DEVELOPMENT OF TRANSGENIC LYSINE RICH RICE VIA AGROBACTERIUM-MEDIATED TRANSFORMATION

Tran Thi Xuan Mai, Tran Thi Cuc Hoa

Summary

In this study the DHDPS-r1 gene from a mutant *Nicotiana sylvestris*, which encodes a DHDPS enzyme insensitive to feedback inhibition, was used to enhance the lysine content in rice seeds. For construction of the vector pPGDSr1, the backbone used for the construct was vector p1380PMI which had a CaMV 35S promoter-driven PMI gene for selection of transformants on mannose sugar. The DHDPS-r1 gene fragment was inserted into multiple cloning sites of p1380-PMI, to restrict targeted gene expression to only the endosperm, a rice endosperm-specific globulin promoter was cloned and was placed immediately upstream of the DHDPS-r1 gene. The constructed vector was then successfully introduced into Taipei 309 rice variety via *Agrobacterium tumefaciens* LBA4404 with transformation frequency of 6.5%. PCR analysis showed that all these putative transgenic rice plants gave positive result. Southern blot analyses of five chosen transgenic rice lines including RL1, RL2, RL3, RL4 and RL5 confirmed that the T-DNA had been integrated into the rice genome. Analysis of total amino acid of T1 seeds from RL1, RL2 and RL3 rice lines revealed that total lysine content in RL1 seeds was enhanced by up to 38% compared to non-transgenic rice seeds. The results of this study indicated that expression of DHDPS-r1 gene in rice seeds may have promising applications for increasing lysine levels in rice to improve nutritional quality of rice plants.

Keywords: *Agrobacterium tumefaciens, DHDPSr1, Lysine content, Taipei 309, Transgenic rice.*