Dynamic Genetic Conservation in the Presence of Invasive Insect and Pathogen Threats to Forest Tree Species of the United States[1]

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Ex-situ genetic conservation focused on collection and storage of seed can play an important role in conserving the genetic diversity of species under grave threat by biotic organisms or a changing climate. However, *ex-situ* genetic conservation is primarily a static activity and does not allow for evolution of the species under a continuing, persistent impacting agent. Invasive insects and pathogens, once established, usually become permanent components of the ecosystem, continuously interacting with the target species. Dynamic genetic conservation seeks to actively harness the genetic variation within the species to develop a new equilibrium under which species restoration can proceed with a realistic chance of at least partial recovery and persistence of the affected tree species. The iterative process of traditional tree improvement has a long history of utilizing genetic variation to increase population level resistance to insects and diseases, and (when done right) is highly compatible with and promotes the primary goal of dynamic genetic conservation of maintaining evolutionary processes. This approach is being taken to achieve dynamic genetic conservation of several threatened species including species of ash (*Fraxinus* spp.) that are gravely threatened by emerald ash borer (*Agrilus planipennis*). Given that the introduction and establishment of invasive insects and diseases will likely continue, we suggest that the time is right to strengthen, expand, and invest in forest genetics and tree improvement programs in order to implement dynamic genetic conservation programs for the ever increasing number of threatened forest tree species. Biotechnology and genomics may provide tools to potentially accelerate breeding programs, but such tools are not necessary for, nor can they replace the need for, successful breeding programs. To maximize the likelihood of operational application of such tools, they should be developed within the context of existing breeding programs. As the development and application/deployment of these tools are completely dependent on integration with a breeding program, if funding is limiting, the breeding program should be the priority.

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