

HYPER-ACCELERATING BREEDING AND ADAPTATION OF LOBLOLLY PINE USING GENOMIC SELECTION

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Increasing in demand for wood products and growing evidence of climate change creates a pressing need for the development of more productive germplasm that is adapted to existing and novel sources of biotic and abiotic stress. Marker-assisted selection (MAS) was previously proposed as an approach to accelerate genetic improvement of conifers. However, the very limited proportion of the total genetic variation captured by the markers identified in association studies hinders their practical application in breeding program. Alternatively, the combined effect of all available markers may be estimated simultaneously, and used to predict the genomic breeding value of progeny in future generations. This approach of Genomic Selection (GS) has become widely adopted in animal breeding and is now of increasing interest to tree breeders. GS greatest impact is expected in breeding of conifers, by significantly reducing the breeding cycle and facilitating early selection of traits expressed late in the rotation, with low heritability. In this presentation the implementation of GS in conifer tree breeding programs will be discussed in light of our experience in developing prediction models for a breeding population of loblolly pine. The results to be discussed demonstrate the feasibility and remarkable gain that can be achieved by incorporating GS in breeding program of conifers, compared to traditional breeding. However, there are clear limitations in the use of prediction models across breeding zones and ages, and obstacles in model transferability across populations should not be underestimated.