Genotype X Environment Interaction in Florida Sources of Loblolly Pine Across the Lower Coastal Plain of the Southeastern USA

Mark J. Dieters¹ and Dudley A. Huber²

¹The University of Queensland, School of Land, Crop and Food Sciences, St Lucia, Queensland 4072 Australia

²CFGRP, The University of Florida, School of Forest Resources and Conservation, IFAS, Gainesville, FL USA

Florida sources of loblolly pine (*Pinus taeda* L.) have previously been reported to exhibit a high level of genotype x site interaction (GxE) when compared to other sources of loblolly in one set of progeny tests established by the Cooperative Forest Genetics Research Program (CFGRP). This may indicate the need for regionalization of breeding and deployment by separating sites on the coastal plains of the Atlantic and Gulf costs to minimize the level of within-region GxE. The study presented here aimed to elucidate patterns of GxE in Florida loblolly pine utilizing data on individual tree volume at 10-15 years of age collected from a total of 36 tests (27 open-pollinated and 9 control-pollinated tests) established by the CFGRP and its members across a diverse range of sites on the lower coastal plain of the south-eastern

USA. These tests were established over a 19-year period from 1970 to 1988 and comprised: five, largely genetically disconnected series of progeny tests; and, progeny from 117 plus-trees selected in a number of Florida counties, but chiefly from the Marion (46), Levy (22) and Nassau (19) counties. Climatic data was collated for each of the test-sites for the period from planting to the age of measurement. This climatic data, along with site characteristics calculated from the growth data (i.e. site index, and rust hazard) were used to classify the environment types represented by the progeny tests. Sites spaned a broad range of environment-types: Greene Co., MS to Levy Co., FL and Laurens Co. GA; site indexes ranging from 15.5 to 37.1m; and, rust hazard varying between 2 and 98%.

Heritability estimates for individual tree volume varied considerably between tests - average of 0.16 ± 0.19 , and range between 0.00 and 0.62. Type B genetic correlations estimated within each series, and varied between a low of 0.39 ± 0.095 to a high of 0.84 ± 0.092 . If data were available only from an individual test series, this would have indicated that GxE for volume in Florida loblolly was variously either very high or inconsequential. By contrast, rust incidence generally demonstrated much less GxE with estimated type B genetic correlations varying between 0.71 ± 0.16 and 1.0 ± 0.00 across the test series. Within each test series, multivariate analyses of variance were conducted to estimate the genetic correlation between each pair of tests. Results tended to indicate that particular tests or test combinations were largely responsible for the low, pooled type B genetic correlations across all tests within a test series. Pattern analysis (i.e. a combination of ordination and classification) of the climatic data, indicated that it was possible to delineate environment-types based on a set of minimum temperature variables, which broadly (with some exceptions) followed geographic location of the tests. On the basis of these results it is believed that the observed GxE in volume of Florida loblolly pine can largely be explained by: a) testing across frost-hardiness zones, b) inclusion of a few atypical test sites (e.g. calcareous soils or Phosphorus-deficiency), c) large differences in rust hazard, and possibly also, d) problems with test establishment and management.