beetle-induced tree mortality in the Selway-Bitterroot Wilderness Area. Final Report to the USFS Research Joint Venture Agreement #RMRS-99611-RJVA. http://www.ltrr.arizona.edu/~kurt/research/kkipf_beetles.pdf.

Koteen L. 2002. Climate change, whitebark pine, and grizzly bears in the Greater Yellowstone Ecosystem. Pages 343-414 *in* S.H. Schneider and T.L. Root, editors. Wildlife responses to climate change: North American case studies. Island Press, Washington, D.C., USA.

Logan, J.A., and J.A. Powell. 2001. Ghost forests, global warming, and the mountain pine beetle (Coleoptera: Scolytidae). American Entomologist 47(3):160-172.

Mattson, D.J. 2000. Causes and consequences of dietary differences among Yellowstone grizzly bears (*Ursus arctos*). Dissertation, University of Idaho, Moscow, Idaho, USA.

Mattson, D.J., B.M. Blanchard, and R.R. Knight. 1992. Yellowstone grizzly bear mortality, human-habituation, and whitebark pine seed crops. Journal of Wildlife Management 56:432-442.

Mattson, D.J., K.C. Kendall, and D.P. Reinhart. 2001. Whitebark pine, grizzly bears and red squirrels. Pages 121-136 *in* D.F. Tomback, S.F. Arno, and R.E. Keane, editors. Whitebark pine communities: ecology and restoration. Island Press, Washington, D.C., USA.

McDonald, G.I, R.J. Hoff. 2001. Blister rust: an introduced plague. Pages 193-220 *in* D.F. Tomback, S.F. Arno, and R.E. Keane, editors. Whitebark pine communities: ecology and restoration. Island Press, Washington, D.C. USA.

Perkins, D.L., and D.W. Roberts. 2003. Predictive models of whitebark pine mortality from mountain pine beetle. Forest Ecology and Management 174:495–510.

Six, D.L., and M. Newcomb. In preparation. A rapid method for rating whitebark pine incidence, severity, and distribution within individual trees in whitebark pine. Western Journal of Applied Forestry.

Steele, R., S.V. Cooper, D.M. Ondov, D.W. Roberts, and R.D. Pfister. 1983. Forest habitat types of eastern Idaho-western Wyoming. USDA Forest Service General Technical Report INT-144. 122pp.

Tomback, D.F., S.K. Sund, and L.A. Hoffmann. 1993. Post-fire regeneration of *Pinus albicaulis*: height-age relationships, age structure, and microsite characteristics. Canadian Journal of Forest Research 23:113-119.

Tomback D.F., S.F. Arno, and R.E. Keane. 2001. The compelling case for management intervention. Pages 3-25 *in* D.F. Tomback, S.F. Arno, and R.E. Keane, editors. Whitebark pine communities: ecology and restoration. Island Press, Washington, D.C. USA

Tomback, D.F., R.E. Keane, W.W. McCaughey, and C. Smith. 2004. Methods for surveying and monitoring whitebark pine for blister rust infection and damage. Whitebark Pine Ecosystem Foundation, Missoula, Montana, USA.

Tomback, D.F., R.E. Keane, W.W. McCaughey, and C. Smith. 2005. Methods for surveying and monitoring whitebark pine for blister rust infection and damage. Whitebark Pine Ecosystem Foundation, Missoula, Montana, USA. (revision of Tomback et al. 2004).

U.S. Forest Service. 2002. Common Stand Exam Guide for Region One. U.S. Department of Agriculture, U.S. Forest Service, Region 1, Missoula, Montana, USA.

U.S. Fish and Wildlife Service. 1993. Grizzly bear recovery plan. U.S. Fish and Wildlife Service, Missoula, Montana. 181pp.

U.S. Fish and Wildlife Service. 2003. Final conservation strategy for the grizzly bear in the Yellowstone Ecosystem. U.S. Fish and Wildlife Service, Missoula, Montana, USA.

Van Arsdel, E., A. Riker, and R. Patton. 1956. The effects of temperature and moisture on the spread of white pine blister rust. Phytopathology 46:307-318.