

GGG Prize 2017

The Editors and Advisory Board of Genes & Genetic Systems (GGS) are pleased to announce that the *GGS Prize 2017* has been awarded to the authors for their paper:

From the laboratory to the field: assaying histone methylation at *FLOWERING LOCUS C* in naturally growing *Arabidopsis halleri*

By Haruki Nishio, Diana Mihaela Buzas, Atsushi J. Nagano, Yutaka Suzuki, Sumio Sugano, Motomi Ito, Shin-Ichi Morinaga and Hiroshi Kudoh, published in *Genes & Genetic Systems* (2016) **91**, 15–26.

This paper was selected by the editors and members of the advisory board as one of the best articles published in GGS in 2013–2016.

Arguments supporting this decision were:

“This study demonstrated that a standard chromatin immunoprecipitation (ChIP) protocol for analyzing histone modifications in the laboratory can be adapted for field samples. The authors used naturally growing *Arabidopsis halleri*, a close relative of *A. thaliana*, and modified the experimental conditions so that they could perform sampling and sample preservation in the field. They showed that these conditions give robust results, comparable with those from laboratory samples. In this study, the floral inhibitor gene *FLOWERING LOCUS C* was analyzed. The data obtained revealed largely similar trends in histone modification dynamics between laboratory and field samples, but also identified some possible differences. The authors predict that their ‘field ChIP’ method will facilitate comprehensive *FLC* chromatin analysis to contribute to our understanding of gene regulation in fluctuating natural environments.”

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The Editors and Advisory Board of Genes & Genetic Systems (GGS) are pleased to announce that the *GGS Prize 2017* has been awarded to the authors for their paper:

Identification of gamma ray irradiation-induced mutations in membrane transport genes in a rice population by TILLING

By Jung Eun Hwang, Duk-Soo Jang, Kyung Jun Lee, Joon-Woo Ahn, Sang Hoon Kim, Si-Yong Kang, Dong Sub Kim and Jin-Baek Kim, published in *Genes & Genetic Systems* (2016) **91**, 245–256.

This paper was selected by the editors and members of the advisory board as one of the best articles published in GGS in 2013–2016.

Arguments supporting this decision were:

“In the present study, a TILLING population was generated in rice using gamma ray irradiation. The authors revealed the success of reverse genetic analysis using the TILLING population. They identified some mutants by TILLING for membrane transport genes that affected the plant’s tolerance to high-salt conditions. After the TILLING assay, a total of 41 mutant lines containing SNPs in the target genes were identified and screened. Among the 41 lines, nine had altered sequences in the exon region of the genes. Of these nine lines, seven were tolerant to salt stress after exposure to 170 mM NaCl for three weeks, while the other two lines were not more salt-tolerant than the control lines. Furthermore, five mutant lines containing SNPs in the coding region of *OsAKT1*, *OsHKT6*, *OsNSCC2*, *OsHAK11* and *OsSOS1* showed changed expression levels for each gene. The authors conclude that variation in membrane transport genes, such as expression levels and protein structures, may affect the rice plant’s tolerance to salt stress. The present study revealed that TILLING is a powerful tool for reverse genetic analysis in rice.”