

# Why and How We Improve Ontario's Forest

## Forest Genetics Ontario

Tree improvement in Ontario's forests is the opposite of high-grading.

Under high-grading practices of past generations, many of the trees left on the land when the best trees were removed tended to be the slower growing, malformed, or diseased individuals, and they formed the gene pool for the next forest.

The objective of tree improvement is to ensure that genes from the best trees on the landscape go into creating the next forest.

We select the finest specimens from a given area, collect and plant their seeds, and bring the seedlings together into a common garden, which we call a seed orchard. We test seedling families and remove the poorer performers, leaving the fastest-growing, straightest, healthiest trees to breed and thereby create the seed for the forest plantations.

Selecting good performers and saving seed is something backyard gardeners do, and indeed has been the foundation of agriculture down through the centuries. The gardener chooses the earliest-ripening tomato, the tastiest sweet corn, the heaviest-yielding squash, from which to save seed for next year's garden (Bubel 1988). In this way, centuries ago the aboriginal peoples of this continent developed maize, through repeated selection of the largest seed producers among wild grasses. Generations of this work led to the development of five distinct types of maize, before European colonization (Heiser, 1979). This is no different from what we are doing in our first generation of tree improvement in Ontario.

Genetic diversity is maintained, and even enhanced, in the future forest through these methods. Wild seed collected from random stands will have a significant relatedness. The nearest neighbours of

forest trees are generally relatives, as seed doesn't travel far – therefore, pollination takes place among a group of related individuals. When we bring the best and healthiest individuals we can find together in our seed orchard, they are surrounded by unrelated individuals with which to mate.

In our second generation work, we have chosen the best performing families among our seed orchard selections, and deliberately cross bred them with other high performing families. This is the same process Gregor Mendel used in his famous pea experiments in the mid-1800s, which led to the modern science of genetics (Mendel, 1866). Indeed, it is what backyard gardeners do when there are insufficient pollinators – not enough bees means not enough squash blossoms are pollinated. The gardener takes matters into his own hands – collecting male flowers and transferring pollen to female flowers of the same species.

We in Ontario do not use the techniques of genetic engineering to work with the forest gene pool. We do not transfer genes from cell to cell, we do not breach the cell wall or introduce genes in artificial ways. We work with nature's way of combining genes – bringing male and female cells together within the natural reproductive structures of the flower.

The resulting seed is grown into seedlings, which are planted in newly harvested forest areas. Unlike agriculture, we do not intensively control natural regeneration of the species that we are planting. Therefore the developing stand will have a combination of the genes from the orchards and the genes that are a natural legacy on the site. We also harvest in patches and over an 80–100 year rotation. So the improved genetic base will be slowly introduced to the natural landscape. Our future forest will be healthier and more diverse for this.

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Bubel, N. 1988. *The New Seed-Starters Handbook*. Rodale Press, Emmaus, PA. 363 pp.

Heiser, C.B. 1979. Origins of Some Cultivated New World Plants. *Annual Review of Ecology and Systematics*, 10: 309-326.

Mendel, J.G. 1866. Versuche über Pflanzenhybriden *Verhandlungen des naturforschenden Vereines in Brünn*, Bd. IV für das Jahr, 1865 Abhandlungen: 3-47. For the English translation, see: Druery, C.T and Bateson, W. 1901. Experiments in Plant Hybridization. *Journal of the Royal Horticultural Society* 26: 1-32.

<http://www.esp.org/foundations/genetics/classical/gm-65.pdf>