PARTICIPATORY GENETIC IMPROVEMENT: LONGLEAF PINE

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University-industry-state cooperative tree improvement has been highly successful in the southern United States. Over nearly 60 years, three cooperative programs have led the way in developing and deploying genetically improved planting stocks for loblolly (*Pinus taeda* L.) and slash (*P. elliottii* Engelm.) pines. However, much lower levels of success have been achieved for species of lesser economic importance such as longleaf (*P. palustris* Mill.) and shortleaf (*P. echinata* Mill.) pines and the many southern hardwoods. The result is that many important forest tree species are in need of sustained genetic enhancement for both short-term silvicultural and long-term conservation purposes. To address this need, we are studying the concept of participatory plant breeding (Atlin and others 2001, Ceccarelli and Grando 2007) for application in forest trees. In particular, we are working on a program for longleaf pine where three types of forest landowner participants would be involved covering the main functions in tree breeding: mother tree selection, progeny testing, and seed production. The program would be organized through a web portal with a back-end database containing the tree, test planting, and orchard data. The program's goal is to provide landowners with an opportunity to actively participate in a region-wide longleaf pine genetic improvement and gene conservation program. In addition, all landowners would benefit from the low-cost availability of well-bred longleaf pine planting stock for optimal performance in a changing climate.

Several decisions are required in establishing a participatory tree breeding program including base population and population structure, target participants and their environmental conditions, the breeding and testing scheme, the improved materials deployment scheme, and how the work is organized among the participants. For longleaf pine, we suggest a base population of about 200 trees per ecoregion and maintaining this size over generations (fig. 1). An ecoregion partially gets at the environmental conditions question in that the associated population is tested and selected for performance within these areas. The areas are defined by similar climate and photoperiod conditions. Within each ecoregion, more specific environmental conditions can be defined (sand hills versus piedmont versus montane), and we suggest that these be used for deployment. For example, within an ecoregion, progeny tests may be established on different physiographic regions or major soil types. Selections from these tests may be used to set up clonal seed orchards specific for the within ecoregion environmental type, or if converting the progeny tests to seedling seed orchards, their seeds can be directed towards similar environmental types. Ecoregions can be defined in many different ways. A couple of approaches seem most useful for longleaf pine, including Craul and others (2005) (site zones) and Griffith and others (2008) (EPA levels III, IV), especially when combined with winter hardiness information (Schmidtling 2001). Potter and Hargrove (2012) have developed a quantitative method for determining ecoregions and projecting their future locations based on climate models that may prove more useful. In addition, practicalities concerning participants' locations and interests and the need to sample and conserve the whole species will affect the number of ecoregions and their borders. One possible case is depicted in figure 1, where six ecoregions are defined, resulting in an overall base population size of about 1,200 trees.

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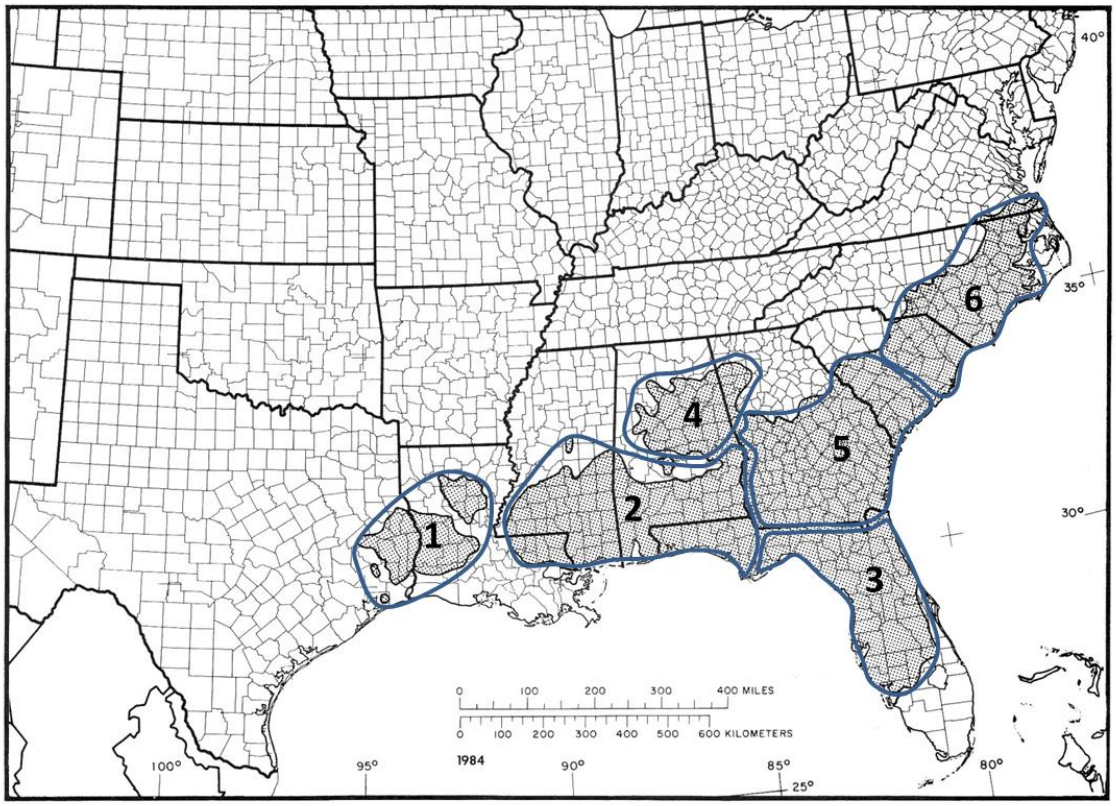

