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Molecular functional of transgenic rice introduced genes encoding fructan biosynthasis

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Objectives

We have tried to bred transgenic rice by using *Agrobacterium tumefaciens* and successfully obtained T2 and T3 generation integration genes encoding fractan biosynthasis. These transgenic lines were higher expressed to environment stress.

Materials and Method

1. Material

Plant- Rice (*Oryza sativa. L)*

Agrobacterium strain- LBA4404/KJGV-B2

2. Method

Breeding of transgenic plants using *Agrobacterium tumefacience*, Molecular characterization: (Southern blot, RT-PCR analysis, RealTime PCR, Northern blot) and Biochemical analysis: (TLC analysis)

Result

Embryogenic callus of rice *(Oryza sativa. L)* was transformated via *Agrobacterium tumefaciens* that LBA4404/KJGV-B2 harbored genes for 1-sucrose : sucrose fructosyl transferase(1-sst), 1-fructan : fructan fructosyl transferase(1-fft). Transgenic lines carrying of transgene was confirmed for integration into the rice genome using Southern blot hybridization. Transcription of transgene in various transgenic lines was determined using RT-PCR or Northern blot analysis. The content of soluble carbohydrates in the transformed plants were analyzed by using thin layer chromatography(TLC). TLC analysis of plants extracts indicated the presence of fructose-containing compounds migrating at the same rates as the standard compounds GF2, GF3, and GF4 in four of the lines analyzed. This analysis confirmed the presence of low-molecular-weight fructan in the seedling of the transgenic rices. Therefore, transgenic rice introduced genes (1-sst and 1-fft) encoding fructan biosynthasis resulted in a dramatic change of the main type of storage carbohydrate, and sucrose was nearly totally converted into low-molecular-weight fructans.

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