

04-1-21

## Alteration in transgene expression level by a mutation in nos terminator sequence in transgenic poplar

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### Objective

The study was to express the prokaryotic *tzs* gene in poplar and to determine its effect on plant development.

### Materials and Methods

The *tzs* gene from a nopaline type *Agrobacterium tumefaciens* (pTiC58) was modified and transferred to poplar plants *via Agrobacterium* vector. The transgenic plants were assayed by Southern, Northern and hormone assay.

### Results and Discussion

The transgenic poplars carrying bacterial *tzs* gene under the control of CaMV 35S promoter showed drastic changes including multiple shoots on hormone free media, thick stem, small leaves, and suppression of root formation. However, during subcultures, a mutant shoot bolted from the bushy shoot cluster and rooted on root induction medium. Southern blot analysis showed that the transgene was detected in all the transgenic poplars. Northern analysis showed that although the transgene was transcribed at similar level in both the bushy and the mutant types of plants, they differed in the transcript length. Whereas the transcript in bushy type was around a 900 base transcript, that of the mutant plant was around 1300 base. Sequencing revealed that there was a mutation in *nos* terminator region in the mutant plant.

The bushy type transgenic plants contained about 0.5ng of cytokinin/g f.w. In contrast, the mutant had slightly higher cellular cytokinin level than did control plants and thus showed lower degree of cytokinin-related phenotypes. The mutant plants transferred to nursery are characterized by more number of shoots, toothed leaves, thicker stem, larger cells, less secondary xylem layer, shorter xylem fibers, shorter vessel elements, and less root development than untransformed control plants.



Fig 1. Northern analysis of transgenic poplars. The right two lanes are the mutants.

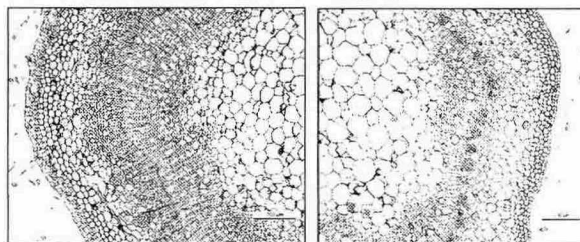


Fig 2. Cross stem sections of control (left) and mutant plant (right)