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Genetic analysis of early field growth of loblolly pine clones and seedlings from the same full-sib families

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Abstract: Field trials established with clones and seedlings from the same families provide an opportunity for comparing full-sib family performance across propagule types. More than 1200 different clones together with over 14 000 zygotic seedlings from the same 61 full-sib families of loblolly pine (*Pinus taeda* L.) were tested on multiple sites across Florida and Georgia. The genetic variance associated with several early growth traits partitioned differently depending on propagule type. Most of the genetic variance associated with growth in the clonal population was additive, while the estimate of dominance in the seedling population was greater than estimates of dominance in the clonal population, based on single-site analyses. Apparently, a lack of randomization of the seedlings prior to field establishment caused full-sib families to appear more different, inflating estimates of dominance genetic variance. Parental and full-sib family ranks were stable regardless of propagule type as indicated by type B genetic correlations. In the clonal population, little genotype \times environment interaction was observed across sites at the parental, family, and clonal levels for all traits. The high genetic correlations between propagule types provide further assurance that selections made through traditional tree-improvement activities for recurrent selection for general combining ability in seedling trials can also be used successfully for breeding families to test in a clonal forestry program.

Résumé : Les plantations comparatives établies à l'aide de clones et de semis provenant des mêmes familles permettent de comparer la performance des descendance biparentales à partir des deux types de propagules. Les auteurs ont testés plus de 1200 clones différents ainsi que 14 000 semis zygotiques provenant des mêmes 61 descendance biparentales de pin à encens (*Pinus taeda* L.) dans plusieurs stations en Floride et en Georgie. La variance génétique reliée à plusieurs caractères de croissance juvénile se répartissait différemment selon le type de propagules. La plus grande partie de la variance génétique reliée à la croissance était additive chez la population clonale alors que l'estimation de la dominance était plus grande pour la population de semis que pour la population clonale lorsque les stations étaient analysées séparément. Apparemment, un manque d'aléation des semis avant leur établissement au champ a entraîné des différences plus grandes entre les descendance biparentales, gonflant ainsi les estimations de variance génétique reliée à la dominance. Le rang des parents et celui des descendance biparentales étaient stables peu importe le type de propagules, tel que l'indiquaient les corrélations génétiques de type B. Chez la population clonale, il y avait peu d'interaction entre le génotype et l'environnement dans l'ensemble des stations à l'échelle des parents, des familles et des clones pour tous les caractères. Les fortes corrélations génétiques observées entre les types de propagules fournissaient une assurance additionnelle confirmant que les sélections effectuées par le biais des activités traditionnelles d'amélioration des arbres, basées sur la sélection récurrente en fonction de l'habileté générale à la combinaison à partir de tests de semi, peuvent aussi être utilisées avec succès dans le cas des descendance issues de croisements dirigés pour effectuer des tests dans le cadre d'un programme de foresterie clonale.

[Traduit par la Rédaction]

Introduction

Loblolly pine (*Pinus taeda* L.) is the most important commercial tree species in the United States, with over one billion seedlings planted annually (McKeand et al. 2003).

Tree-improvement programs for loblolly pine are now beginning their third generation of breeding and testing (McKeand and Bridgewater 1998) and have relied on recurrent selection for general combining ability for improving a few key traits. Traditional tree-improvement programs using open-

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