

# WHAT IS NEXT IN THE APPLICATION OF GENOME-WIDE INFORMATION TO TREE BREEDING?

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Almost three decades have passed since the first quantitative trait loci were identified in tree mapping populations. Despite the early excitement, the wide application of genomic information to forest breeding programs has hardly ever materialized. The difficulties in implementing genomic data in breeding programs have been many, but the most significant impediments have been the inability to uncover the majority of loci that control complex traits and high costs of genotyping technology. Recently, new developments in genome-wide prediction methods and the dramatic reduction in genome services have created a renewed interest in these approaches. Still, it remains unclear if current advances will be sufficient to unleash the wide use of genomics in tree breeding, or if they will once again remain the domain of academics.

I will briefly review the current application of genome-wide information to tree breeding and the outcomes of numerous pilot studies already completed or under way. While the preliminary results from these studies are exciting, they may not be sufficient to entice most tree breeders to incorporate genomic technology, unless decreasing costs and added value and efficiencies can be created. Thus, I will focus largely on what are likely to be the next major leaps in the use of genome-wide information in tree breeding, including the application of prediction models to guide the establishment of the most productive crosses based on specific combining ability, the use of methods that pool progeny to generate accurate predictive models at a fraction of current costs, and the application of low-density, ultra-low cost and high throughput methods of genotyping based on sequencing.

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