

# Attractive title

## ACCELERATED BREEDING THROUGH INDUCTION OF EARLY FLOWERING

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### Introduction

Accelerated breeding is a novel breeding technique that makes use of genetic modification to speed up breeding by induction of early flowering. In the final breeding steps, the genes used for the genetic modification are crossed out, resulting in end-products that are completely free of genetic modification.

### Need for Accelerated Breeding

In comparison to herbaceous plants, the breeding of trees is more time-consuming due to their long generation time. Hence, in forest tree breeding, the concept of “Selection breeding” has been created. This concept is based on the assessment of an F<sub>1</sub> progeny of two elite or ‘plus’-trees with respect to forestry relevant trait (Hybrid breeding). However, in forest tree species, the production of backcrossing is practically excluded because of the long generation cycle. Therefore, shortened juvenility and precocious flowering is the important breeding goals. Initial experiments have in Apple shown that generation time can be reduced from 5-7 years to just one year for each backcrossing (Flachowsky *et al.*, 2007).

### Steps in Accelerated Breeding

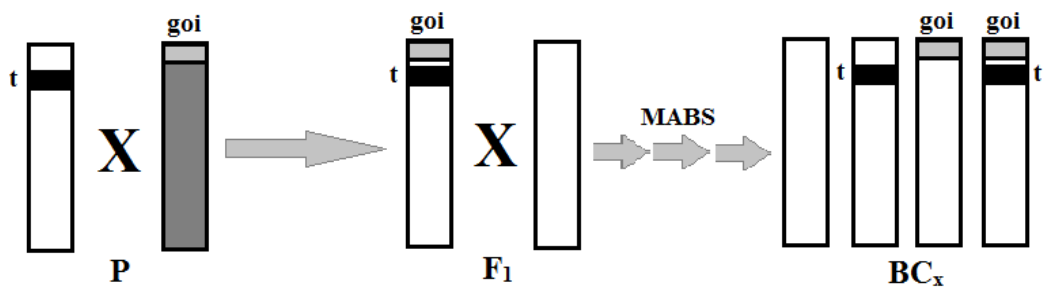
- 1. Cloning of genes:** Flower initiation has been intensively studied in *Arabidopsis* and homologues of genes involved in the flowering initiation (*LEAFY (LFY)*, *APETELAI (API)*, BpMADS4) and juvenility maintaining gene (*TERMINAL FLOWER (TFL1)*) has been cloned in many forest tree species (Kotada and Wada, 2005).
- 2. Transformation of the forest tree species:** *Agrobacterium rhizogenes* contain Ri-plasmid along with suitable T-DNA gene construct of constitutive CaMV35S promoter and cloned gene is used in the development of transgenic forest tree.
- 3. Method for inducing early flowering:** Early flowering induction can be done either by reducing the activity of juvenility maintaining gene, such as *TFL1*, by gene silencing approach (RNAi) or by overexpression of MADS-box and other floral regulatory genes, such as BpMADS3 to achieve early flowering in the transgenic forest tree.

34 **4. Know-out of transgene:** In the final breeding step, the transgenes used for induction of  
 35 early flowering will be crossed out and plant line that is completely free of genetic  
 36 modification-related DNA sequences will be selected.

37 **Accelerated Breeding Procedure**

38 Genetically modified tree species produced using gene silencing or overexpression  
 39 constructs that flower much earlier was crossed with its wild progenitor to transfer useful gene.  
 40 The F<sub>1</sub> progeny containing the transgene gene (**t**) and the gene of interest (**goi**) is selected and  
 41 backcrossed to the parental line which doesn't contain transgene. Marker assisted backcross  
 42 selection procedure is used to select progeny with **t** and **goi** along with maximum parental line  
 43 genome recovery and selected progeny are used again for backcrossing. In the final step,  
 44 reliable selection is made for parental plant lines that are completely free of transgene **t** and  
 45 contain **goi**.

**One colour figure is must**



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**Fig.** Gene-flow during accelerated breeding

48 Standard PCR techniques are employed to confirm the presence or absence of transgene  
 49 in the selected line. Southern blotting using the complete T-DNA construct as a probe gives  
 50 addition evidence for the genetic modification free status of the selected lines.

51 **Conclusion**

**Inference/Opinion**

52 Transgenic trees could be an important tool for speeding up breeding cycle for traits  
 53 that can be rapidly determined in juvenile plants or directly accessed via molecular markers.  
 54 The new varieties produced by this method do not contain any genetic modification- related  
 55 DNA sequences and will be similar to those of the conventionally bred varieties.

56 **References**

**References arrangement**

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