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| Please use this form to clearly and concisely report on project progress. The information included should reflect quantifiable results that can be used to evaluate and measure project success. Comments should be limited to the designated boxes. Technical reports, no longer than 4 pages, may be attached to this summary report. | |
| Project Number: |  |
| Project Title: | Identification and confirmation of natural tolerance to off-target Dicamba damage in non-Xtend soybeans |
| Organization: | University of Missouri |
| Principal Investigator Name: | Pengyin Chen |
| Other investigators: | Caio Canella |
| Report Period: | March 15 to June 15, 2022 |
| **Research updates**:  In this last quarter, the team has finalized the planning and preparation of all field trials to be conducted in 2022. Planting has been completed for the majority of yield trials and dose-response and mapping studies will be planted in the upcoming days. Below is a summary of field trials and respective objectives:  **Table 1**. Summary of field trials to study dicamba tolerance in soybean   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **Test** | **Entries** | **Locations1** | **Replications** | **Data** | **Objective** | | 22-AYT | 259 | Portageville (3) Mid-South (6-8) | 3 Portageville 2 Mid-South | Yield, Soy6K SNP, Dicamba R3, UAV R3 | Identification and selection of **high-yielding tolerant** advanced lines | | DIC-Map2 | 450 | Portageville (2) | 2 | Yield, Soy6K SNP, Time-series Dicamba, Time-series UAV | Genomic studies to identify **significant marker-trait associations** | | DIC-Dose3 | 8 | Missouri (2) Illinois (1) | 3 | Soy6K SNP, Time-series Dicamba, Time-series UAV | Dose-response studies to identify **tolerance exposure thresholds.** Total of 6 treatments. |   1Mid-South locations include Arkansas, Illinois, Louisiana, Mississippi, Missouri, Tennessee, and Virginia. 2DIC-Map consists of two bi-parental populations derived from a susceptible breeding line and a tolerant plant introduction (PI).3DIC-Dose study includes multiple dicamba rates sprayed every 7-10 days after the mid-vegetative stage to simulate the prolonged off-target exposure.  In addition, we are currently advancing 8 bi-parental populations derived from a non-Xtend tolerant breeding line and a high-yielding breeding line in an off-season nursery in Costa Rica. The forward-breeding scheme is aiming to develop new tolerant, high-yielding breeding populations. Progeny rows (~800 F4:5 lines) are expected to be grown in summer 2023. For this year’s crossing block, we have entered 5 high-yielding, tolerant parents and will attempt to develop 8-10 new breeding populations.  The team also made good progress in unveiling the molecular and physiological mechanisms associated with resistance. Preliminary genome-wide association studies using the PI panel have highlighted two genomic regions in chromosomes 10 and 13 with genes related to physiological mechanisms of plant detoxification to herbicides (Figure 1). Further analyses are currently being conducted and finalized results will be available in the next quarterly report.    **Figure 1**. Manhattan plot detecting significant marker-trait associations in chromosomes 6, 10, and 13. Genes located in these genomic regions are associated with multidrug resistance protein (phase 3 of plant detoxification) and oxidoreductase activity (phase 1 of plant detoxification).  **Summary and Highlights:**   * The two publications submitted to Crop Science and Remote Sensing have been accepted and printed. * The team is partnering with GDM Seeds to expand the applications of the UAV-based phenotyping platform. * Molecular studies are ongoing and preliminary results have highlighted genomic regions associated with physiological mechanisms of plant detoxification to herbicides. | |
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