

Map-based cloning of the yellow embryo lethal (yel) gene in rice (*Oryza sativa* L.)Backki Kim¹, Gileung Lee¹, Yunjoo Lee¹ and Hee-Jong Koh^{1*}¹Department of Plant Science and Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151–921, Republic of Korea**[Introduction]**

The COP1 (constitutive photomorphogenic 1) acts as an E3 ubiquitin ligase at the central of light signaling to repress light signaling by targeting photoreceptors and downstream transcription factors for ubiquitination and degradation. Mutations in the COP1 gene are either homozygous lethal or lead to severe phenotype and anthocyanin accumulation was detected under continuous red light in *cop1* in *arabidopsis thaliana*.

[Materials and Methods]

We generated a yellow pericarp and embryo lethal mutant from the chemical mutagenesis using N-methyl-N-nitrosourea (MNU) on a japonica rice cultivar, Hwacheong. In this study, we fine mapped and cloned the gene responsible for yellow pericarp and embryo lethal phenotype using a map-based approach.

[Results and Discussions]

Fine mapping revealed that the mutant gene (*yel*) was located on the long arm of chromosome 2. Sequencing of the candidate genes analysis showed a 706-bp deletion in the 5'UTR and first exon including start codon of *OsCOP1* (Constitutive Photomorphogenic 1). *OsCOP1*, orthologs of *Arabidopsis COP1* encodes a protein of comprising RING-finger, coiled-coil and WD40 domains. To confirm the function of *yel* gene on yellow pigmentation and embryo lethality, we introduced *YEL* overexpression vector into the mutant heterozygous plant. Overexpression of *YEL*, containing normal RING-finger domain restored the pericarp color from yellow to white, while the embryo color was still black and maintained lethality. Gus staining signals were primarily detected in the embryo, pericarp, pollen and nodes. These results indicated that yellow embryo lethal (*yel*) gene might be involved in yellow pericarp color and the flavonoids biosynthetic pathway in rice seed.

[Acknowledgements]

This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No.PJ011790), Rural Development Administration, Republic of Korea

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