***Overview of planned data analyses for Jenny and Joan***

(1) Determine the current extent, severity, and rate of spread of WPBR infection:

Using field data collected during the summers 2015 and 2016, we will calculate plot-level estimates of extent, severity, and spread rate for each white pine species. All calculations will be based on data from the permanent monitoring trees. We define extent (E) simply:

where *Nit* is the number of plots at time t (i.e., first resurvey in 2015/2016) with at least one infected individual and *Nt* is the total number of plots surveyed at t. We will calculate two measures that address the severity of the disease – the frequency of the infection in the population, defined as incidence (*I*), and tree-weighted index of disease progression (*DP*). Incidence is defined as:

where is the number of trees in plot j at time t with signs of WPRB and is the number of white pine trees in plot j at time t. DP is defined as:

where *k* is the number of white pine trees in the plot and is the blister rust index for tree k. *RI* is calculated from the count of cankersand size of infected pines (Duriscoe and Duriscoe 2002):

where *cs* is 0 for 0 branch cankers, 1 for 1-3 branch cankers, 2 for 4-9 branch cankers, 3 for 10-25 branch cankers, 4 for >25 branch cankers, and 5 for bole canker; DBH is the tree diameter at breast height (in inches – if tree diameter is greater than 25 inches, then DBH = 25), unless the *cs* component is zero, in which case *RI* = 0.

Our primary estimate for spread rate (SR) among plots is:

where *I1*is the incidence of WPRB at time *1* (2013-2016), *Io* is the incidence at time 0 (1995-1999), and ∆*t* is the sampling interval in years between sample times *t1*and *t0.*

To summarize plot-level changes in WBRP distribution and dynamics, we will bin our plots by two classifications: 1) species of the dominant white pine host; 2) the three major watersheds in SEKI. We will then compare extent, incidence, disease progression, and spread rate of WPBR among bins. For the three metrics with replication (*I, DP*, and *SR*), we will report the means and standard errors and test for significant change using an ordinary t-test for *SR* and a paired t-test for *I* and *DP*. We will also describe other plot and tree-level statistics. For example, we will test for differences in growth rate, measured by DBH between sample times *t1*and *t0* , among trees previously infected with blister rust, currently (but not previously) infected with blister rust, and blister-rust free trees. For each white pine species, we will calculate means and standard errors of associated *Ribes* and *Pedicularis* spp. crown cover and presence/absence, as well as the average number of trees with *Dendroctonus* spp. infestations. We also will also attempt to isolate the effect of fire vs. other mortality agents on white pines by adding fire as a treatment effect.

Based on our summaries and analysis of the field data, we will create tables designed to inform managers. The summary statistics will be organized into two tables that describe: 1) our WPBR results and the plot characteristics for each white pine species, and 2) WPBR results and plot characteristics grouped by the major watersheds. The table that describes WPBR results for every SEKI’s white pines will display the summaries for *E, I, DP, RI,* and *SR.* Plot characteristics to be included in a table will be: DBH, crown cover + presence/absence of *Ribes* and *Pedicularis* spp., and number of trees infested with *Dendroctonus* spp.

Using a subset of the summary data, we will develop a SEKI-wide blister rust map, as well as WPBR maps by major watersheds. WPBR plot-level *I* and *DP* will be projected on a SEKI-wide map that displays all white pine plots with and without blister rust and disease progression (visually described by icon size). We will create a similar map for SEKI’s watersheds with their associated WBPR incidence and disease progression to help prioritize areas that are more threatened by WPBR.