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IDENTIFYING SITE TYPES FOR PINUS RADIATA GENETIC EVALUATION IN AUSTRALIA

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In "rolling front" breeding programs there is often low genetic connection between sites planted more than a few years apart. For program wide genetic evaluation, there is probably enough connectedness between sites to estimate unbiased genetic values for different site-types, if the site-types are well defined and the correlation between the site-types can be estimated. Genotype by environment interaction (GxE) analysis methods which rely on (nearly) balanced treatment representation across sites are difficult to use when connection is low and may unnecessarily restrict the sampling of the different environments that the sites represent. Use of all possible sites with sufficient pair-wise connection ensures a broader sampling of environments and may allow better site-type definition. A database of site-site, trait-trait and age-age genetic correlations was created from single site and paired site analyses of over 60 trials. Additive correlations for DBH at ages up to 10 years were modelled with terms to account for age-age and site-type correlations. Error were weighted by the standard errors of the estimates, the number of estimates per site, and the last eigenvalue of the site-type correlation matrix to ensure positive definiteness, where needed. Site-types were identified by checking all possible cut off values of continuous variables (or groups of categorical variable levels) of long term environmental (mostly climatic) values which minimised the weighted error sum of squares of the model. Site-types based on additive correlations were identified from minimum temperature, and then rainfall within cool sites, and such a classification was better than the current a priori regional site-type grouping. Genetic values less confounded by poor groupings of sites should result.