A NEW “OMICS” PLATFORM TECHNOLOGY FOR APPLIED CYTOGENETICS AND IMPLICATIONS FOR GERMPLASM ENHANCEMENT IN ALLIUM

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Yamaguchi University is a core organization in Asia for Allium germplasm collection. Our gene preservation lines mainly consist of asexually propagated vegetable crops, such as shallot, wakegi onion, Japanese bunching onion, garlic, rakkyo and their wild relatives. The constituent of artificially manipulated genetic stocks are interspecific hybrid, polyploid, haploid, doubled haploid (DH), alien chromosome addition line, alloplasmic line, segregating population, etc. Our research via the usage of these genetic resources aims to enable a holistic approach to profile the phytochemical composition as well as its related gene expression of Allium vegetables for plant breeding studies, through collaborative development of resources for metabolomics-high throughput chemical profiling by mass spectrometry, together with transcriptomics assay metadata by RNA-Seq. Conventional and advanced metabolomics analyses in a complete set of eight monosomic addition lines proved to be very effective in revealing the effects of single alien chromosomes from shallot on the production of several functional chemical compounds in the leaf tissue of A. fistulosum. Another study based on phytopathological aspect was carried out to evaluate the antifungal effect of shallot metabolites on Fusarium oxysporum and to determine the shallot chromosome related to Fusarium wilt resistance using these addition lines. Our main focus will be to map the resistance gene of shallot with a large number of SNP markers together with a number of metabolome quantitative trait loci by using the mapping population derived from F1 hybrids between two morphologically and physiologically distinct doubled haploids, shallot DH and bulb onion DH. An omics approach will be used to characterize variation in these unique genetic stocks, developing capability and plant materials to support metabolomics-informed plant breeding studies of whole plants, as well as enabling detection of associations between phytochemical content, gene expression and specific genome regions. The knowledge and technologies will be applicable for targeting breeding towards enhanced functionality as well as disease resistance.

Key Words: germplasm, doubled haploid, alien chromosome addition line, omics, Fusarium