Figure 1—*The native range of longleaf pine.*

Figure 1--The native range of longleaf pine (gray shade) with proposed longleaf pine breeding zones (ecozones, numbered 1 to 6).

The breeding and testing scheme needs to meet a few criteria, including maintaining large enough base populations to insure gene diversity and the potential for artificial and natural selection (Eriksson and others 1993), and be small and simple enough to allow participants to manage and maintain the program indefinitely. We meet the first criteria by starting with 200 unrelated trees per ecoregion and six ecoregions (Echt and others 2011, Gapare and others 2008, Lawrence and others 1995). These trees are provided by the participants and should meet some minimum standard of condition in their native environment. This could be a tree that has tested well in a previous tree improvement program or one that exhibits a good phenotype and cone crop potential. Of course, availability of fresh cones or viable seeds is needed as well, since the scheme relies on progeny performance in the next generation for forward selection. Seeds will be germinated and seedlings transplanted into progeny tests that provide family and individual-tree performance information serving as a basis for selection to establish both seedling and clonal seed orchards. All progeny will be from wind pollinations, further simplifying the participants' workload with recurrent selection. Figure 2 depicts the open-pollinated, recurrent breeding and selection scheme (adapted from Simmonds 1979) through three generations with seed orchard development and seed deployment options at each generation.

Participatory tree improvement offers the forestry community an opportunity for collectively developing and maintaining genetic materials for tree planting and gene conservation. It can range from a highly centralized program that may resemble university-industry-state cooperatives to a decentralized program where essentially all components of the program are managed and conducted by the participants. An intermediate approach seems most likely to succeed in species such as longleaf pine that have some economic and ecologic importance but not to the

