



INVITED REVIEW

Managing the rate of increase in average co-ancestry in a rolling front tree breeding strategy

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Summary

In breeding forest trees, as for livestock, the goal is to capture as much genetic gain as possible for the breeding objective, while limiting long- and short-term inbreeding. The Southern Tree Breeding Association (STBA) is responsible for breeding Australia's two main commercial forest tree species and has adopted algorithms and methods commonly used in animal breeding to achieve this balance. Discrete generation breeding is the norm for most tree breeding programmes. However, the STBA uses an overlapping generation strategy, with a new stream of breeding initiated each year. A feature of the species bred by the STBA (*Pinus radiata* and *Eucalyptus globulus*) is the long interval (up to 7 years) between when an individual is mated and when its progeny is first assessed in field trials and performance data included in the national performance database. Mate selection methods must therefore recognize the large pool of unmeasured progeny generated over recent years of crossing. In addition, the substantial delay between when an individual is selected in a field trial and when it is clonally copied into a mating facility (breeding arboretum) means that selection and mating must occur as a two-step process. In this article, we describe modifications to preselection and mate selection algorithms that allow unmeasured progeny (juveniles) to be recognized. We also demonstrate that the addition of hypothetical new progeny to the juvenile pool is important for computing the increase in average co-ancestry in the population. Methods outlined in this article may have relevance to animal breeding programmes where between mating and progeny measurement, new rounds of mating are initiated.