Genetic Structure Of Northern Red Oak: Implications For Breeding And Silviculture

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Abstract -- Single embryos from each of 40 Northern red oaks (*Quercus rubra* L.) in 8 populations in Pennsylvania (40 embryos per population) were subjected to horizontal starch gel electrophoresis. Embryo tissue was electrophoresed without any stratification or germination and allele frequencies were tallied for 13 enzyme loci. The average expected heterozygosity over all loci and populations, Ht, was 0.233. An analysis of genetic structure with F- statistics indicated that red oak populations were nearly panmictic (Fis = -0.008). Red oak populations were very weakly differentiated with respect to isozyme allele frequencies (Fst = 0.009) with only about 1% of the observed genetic variation distributed among populations. In two populations, 30 additional acorns per tree were collected from 20 out of the 40 acorn-bearing trees to provide progeny arrays for a study of the mating system. The multilocus estimate of outcrossing, t, was 1.002 for stand 1 and 1.015 for stand 2. Neither estimate was significantly different from complete outcrossing (t = 1.0). An analysis of individual outcrossing rates indicated significant tree-to-tree variation in both stands, although 28 out of 32 individual outcrossing estimates were not significantly different from (t =1.0). A significant negative correlation (r = -0.69, p < .01) between family size and departure from complete outcrossing suggests that some of the variation among individual outcrossing rates mat have been due to sampling error. Because a large majority of individual outcrossing estimates were near (t = 1.0), open-pollinated family tests are likely to reflect real differences in mean breeding values of most families. High outcrossing rates also suggest that estimates of additive genetic variances and heritabilities are not likely to be biased upwards by increased genetic correlation among family members. If similar outcrossing rates occur in other red oak stands, then acorns harvested from seed production areas should be genetically diverse and largely non-inbred. Due to the large amount of within-population genetic variation, artificially regenerated stands derived from even a moderate number of seed-producting trees are likely to contain high levels of genetic variation. Furthermore, selections made only at the provenance level will probably still maintain high levels of genetic variation, although the relative magnitude of height growth variation among populations, within populations and within families suggests that maximum genetic gain could probably be achieved by selecting at all three levels.

Additional Keywords: isozyme, mating system, tree improvement.

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