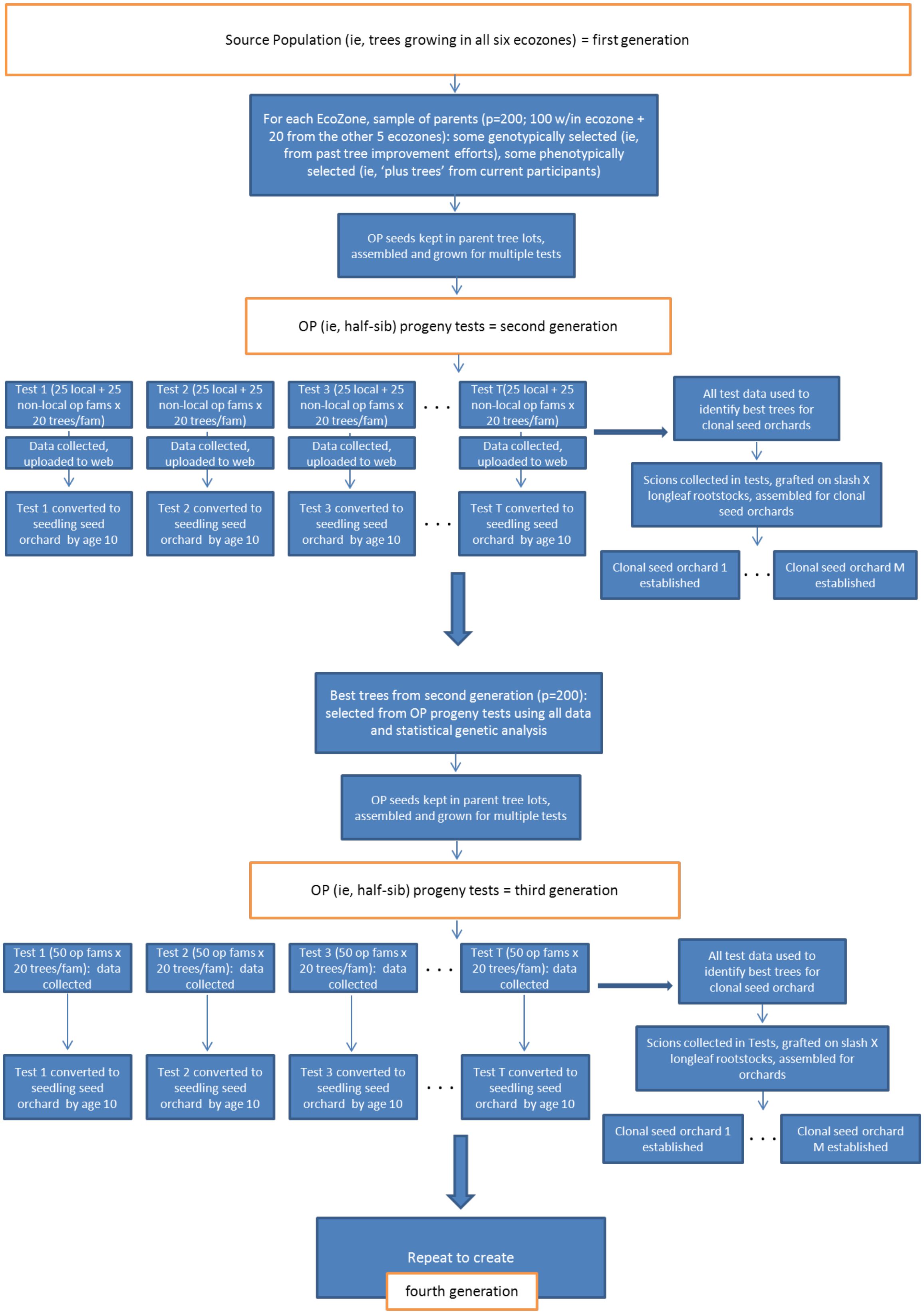

Figure 2--Proposed participatory breeding plan for longleaf pine.

level of the major industrialized species such as loblolly pine or the very high-valued hardwoods such as black walnut (*Juglans nigra* L.). In such a program, we can anticipate a geneticist coordinating the program with limited technical and clerical support and a network of participating landowners. These landowners could range from private individuals or companies to non-governmental organizations to public agencies, where they fall into three basic functions: plus-tree identification, performance testing, and cone/seed production. Plus-tree identification participants collect open-pollinated cones from their favorite tree(s) and document the tree(s) in the project's online database. The coordinating geneticist will ensure that the plus trees meet a basic phenotypic standard (i.e. desirable traits or physical attributes) and originate on a variety of site types (i.e. uplands, sand hills, flatwoods) and their respective plant associates (e.g. wiregrass, bluestems, saw palmetto). Performance testing participants (a landowner or a group of landowners) will identify potential sites, choose the test planting sites, establish tests, and grow the trees. This group will also collect the needed data and collect cones for establishing next-generation performance tests. Cone/seed production participants (a landowner or group of landowners) will produce seed from the rogued performance tests (i.e. seedling seed orchards), or they may establish a grafted (i.e. clonal) seed orchard to produce the highest genetic quality seed. Clear, reliable, and timely communications facilitated by the internet and mobile/cloud computing offer new opportunities for distributed forest research and monitoring and tree improvement should benefit from this development.

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LITERATURE CITED

Atlin, G.N.; Cooper, M.; Bjørnstad, Å. 2001. A comparison of formal and participatory breeding approaches using selection theory. Euphytica. 122: 463-475.

Ceccarelli, S.; Grando, S. 2007. Decentralized-participatory plant breeding: an example of demand driven research. Euphytica. 155: 349-360.

Craul, P.J.; Kush, J.S.; Boyer, W.D. 2005. Longleaf pine site zones. Gen. Tech. Rep. SRS–89. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station. 23 p.

Echt, C.S.; Crane, B.S.; Nelson, C.D. 2011. Establishing restoration seed reserves in national forest system seed orchards. In: Nelson, C.D.; Rousseau, R.J.; Yuceer, C., eds. Proceedings of the 31st southern forest tree improvement Conference: 46-49.

Eriksson, G.; Namkoong, G.; Roberds, J.H. 1993. Dynamic gene conservation for uncertain futures. Forest Ecology and Management. 62:15-37.

Gapare, W.J.; Yanchuk, A.D.; Aitken, S.N. 2008. Optimal sampling strategies for capture of genetic diversity differ between core and peripheral populations of *Picea sitchensis*. Conservation Genetics. 9:411-418.

Griffith, G.E.; Omernick, J.M.; McGinley, M. 2008. Ecoregions of the United States - level IV (EPA). Environmental Information Coalition, National Council for Science and the Environment. http://www.eoearth.org/article/Ecoregions_of_the_United_States-Level_IV_(EPA). [Date accessed: August 24, 2011].

Lawrence, M.J.; Marshall, D.F.; Davies, P. 1995. Genetics of genetic conservation. I. Sample size when collecting germplasm. Euphytica. 84: 89-99.

Potter, KM; Hargrove WW. 2012. Determining suitable locations for seed transfer under climate change: a global quantitative method. New Forests. 43.5-6: 581-599.

Schmidtling, RC. 2001. Southern pine seed sources. Gen. Tech. Rep. SRS-44. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station. 25 p.

Simmonds, N.V. 1979. Principles of crop improvement. New York: Longman, Inc. 408 p.