Genomic prediction of complex traits: genomics and quantitative genetics converge to innovate *Eucalyptus* breeding in Brazil

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Genetically improved seeds or clonal stocks have been successfully delivered by systematic tree breeding, but several challenges remain. Long life cycles, late flowering, poor juvenile-mature correlations and changes in market demands and climate, frequently make the progress of tree breeding slow and uncertain. Following the largely fruitless attempts to develop MAS (Marker Assisted Selection) for forest trees, based on the unrealistic concept of dissecting a complex trait in its individual components, the convergence of high-throughput genomics and quantitative genetics has established the paradigm of genomic prediction of breeding values as a way to accelerate breeding of complex traits. Additionally, the adoption of realized genomic relationships, provide innovations in breeding approaches and genetic parameters' estimation by accounting for the random Mendelian segregation in pedigrees. Using the Eucalyptus genome sequence we developed a breeder-friendly and cost-effective SNP genotyping "chip" that provides high-density genotyping for eucalypts. Using this platform in several breeding programs in Brazil, we have shown that genomic selection (GS) matches the accuracy of phenotypic selection for growth and wood traits, nevertheless enhancing the rate of genetic gain by increasing selection intensity, radically reducing generation interval and improving the accuracy of breeding values. Yet, predictive abilities are impacted by GxE interaction and driven mainly by relatedness, such that population-specific predictive models are necessary. We are on the brink of adopting GS in operational eucalypt breeding in Brazil. Strategic and logistics aspects for the adoption of GS are now the challenges to fully integrate this new breeding technology into routine tree improvement.

The *Eucalyptus* SNP array initiative: second-generation SNP arrays for low-cost operational genomic selection and very high-density genotyping for advanced genomic and breeding applications

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Following the development and worldwide adoption of the *Eucalyptus* EuCHIP60K SNP, we have now advanced a new initiative to build second-generation SNP arrays. The objective of the ESAI (Eucalyptus SNP Arrays Initiative) was to provide an improved performance 65k SNP genotyping array with wider applicability and significantly lower cost for operational genomic selection and a very high-density (HD) array with 500,000 to 1,000,000 SNPs for advanced genomic investigation and breeding applications. The new arrays were developed on the Axiom myDesign technology platform and provide a larger number of SNPs than the previous chip. A total of 1.3 million SNPs with coordinates to *Eucalyptus grandis* genome sequence assembly v2.0 were screened bioinformatically, including previously validated SNPs and a large set of newly discovered ones from new sequencing data for *Eucalyptus* species of subgenus *Symphyomyrtus* and genus *Corymbia*. This screening was carried out with 960 samples, including germplasm sources of 18 *Eucalyptus* and 3 *Corymbia* species contributed by the 17 ESAI participating organizations, allowing selection of an optimized set of SNPs. The newly developed ESAI65K SNP array includes a set of ~10,000 SNP for *Corymbia*, a set of cpDNA SNPs for inferring maternal lineages and a set of SNPs making the previous SNP chip data fully portable to this new one. The ESAIHD array with > 500,000 SNPs was used to genotype parents of breeding populations, subsequently allowing SNP imputation to high-density for offspring individuals genotyped with the ESAI65K to improve accuracy and longevity of prediction models along generations of genomic selection.

Cooperative research effort for the production of pine solid wood and resin in Brazil

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Companies working with pines in the solid wood and resin segments in Brazil highlight scientific developments in the areas of gene conservation, genetic improvement and silviculture as basic priorities. However, the required long term research activities in forestry are costly and companies usually face budgetary and structural limitations. High investments are necessary and routine activities are complex, involving procurement of genetic material, specialized personnel, laboratory facilities and establishment and maintenance of both short- and long-term field experiments. In a quest to reduce costs and optimize efficiency in the implementation of research with support from Embrapa Florestas, forest companies associated with APRE (Associação Paranaense de Empresas de Base Florestal) and ACR (Associação Catarinense de Empresas Florestais) set up PCMP (Projeto Cooperativo de Melhoramento de Pinus), a cooperative project for the improvement of pines, and Funpinus (Fundo Cooperativo para Melhoramento de Pinus), a cooperative fund for the improvement of pines. Funpinus provides the administrative structure and financial organization for the implementation of PCMP. The cooperative currently has ten associated companies (resin and solid wood production) from the states of Santa Catarina, São Paulo, and Paraná. The objective of PCMP is to focus efforts on the development of improved pine genetic material, including interspecific hybrids to meet growing demands for high-quality raw material and higher productive efficiency. The PCMP began operations in 2017, with the basic premise to offer an addition to the work developed by individual companies, so that independence and autonomy of each participant company's particular work is honored.