2nd INTERNATIONAL

Molecular Plant Protection Congress

ORHANGAZİ • BURSA

May 15-18, 2023

INNOVATIONS IN
PLANT PROTECTION

PROGRAM AND ABSTRACT *BOOK*

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Tanıtım nüshasıdır, para ile satılmaz. Bandrol uygulamasına ilişkin usul ve esaslar hakkındaki yönetmeliğin beşinci maddesinin ikinci fıkrası çerçevesinde bandrol taşıması zorunlu değildir.

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O-20

Development of resistance against broomrape (*Orobanche* spp., *Phelipanche* spp.) using CRISPR/-cas9 technology in tomato (*Solanum lycopersicum*)

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Weeds are among the most important factors that cause significant yield and quality losses in tomato (*Solanum lycopersicum*). Thanks to the strigolactone (SL) compounds synthesized from the tomato roots of the fully parasitic broomrape (*Orobanche*/*Phelipanche* spp.), they weaken the plant and even cause plant death by feeding from the root after germination in the soil. In this study, it was aimed to obtain genetically resistant tomato lines against broomrape with the CRISPR/Cas9 system designed to modify the "Carotenoid cleavage dioxygenase 7" (SlCCD7) gene, which is involved in the SL pathway in tomato. As a result of the transformation via the Agrobacterium-mediated method, a mutation causing a biallelic heterozygous deletion of 18 and 186 nucleotides (nt) occurred in the T0 generation. The 186 nt unique mutation resulted in an inframe modification between Thr42-Val105 in the SlCCD7-exon 1 region that resulted in the deletion of 62 amino acids. In the T1 generation, 2 of the 4 plants with 186 nt homozygous deletion were identified as marker-free (not carrying Cas9 gene). In plants carrying 186 nt homozygous deletion, broomrape resistance was obtained without undesirable agro morphological changes. Genetic resistant lines against broomrape can be used for commercial purposes in upland-greenhouse cultivation, open field industry and table tomato cultivation where solarization is not possible. It is predicted that the use of resistant varieties will greatly reduce the yield and quality losses caused by the parasitic weed.

Key words: Gene editing, Agrobacterium-mediated transformation, ccd genes, strigolactone pathway

O-21-STU

Determination of the resistance status of wild mustard (*Sinapis arvensis* L.) collected from wheat cultivation areas in Amasya, Çorum, Tokat and Yozgat provinces against tribenuron methyl by molecular methods

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Different crop plants are grown for the plant nutrition of people around the world. One of these agricultural products is wheat. Agricultural products obtained from wheat gained importance for being used in several ways, such as feeding human beings and ani Although wheat is an important agricultural production material, product losses of up to 100% due to diseases, harmful animal organisms, and weeds have been revealed by many researchers. Even the weeds seen in wheat can cause the entire product to become unusable. The producers generally prefer herbicides since wheat is not a hoe plant; accordingly, there is a limited control method. Due to the regular use of the same group of herbicides, herbicide resistance problem arises in weeds. In this study, wild mustard (*Sinapis arvensis* L.) seeds were collected from 310 different locations from wheat fields in Amasya, Çorum, Tokat and Yozgat provinces to investigate the current resistance status of weed against Tribenuron methyl, which is used extensively in this region. As a result of the bioassay tests, it was determined that 13 of the wild mustard populations collected from 310 fields survived at the registered dose (10 g/ha) of herbicide. According to these results, a dose-response test was performed, and point mutation against ALS group herbicides was investigated molecularly. As a result of the PCR and sequencing study, it was determined that there was a point mutation for Leucine in the amino acid Trp-574 in one population. In this study, resistance to an ALS group herbicide of wild mustard found in wheat growing areas of Amasya, Çorum, Tokat and Yozgat provinces was investigated, and Trp-574 mutation was detected for the first time in Türkiye in a population collected from the Tokat region.

