

Genotype-by-environment interaction, in *Corymbia citriodora* hook

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Corymbia citriodora is one of the most cultivated forestry species in Brazil, it combines a high growth rate with high wood density. Its timber is used in products, such as poles, railway sleepers, posts, scantlings, wharves and construction lumber. Genotype-by-environment interaction (GE) is one of the most important elements in the management of a tree breeding program. It is used to define breeding zones and to select genetic material which can be targeted to address specific environmental conditions. The aim of this research was to estimate genetic parameters and to understand GE patterns based on *C. citriodora* progeny tests. The experiment was established using 56 open-pollinated families in three different locations within the Luiz Antônio's experimental station, Brazil. The three sites differ contrastingly on their soil type (1: Red Latosol, 2: Quartzarenic Neosol, 3: Clay Latosol). The following traits were measured at 30 years of age: height (HT), diameter at breast height (DBH), stem form and survival. Based on this data the individual stem volume (VOL) was calculated. The MHPRVG (harmonic mean relative performance of genetic values) predicted by BLUP was used to analyze productivity, stability and adaptability. The GE was not found to be significant regarding all growth traits. A complex GE was detected only for survival, confirming the importance of choosing the correct genetic material of the species for specific sites. The joint analysis showed a significant difference between families for DBH, survival and VOL. In the individual analyses, family growth trait performances were different only in site 2. The estimated gains presented low and moderate values peaking at 11% in site 2. In summary, the material studied here presents the potential to obtain genetic gains through selection. However, to keep these gains continuous over the next selection cycles it is necessary to incorporate new genetic materials in order to increase the diversity observed among the progenies

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