COMMON MISCONCEPTIONS ABOUT FOREST TREE BREEDING, A VALUABLE TOOL FOR ADDRESSING FOREST HEALTH ISSUES

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ABSTRACT

Breeding programs are an important tool for managing invasive insects and diseases causing high mortality rates and even threatening extinction of some of our forest tree species. The emerald ash borer (EAB) invasion of North America, as one example, has resulted in five North American ash species being listed as “critically endangered” on the IUCN red list (IUCNredlist.org). Impacts from such significant losses are far-reaching. Wildlife species that depend on threatened tree species can also be at risk of extinction, Mortality of riparian tree species such as Eastern hemlock, currently under attack by the hemlock woolly adelgid, can impact water quality. Economic impacts can be far-reaching, and include the costs of removing and replacing trees, and the loss of valuable income sources. This income loss is especially pertinent to rural communities reliant on both traditional – such as lumber, pulp, paper, and fiber and non-traditional forest products – ginseng, morels, and goldenseal. Additionally integral to rural economies are recreational opportunities provided by healthy forests, such as camping, hiking, canoeing, kayaking, hunting and fishing. In Hocking County, Ohio, for example, recreational tourism supports one out of every seven jobs and generates more than 115 million dollars annually (Apsley et al. 2014). Hemlock trees are cornerstone species in these recreation areas and their loss due to hemlock Wooly Adelgid (HWA) pose a serious threat to local communities.

Once an invasive insect or disease has become established, it is difficult, if not impossible, to remove. Breeding programs develop seed sources with appropriate levels of resistance for restoration, and are sometimes are the only available option for managing forest health issues. Tree breeding is a repetitive process of selection, mating and testing trees with the goal of producing improved populations of parent trees to produce genetically diverse, adapted seed. Each generation of breeding will produce seed lots with an increased proportion of resistant individuals and the average level of resistance of the popula- tion will be higher. The goal is to incorporate many different types (genes, gene variants) of resistance and preserve genetic diversity so that resistance cannot easily be overcome and the population maintains the ability to adapt to future threats and changing environmental conditions. Not every seedling will be resistant, but improved seed lots that have undergone rigorous testing, give forest managers an idea of what rate of mortality can be expected, and they can adapt their planting plans accordingly. However, programs to breed for improved host-resistance are often not pursued, or are only considered once all other options have failed, costing valuable time. Misconceptions about forest tree breeding programs may contribute to hesitation on the part of managers to pursue them as a forest health priority. These misconceptions will be discussed below, to offer clarification of both the potential and the limitations of breeding programs.

Myth: a resistant tree must be completely “bulletproof.” When an invasive pest is introduced, the popula-

tion of host trees have not been previously exposed, so they have not been able to develop resistance over a long period of co-evolution. This does not mean that the population is completely devoid of resistant trees. Each tree is a unique individual with its own set of unique traits. Within genetically diverse populations, individual trees can have a wide range of responses, or phenotypes, to the invasive threat. The naturally occurring high levels of genetic diversity found in most forest tree species provides one of the most valuable tools for addressing forest health issues. Although trees that are highly susceptible to the insect or disease are likely to be most common, because there has been no selective advantage to such traits prior to introduction of the invasive pest or pathogen, there may be some infrequently occurring individuals with certain combinations of genes or gene variants that confer a variety of resistance traits, ranging from partial resistance or tolerance to high levels of resistance. Trees with partial resistance may only be able to live a few years longer than susceptible trees, but this does not mean that they are not "resistant" enough to provide a solution. When two partially resistant parent trees are bred, they may produce some progeny that get the best genes from each parent, and as a result are more resistant than both parents. For example, "lingering ash" trees that have survived long term EAB infestation when all surrounding ash trees have died, have been shown to have increased measurable mechanisms that allow them to mount a defense against EAB (Koch et al. 2015). Preliminary results indicate that breeding two lingering ash trees does produce some progeny with even greater defenses against EAB than either parent.

