◎ 재배·생리·품질·가공분야

A01

Differential Expression of C4H (*cinnamate-4-hydroxylase*) and F5H (*ferulate-5-hydroxylase*) genes in Rice (*Oryza sativa* L.) by Gamma-irradiation

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Objectives

Gamma-radiation can improve the resistance to environmental stress factors such as photoinhibition and UV-B stress in several plant species. In this study, we attempted to reveal a relationship between the gamma-irradiation and expression of C4H and F5H genes in rice plants.

Materials and Methods

- *Plant materials*
  - Rice cultivars: Illpoombyeo, a Japonica type, and IR-29, an Indica type
- *Conditions for gamma-irradiation and RT-PCR analysis*
  - For gamma-irradiation, 3-month-old plants were exposed to gamma rays of 0, 5, 10, 50, and 100 Gy for 4 hr, and then stem and leaf fragments were harvested 0, 5, 12, 24, 48 and 72 hr after the irradiation.
  - Total RNA extraction for synthesis of the first strand cDNA was performed using the Trizol reagent. For RT-PCR analysis, an aliquot (1μg) of total RNA was reverse-transcribed in an RT system, AccuPower RT Premix (Bioneer, Daejeon, Korea). The subsequent PCR was performed with a total 20μl cDNA reaction mixture in a PCR system, Perfect premix ver. 2.1 (Takara Korea Biomedical Inc., Seoul, Korea)

Results

- The expression of *OsC4HL* in the leaf tissues of Ilpoombyeo was the most distinguishable in the 50- and 100-Gy groups as compared with that in the control.
- Similarly, the expression of *OsF5HL* in Ilpoombyeo was kept higher in the irradiated groups during the post-irradiation period than in the control.
- In contrast, the high expression of *OsC4HL* in IR-29 was noticeable only until 12 hr after the irradiation in the 100-Gy group. Moreover, the expression of *OsF5HL* in IR-29 was less changeable during the post-irradiation period.
- Lastly, the expression patterns of two genes in the stem tissues were more complex in both cultivars. Although their expressions were different between the control and 50-/100-Gy groups, such differences did not appear in the same pattern during the post-irradiation period. Therefore, the expression of two genes in the stem tissues still need to be further analyzed.

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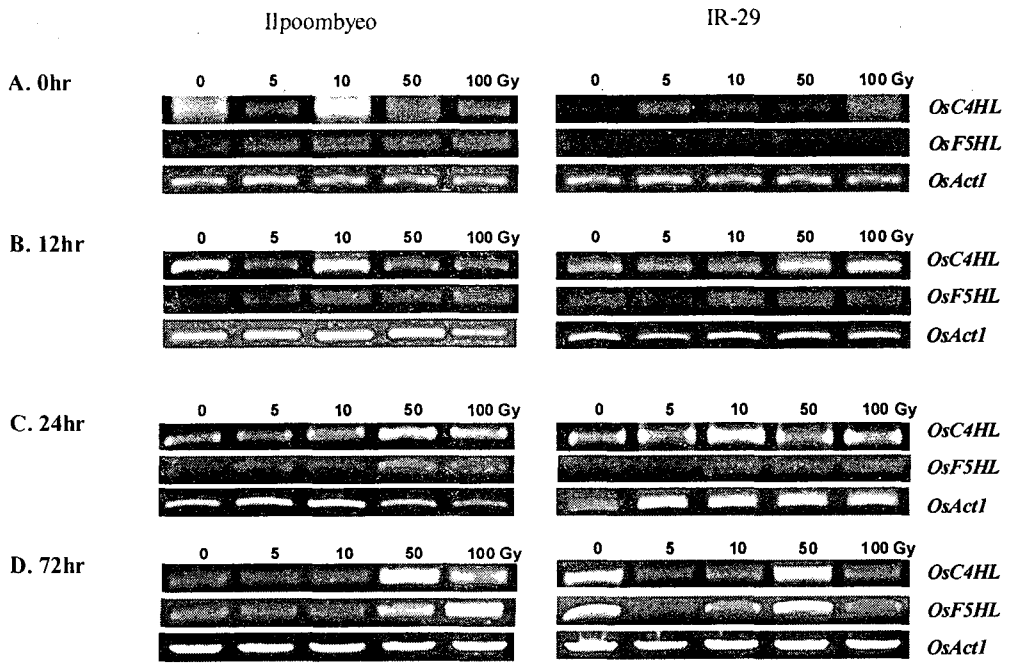

Fig. 1. RT-PCR analysis of two genes in the leaf fragments.

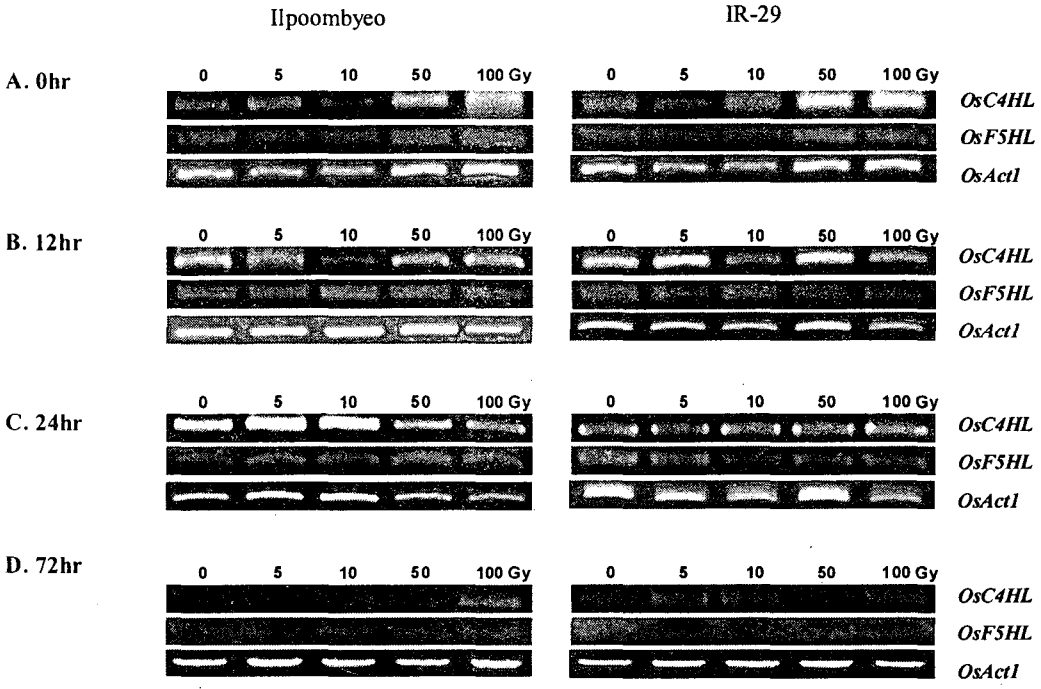

Fig. 2. RT-PCR analysis of two genes in the stem fragments.