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Carotenoid-accumulating rice by multi-gene expression system

Sun-Hwa Ha¹, Ha-Rin Jung², Kyoung-Ji Chung¹, Donghern Kim¹, Seok-Cheol Suh¹, Ju-Kon Kim²

¹National Institute of Agricultural Biotechnology, RDA, Suwon 441-707, South Korea

²Department of Biological Science, Myongji University, Yongin 449-728, South Korea

Objectives

We have tried to develop carotenoid-accumulating Korean rice cultivar through methods to express several genes simultaneously for plant metabolic engineering.

Materials and Methods

1. Material

Plant - *Oryza sativa*, *Capsicum annuum*

Gene - carotenoid biosynthetic genes, IRES, 2A sequence

2. Methods:

Vector construction by three different multi-gene system (1. simple PCR fusion, 2. viral internal ribosome entry site (IRES) sequence, 3. self-processing virus 2A polyprotein sequence) for rice transformation

Results and Discussion

In humans, carotenoids are essential components of the diet as a source of provitamin A and also play roles in decreasing human age-related-macular degeneration, some cancers and heart disease. Given the importance of carotenoids to agriculture and human health, many groups have targeted the pathway for engineering. As one of efforts to complement these approaches, we are trying to establish multi-gene expression system with carotenoid biosynthetic genes. To accumulate carotenoids in rice endosperm, gateway vector including rice globulin promoter was used as a backbone plasmid for vector construction. Carotenoid biosynthetic genes originated from pepper plant and *Erwinia* were used to make three different vector system: 1. multi-gene fusion by PCR, 2. viral internal ribosome entry site (IRES) sequence, 3. self-processing virus 2A polyprotein sequence. Now, we are developing transgenic rice plants and analyzing their activity and function by molecular biological and biochemical tools. By this approach we hope to develop useful method to express several genes simultaneously for plant metabolic engineering. Furthermore, we expect carotenoid-accumulating Korean rice crops through higher technology.