Myth: breeding takes too long, is too expensive and isn't successful. Although every program may not be successful, there are many examples of programs that have achieved success, and some that have done so in relatively short periods of time (Sniezko and Koch 2017). For example, the first Port-orford cedar seed lot having increased resistance to the root rot pathogen, *Phytophthora lateralis*, was released within five years after the start of the resistance program at the Forest Service's Dorena Genetic Resource Center. Resistant seedlots were available for seven out of thirteen breeding zones of Port-Orford cedar within fourteen years (Sniezko et al. 2012). This rapid success contributed, in part, to Port-Orford cedar being downgraded from being listed as a "vulnerable" species on the IUCN red list in 2011, to "near threatened" in 2013 and is anticipated to be considered a species of "least concern" within 10 years (Farjon 2013). Another example is the U.S. Forest Service Northern Research Station's program breeding for American beech with resistance to beech bark disease, which deployed its first resistant seedlings within ten years of the start of the program and currently has nine regional seed orchards in seven states in various stages of development (Koch and Heyd 2013).

The length of time it takes for a breeding program to achieve successful deployment of seed with improved resistance is dependent on many different factors. For example, the genetic complexity of resistance and the ease or difficulty in being able to identify appropriate trees can influence timelines. The more genetically complex resistance is, the more difficult it may be to breed for, leading to potentially longer time periods (more generations of breeding) until appropriate levels of resistance can be deployed. However, if substantial resistance (frequently occurring and high level of resistance) can be identified in existing natural populations, this can reduce the amount of time to produce improved seedlots. Developing methods to identify resistance in seedlings and parent trees plays an important role in breeding programs. Protocols that allow efficient high-throughput screening to select resistant material can reduce both the time and cost involved in a successful breeding program. The biology of the tree species can also impact the length of time a breeding program requires. For example, the time it takes for a tree to reach sexual maturity and produce seeds can range from less than ten years up to several decades. Hormone treatments and various lighting and cultural regimes are commonly used in some tree species to induce flowering as early as one to three years of age. Another important factor is continuous support of the breeding program; programs that go through rounds of starting and stopping, typically tied to success or failure of obtaining sources of "soft" funding, are much less efficient than those that have continuously committed resources.

Nevertheless, the time frame of these examples and many other breeding programs is consistent with the length of time and resources dedicated to alternative management strategies, such as the development of biocontrol. Despite significant resources being committed to the development of EAB and HWA biocontrol programs over a period of more than 15 years, and significant progress being made, there is yet to be definitive evidence of biocontrol leading to improved tree health. Combining both biocontrol and improved host resistance through breeding programs may be the best strategy for retaining the tree species these invaders are currently threatening (Duan et al. 2015).

Myth: genomics and biotechnology alone can solve the problem. The advent of molecular biology and the age of genomics, has created much enthusiasm about the use of genomics and genetic modification to accelerate the production of resistant trees. The use of genomics to develop methods such as marker assisted selection (MAS) or genomic selection (GS), can streamline the breeding process by using markers to select seedlings or parent trees that are resistant. However, the development of such strategies depends on resources produced by breeding programs – large numbers of trees or seedling with known parentage and phenotypes (resistant or susceptible). Similarly, genetic modification through transgenic or gene-editing technologies, cannot replace a breeding program. These techniques may be able to create a single resistant tree (genotype) that will require costly regulatory authorization to plant in natural forests. For successful landscape scale restoration, the genetically modified tree will need to be integrated with a traditional breeding program to incorporate genetic diversity and maintain adequate adaptive capacity to multiple stresses and environments. Although genomic tools and genetic modification techniques can play an important role in understanding the underlying mechanisms of resistance and have the potential to enhance breeding programs, investing in such research alone will not produce resistant tree. An active breeding program is a prerequisite for the successful development and implementation of such tools, but does not require such tools to be successful. Most, if not all, operational breeding programs do not utilize such tools, often due to high cost of implementation. Careful cost-benefit analysis should be considered prior to pursuing the development of such tools to augment breeding efforts.

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