Abstract UPSC Days 2011

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Forest tree genetics and future breeding: from inbreeding to genomic selection

Forest tree breeding, particularly in species in the boreal zone, is time consuming and has been effect for a limited time compared to agricultural crops. There are several issues of breeding effectiveness and speed that current research and technology can improve. Currently the breeding population and climate zone for deployment are not optimized. By using bio-geo-climatic data we can redefine the breeding zones to increase production. Simulation software such as METAGENE can be used to establish new breeding strategies for higher genetic gain, for example, decouple negatively correlated traits and study possible purging of inbreeding depression. Furthermore, establish the economic weights for solid wood, pulp and bioenergy and how to select for those traits are also important in developing breeding objectives more in tune to todays industry. The rapid progress in high throughput sequencing and SNP scoring can be utilized by applying dense marker maps to capture most genetic variation in traits of interest. These markers can then be utilized in an extended form of marker assisted selection termed Genomic Selection. Genomic selection has great potential in speeding up the breeding process and increase genetic gain in traits that are difficult and/or expensive to measure.