

**PB-032**

## Risk Assessment in the Agricultural Environment of Genetically Modified Drought Tolerance Rice (*Oryza sativa* L.)

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### [Introduction]

According to the global rainfall deficiency summary written by the APEC (Asia-pacific economic cooperation) climate center, the characteristics of drought is random, frequent, and persistent. Developing a new variety through molecular breeding in preparation for drought, but the scientific safety of GM plants has not been fully proven, so there are many limitations. In this research screening release risk in agricultural environment of drought tolerance GM rice with the use of compare each phenotype and gene flow.

### [Materials and Methods]

The LMO (Leaving modified organism) field, located at Gunwi, Gyeongbuk province. Environmental data were prepared based on soil environment meter, anemometer, and RDA (Rural development administration) Agricultural Weather Information Service. Record agricultural characters with the use of plant growth and development screening. Weediness potential test is performed by measuring shattering and germination. Evaluate the viability in natural environment through after wintering germination test. Assess gene transfer by the movement of heritable substance. The collected data were analysed using the SPSS program (IBMSPPS Statistics, version 25, NC).

### [Results and Discussion]

There was no significantly difference in the environmental conditions for two years, suitable environmental conditions to growth and reproduction of rice. Also, the weather that cause infertility did not occur. Yield was recorded under drought conditions in 2018, Ilmi, HV8, and HV23 were  $88.9 \pm 3.1$  kg/10a,  $164.2 \pm 49.1$  kg/10a,  $124.8 \pm 43.2$  kg/10a. In 2019,  $122.0 \pm 2.8$  kg/10a,  $160.2 \pm 20.4$  kg/10a,  $172.7 \pm 7.1$  kg/10a. The protein content of HV8 and HV23 are increased maximum 0.4% than Ilmi. The other agronomic characters did not show a significant difference for 2 consecutive years. After wintering viability recorded 0% at 24 places from 10 m to 40 m around the LMO field. Horizontal and vertical gene transfer did not occur.

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