**Guidelines for Gene Conservation Seed and Cone Collections**

Last revised: February 17, 2010

Because genetic variation is often tied to patterns of environmental variation, the collection strategy emphasizes collections from many diverse locations throughout a species’ range. A stratified sampling design will be used to sample the breadth of genetic variation for each species based on seed zones as defined by local experts. While not all seed zones may be based on scientific data at present, regional geneticists and botanists have used the best information available to delineate current seed zones; these will be modified as information becomes available. The objective is to sample a minimum of 50 trees from a minimum of 10 locations dispersed throughout each seed zone. This number should provide sufficient genetic variation to reestablish the population since it will contain over 95% of the genetic variation found in the population; however, these numbers will not conserve all the low frequency alleles, such an effort is outside the scope of this project.

The following is a set of guidelines for sampling. Up to 5 trees at a location can be counted towards the 50-tree total. Where possible, more trees can be collected at a location. A single location is defined as having sample trees within 1 mile of each other and for which no significant changes are required on the collection sheet other than providing GPS coordinates for the trees. Thus a stand or location is defined in both terms of distance and having a common environment with similar plant associations, soils and landscape position. Collection trees should be spaced preferably at least 100 feet apart to reduce the likelihood of sampling closely related individuals.

For each site, the minimum information will be collected and entered into GENDAT: species, location (lat/long datum, how collected), ownership, elevation, single/multiple tree collection, if multiple tree collection then the number of trees at the site, and the number of seed per tree. Additional information desired includes: habitat, associated species and ecological site descriptor, slope, aspect, and soil type.

In an optimal situation, the first 400 viable seeds from each tree are slated to be put into long-term storage at the USDA-ARS National Center for Genetic Resources Preservation (NCGRP, formally NSSL) in Fort Collins, CO; access to this seed is highly restricted and would require approval from Forest Health Protection in Washington, DC (Gary Man). An additional 100 seed will be stored at local facilities in the Region/station where it was collected for gene conservation purposes or other agreed upon facility (to be further defined). The next 600 seed are to be put into a working collection that will be available to researchers for rust screening and research. Access to this seed requires approval from the Regional Geneticist, Center Geneticist, or Scientist who collected the seed. Any remaining seed would be available for restoration and under the control of the collectors.

If the 1,100 seed target cannot be achieved for an individual tree, then the following minimums should be followed; 200 seed should be put into long-term storage at NCGRP, 50 seed should be stored at “local” facilities.

Finally, if the 250 seed minimum cannot be achieved, collections can be bulked by site (specific details need to be defined). It is preferred that individuals in a bulk should be kept in separate packages as a sub-lot. If such collections are not possible, an existing bulk collection can be used as a gene conservation seed source (if proper documentation is available) until suitable collections are available. The overall goal of a bulked collection would be to have 2,000 seed for NCGRP and 500 seed backed up at local facilities.