Key words: *Sinapis arvensis*, Trp-574, resistance, tribenuron methyl

O-22-STU

Molecular identification of *Fusarium* spp. on infected broomrape (*Phelipanche* spp.) seeds

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Broomrapes (*Orobanche* spp. and *Phelipanche* spp.) are holoparasitic plants that are completely dependent on the host plant for water and nutrients. *P. aegyptiaca* and *P. ramosa* are the most destructive broomrapes species worldwide, causing

serious damage on Solanaceae crops mainly in Mediterranean countries. Therefore, the discrimination of broomrape species are crucial in term of the specific struggling strategy determination such as biological control. In this context, we used the ribosomal protein S2 (rps2) specific molecular markers for observation of differences between *P. aegyptiaca* and *P. ramosa*. Thus, we can determine the management strategy by using *Fusarium* isolates. In this study, nine isolates of *Fusarium* spp. were isolated from *Phelipanche aegyptiaca*. seeds from the heavily infested tomato-growing greenhouses in the South of Türkiye. Three of them were identified based on internal transcribed spacer (ITS) and translation elongation factor (TEF) gene regions sequence by using the ITS1/ITS4 and EF1-728F/TEFLLE-R primers and the isolates were classified as belonging to *F. fujikuroi* at the rate of 99.80% and 100%, respectively. The aggressiveness of the isolates on *P. aegyptiaca* seeds were assessed by the seed inhibition and radicle growth tests. The isolates were found to be pathogenic on the seeds and the disease severity (%) were determined up to 70%. Our recent studies indicate that *F. fujikuroi*, can give a potential contribution to the biocontrol of *P. aegyptiaca.* This is the first report on *Fusarium* spp. on infected *Phelipanche* spp. seeds based on molecular identification, in Türkiye.

Key words: *Phelipanche aegyptiaca, Fusarium fujikuroi*, parasitic weed, molecular identification

O-23 (KEYNOTE SPEECH)

Discovery, development and commercialization of RNA-based biopesticides

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RNA interference (RNAi) is a ubiquitous, naturally occurring mechanism of eukaryotic gene regulation that has received intense study for over twenty-five years since being first discovered in the nematode, *Caenorhabditis elegans.* RNAi is initiated by various forms of duplex RNA that are processed into small interfering RNAs (siRNA). siRNAs direct RNA-induced silencing complex (RISC) to cleave target mRNA in a sequence-specific manner, resulting in suppression of the encoded protein. RNA-based actives open the potential for a wide range of applications in medicine and agriculture. For crop protection, RNA is being developed as a new mode of action to control agricultural pests and pathogens by targeting genes for cellular function or disease. RNA-based biopesticides fit well with sustainable agriculture initiatives aimed at reducing environmental impact and ensuring food security. RNA is an attractive alternative to broadly toxic synthetic chemistry due to its low persistence in the environment and sequence specificity that targets pests. Innovation across disciplines of bioinformatics, RNA biological manufacturing processes, and cellular delivery are being integrated to drive progress for agricultural RNA products soon to be commercialized. GreenLight Biosciences overcame RNA cost hurdles by inventing a large-scale, cost-effective cell free production process for RNA. The first product from Greenlight Biosciences, Calantha™ , targets *Leptinotarsa decemlineata*, the Colorado potato beetle. The active ingredient in Calantha™, known as ledprona, recently received a recently proposed IRAC MoA classification as the first RNA-mediated protein suppressor. This presentation will highlight the product performance of Calantha™ and provide an update on Greenlight Biosciences' pipeline including RNA-based insecticides, fungicides and acaricides.

Key words: Biopesticides, RNAi, RNA based biopesticides

O-24 (KEYNOTE SPEECH)

Alternative structured dsRNAs can enhance RNAi in insects

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Double-stranded RNA-based insecticides offer the potential to control pest insects with minimal impacts on non-target species, which makes them an appealing alternative to the many broad-spectrum chemical pesticides currently in use. Our lab has been focusing on the development of ingestible double-stranded RNA (dsRNAs) for insect control, and one of the unique challenges of this delivery methods is the destruction of the dsRNA within the insect gut before the molecules can enter the gut cells. Our recent research has determined that some structured dsRNAs are more resistant to insect gut nucleases, which could improve their efficacy for insect control. In addition, we have observed that the alternative structured dsRNAs can enter the cells by a clathrin-independent mechanism, and thus bypass the usual route of entry that conventional dsRNAs use to mediate their effects. Combining different structured RNAs with various adjuvants, we have identified effective formulations that improve the efficacy of foliar dsRNA sprays or topically-applied insecticides to protect crops from a variety of insects. The alternative structured dsRNAs, in addition to being equally, if not more effective than linear dsRNAs, offer the possibility to develop RNAi control strategies for insects that are either resistance to or naturally refractory to conventional dsRNAs.

Key words: RNA interference, insect control, cellular uptake