

## **IUFRO Conference 2023**

## Enviromic analysis for prediction of *Eucalyptus globulus* genotypeenvironment interaction and mapping of breeding zones

Callister, A.<sup>1</sup>; Bradshaw, B.<sup>2</sup>; Brawner, J.<sup>3</sup>

<sup>1</sup> Treehouse Forest Research, Check, VA, United States

<sup>2</sup> Australian Bluegum Plantations, Albany, Western Australia, Australia

<sup>3</sup> University of Florida, Gainesville, FL, United States

Received 11 Jul 2023 Accepted 01 Sep 2023 Published 20 Nov 2023  $\square$  Correspondence

Andrew Callister, andrew@treehouse-research.com

Genotype-environment interaction (GE) is pervasive in forest genetics and is a substantial cause of erosion in genetic gain. Delineation of spatial breeding zones (BZs) is fundamental for controlling GE. We developed a BZ classification pipeline for Eucalyptus globulus in 2 Australian regions based on phenotypic, genomic and pedigree data, as well as on a detailed environmental characterization ('envirotyping') and spatial mapping of BZs. First, the factor analytic method was used to model additive genetic variance and site-site correlations (rB) in stem volume across 48 trials of 126,467 full-sib progeny from 2 separate advanced-generation breeding programs. Single-step genomic BLUP (ssGBLUP) was used to create a joint relationship matrix combining both programs for factor analytic analysis. Thirty-three trials were envirotyped using 145 environmental variables (EVs), involving soil and landscape (71), climate (73), and management (1) EVs. Next, sparse partial least squares-discriminant analysis (sPLS-DA) was used to identify EVs that were required to predict classification of sites into 5 non-exclusive BZ classes on the basis of rB. These BZs were then spatially mapped across the West Australian (WA) and 'Green Triangle' (GT) commercial estates by enviromic prediction using EVs for 80 locations and 15 sets of observed climate data to represent temporal variation. Finally, stem volume breeding value accuracy and genetic gain from ssGBLUP across 40 trials were compared using the new enviromic BZ classification and the previous regional BZ classification. The FA model explained 85.9% of additive genetic variation. Our environmental classification system produced within-zone mean rB between 0.76 and 0.84, which improves upon the existing values of 0.62 for WA and 0.67 for GT as regional BZs. One to two sPLS-DA components were required for each BZ definition, with 5 to 8 EV's per BZ. The enviromic BZ classification provided for more accurate breeding values and greater stem volume gain. This work raises highly relevant topics for discussion, including a) the drivers of GE in E. globulus, b) methods of collecting and curating environmental data for envirotyping with eucalypts, c) the advantages and challenges of adopting non-exclusive (i.e. overlapping) BZs, d) the need for developing a phenological system for eucalypts, e) accommodating temporal environmental variation in GE analysis, and f) breeding and improvement strategies for a changing climate.

Keywords: single-step GBLUP, envirotyping, genetic correlation, tree breeding, genetic improvement



Callister A, Bradshaw B, Brawner J. Enviromic analysis for prediction of *Eucalyptus globulus* genotype-environment interaction and mapping of breeding zones. Agrociencia Uruguay [Internet]. 2023 [cited dd mmm yyyy];27(NE2):e1246. Doi: 10.31285/AGRO.27.1246.