



UI Extension Forestry Information Series

Jurassic Forestry

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A revolution has occurred in the science of genetics and the wonderful and horrible possibilities are everywhere you look . . . “Disease Gene Located”, “Medicine Manufactured by Genetically Engineered Bacteria”, “Foreign Gene Inserted into Tomato”, “Dinosaurs on Rampage in Jurassic Park”! The big change is that we can now extract, read, and even change the genetic blueprint (DNA) of any plant or animal. Moral and ethical considerations aside, this is undoubtedly one of the biggest technological breakthroughs in the history of biology.

Changing the genetic code of plants and animals is certainly nothing new. Humans have dramatically altered the genes of every domesticated organism. In the past we’ve done this in two ways: by selecting genetic variation already present (e.g. choosing plants with big fruits to be the parents of next year’s crop will gradually produce a genetically different variety with larger fruits); or by transferring desirable genes from another species via hybridization. Until recently, we could only transfer genes between closely related species that could interbreed. In the process, undesirable traits (genes) would also be transferred to the hybrid.

With modern genetic engineering (biotechnology) we transfer *only* the gene we want and interbreeding isn’t required. Theoretically, we could cut nitrogen fixation genes out of alfalfa and put them into white pine, two plants that could never hybridize. Before we’re able to actually do this, however, we need to learn a lot about the genetic code of both alfalfa and pine.

Genetic engineering of trees is still a few years away, but there are some useful things we can do with DNA right now. My research looks at the DNA of wild plants to learn more about genetic differences. We

tend to think that species are fairly uniform genetically throughout their range, however, when we look at the DNA they frequently are not!

Bitterbrush, an important wildlife and cattle forage species we are studying, provides a good example. Managers have long been frustrated in their attempts to reestablish bitterbrush using commercially available seed. We have found considerable DNA differences throughout the range of the species; all bitterbrush is not alike and indiscriminately transferring seed from place to place does not appear to be wise. We will use our genetic data to create a seed zone map that will hopefully improve management success. We are also currently exploring basic genetic patterns in ponderosa pine, flowering dogwood, willow, and several rare and endangered plant species.

Success in agricultural enterprises has long been dependent on an intimate knowledge of the genetic makeup of the crop species. In contrast, we have attempted to manage wild species with little knowledge of their basic genetics. With DNA analysis, we can finally begin to unravel the genetic complexity of wild species and in turn become more efficient and successful resource managers.

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