[PP-01]

Eggplant Genome Editing Using CRISPR/ Cas9 Technology

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Eggplant (Solanum melongena L.,) is one of the main used vegetables in many countries. It has a long growth period which makes as one of the vegetables that is more exposed to pests, disease infestation, environmental stresses and parasitic weeds.

Orobanche spp. known as broomrape is one of the parasitic weeds that can cause huge damages to yields off eggplant. It is a well- known fact that these parasite seeds for germination need to be exposed to specific chemicals called strigolactones [SLs], which are released by the host roots.

The CCD8 gene is involved in the synthesis of strigolactones and plays an important role in controlling growth and development. CRISPR-Cas9 has been applied to manipulate the SlCCD8 gene in eggplant (Solanum melongena).

Using the Agrobacterium-mediated plant transformation method gRNA and Cas9 were transferred to eggplant. As the material was used eggplant cotyledons. The successful editing of eggplant lines was confirmed by Sanger sequencing. The induced mutations were stably inherited in the T1 progeny. Our findings based using CRISPR-Cas9 technology opens the way to the development of eggplant genotype's resistance to parasitic weeds

Keywords: Agrobacterium tumefaciens-mediated, CCD8, CRISPR-Cas9 technology, Eggplant, Orobanche spp

[PP-03]

Genome-Wide Association Study for Leaf Rust and Stem Rust Resistance in Bread Wheat Growing in Kazakhstan

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Common wheat (Triticum aestivum L.), is one of the main cereal crops cultivated around the world and is important for food security. Kazakhstan is among the ten largest exporters of wheat, with a volume of 11.4 thousand tons produced in 2019. According to the Bureau of National Statistics of Kazakhstan, the sown area under wheat was 12.2 million hectares in 2021, which represents about 76.7% of the total area used for cereal crops in the country. One of the largest problems in wheat production all over the world is foliar diseases, in particular Puccinia graminis f. sp. tritici (Pgt), causing stem rust (SR), and Puccinia triticina Eriks. (Pt), causing leaf rust (LR). One of the most effective ways to prevent wheat rust epidemics is the development of cultivars with durable resistance to pathogens. The development of new cultivars with high productivity and LR and SR disease resistance, including using marker-assisted selection, is becoming an important priority in local breeding projects. Therefore, the search for key genetic factors controlling resistance in all plant stages, including the seedling stage, is of great significance. LR and SR resistance is controlled by a diverse group of genes, designated as Lr and Sr, respectively. In the literature, approximately 80 Lr and about 60 Sr genes have been identified and described in bread wheat, durum wheat, and diploid wheat species. In this work, we applied a genome-wide association study (GWAS) approach using 212 local bread wheat accessions that were phenotyped for resistance to specific races of Pt and Pgt at the seedling stages. The collection was genotyped using a 20 K Illumina iSelect SNP assay, and 11,150 polymorphic SNP markers were selected for the association mapping. Using a mixed linear model, we identified 11 quantitative trait loci (QTLs) for five out of six specific races of Pt and Pgt. The comparison of the results from this GWAS with those from previously