

**[P4] Crop Genetics and Physiology**

Thu. Sep 9, 2021 12:15 PM - 2:00 PM Room 4 (Poster) (Crop Genetics and Physiology)

12:15 PM - 1:00 PM

**[P4-09] Resistant Loci to Physiological Disorder Cupping in Chinese Cabbage (*Brassica rapa* var. *Pekinensis*)**

\*Nominated for Presentation Awards

○Haruto Takamori<sup>1</sup>, Osamu Kawaide<sup>3</sup>, Tokuko Sakaguchi<sup>1</sup>, Minami Nakazawa<sup>1</sup>, Natsuki Ito<sup>1</sup>, Ayuka Furukubo<sup>2</sup>, Minami Amaike<sup>2</sup>, Takashi Ito<sup>5</sup>, Fumio Azuhata<sup>3</sup>, Mashiro Okada<sup>2</sup>, Seiji Chino<sup>5</sup>, Hideo Matsumura<sup>4</sup>, Satoshi Niikura<sup>3</sup>, Nobuaki Hayashida<sup>2</sup> (1., Shinshu University, Japan, 2.Division of Applied Biology, Faculty of Textile, Shinshu University, Japan, 3.TOHOKU SEED CO., LTD., Japan, 4.Gene Research Center, Shinshu University, Japan, 5.Engineering Department, Faculty of Textile, Shinshu University, Japan)

Chinese cabbage (*Brassica rapa* var. *pekinensis*) is one of the major crops in the Brassicaceae, showing form of leafy heads at the later growth stage. Cupping is one of the problematic physiological disorder in Chinese cabbage, caused by the environmental stresses as calcium deficiency. Also, defect of calcium causes other multiple disorder or disease like tip burn and soft rot, leading degradation of its quality. Therefore, we evaluated genetic cupping resistance in Chinese cabbage, as a novel indicator of calcium deficiency, in different environments. Progeny derived from a cross between two Chinese cabbage lines, showing different properties of cupping resistance, were prepared. One thousand of F1-S2 seedlings were grown in the cultivation room for phenotypic observation. Cupping phenotypes at the heading stage were evaluated in the field with replication for four years, resulting that thirty-two hundreds of F1-S2 individuals were scored. Based on these scores and genotyping data obtained from the RAD-seq analysis, QTL analysis was performed. Interestingly, independent QTL peaks appeared in different linkage group (LG) between seedling and heading stages. Unique major peak of the QTL was detected in LG2 for the phenotype at seedling stage. For headings stage, QTLs were found in LG1, LG3, and LG7. Candidate genes for cupping resistance are involved in these QTLs, which expected to contribute to genetic improvements in Chinese cabbage. Also, these genes will be helpful for understanding the mechanisms in various calcium-related traits.