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Genetic parameters for early growth and disease resistance in a cloned F_2 hybrid progeny of *Eucalyptus urophylla* × *grandis*

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The VERACEL breeding program includes several advanced generation *urograndis* hybrids (F2) from crosses of selected F1. To understand the performance and genetics of these F2, we established F2-cloned progeny trials with 1,350 clones from 35 families, each family with 8 to 35 cloned progenies. These families stem from crosses between known F1 *urograndis* female parents and pollen mixtures of other selected parents. The experimental design comprised 15 trials with 95 clones each, arranged in randomized blocks and linked by 7 common commercial hybrid clones. These experiments were performed in two sites contrasting for physiological disorder (PD) incidence. Due to incomplete pedigree of the families, the model fitted assumed the additive genetic relationship between sibs as half-sibs. The non-additive genetic component was estimated from clone effects within half-sib families. A multisite individual tree genetic model was fitted for diameter, height, PD, *Calonectria*, and rust incidence for trees up to 1 year old: yijklmn= μ+gi+gij+sm+cn+tbkl+sgim+sgijm+scmn+eijklmn; where random effects are gij (additive genetic effects), gi (all non-additive genetic effects of clones), and eijklmn (residuals); and fixed effects are sm, which is either site with higher or lower productivity and PD incidence, cn is F1 or F2, and tbkl is trial-block interaction. The same model was used for diseases and PD, but assumed a binomial distribution with a logit link function. PD was analysed only for the higher PD incidence site, thus excluding interactions with the other site. Results indicate that at the high PD incidence site, height and diameter growth was greater (~40%), but it also had higher mortality (40% vs. 22%) and higher PD incidence (51% vs. 23%). Compared with F1 controls, *Calonectria* incidence was higher in F2 (~10%) but similar at both sites, as was rust, although with lower incidence (~5%). Multisite analysis revealed low additive genetic variance and moderate total genetic variance (A+NA) for growth, diseases, and PD. For growth, narrow- and broad-sense heritability were h2=0.11 and H2=0.40. The additive genetic correlation between the two sites was close to 1 (rA~0.9), whereas the non-additive genetic correlation was lower (rNA~0.5). The narrow- and broad-sense heritability for diseases and PD was low (between 0.10 and 0.15). The low additive genetic variance for growth, diseases, and PD constrains substantial gains from parental selection within F1. However, clonal selection would still be effective due to considerable non-additive effects. Further studies using a large set of various populations are needed to validate these findings.

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