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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:  | Development of functional ultra-high stearic acid soybean germplasm |
| Organization:  | University of Missouri |
| Principal Investigator Name: | Dr. Grover Shannon |
| Other investigators: | Caio Canella Vieira, Dongho Lee |
| Report Period: | September 15 to December 15, 2022 |
| **Research updates**:***2022 progeny plots for high stearic project.***A total of 45 high stearic soybean lines (12 conventional / 33 round-up ready) were selected from 2022 progeny plots based on fatty acid profiles and overall agronomic traits, including uniformity, pod load, and plant structure. The yield performance of the selected lines will be tested with commercial soybean checks in 2023 preliminary yield trial.***Breeding populations under generation advancement process.***A total of 10 high stearic breeding populations made in Summer 2021 are being advanced in off-season nurseries in Costa Rica and Puerto Rico. Roughly 100 F4:5 lines per population will be planted in 2023 progeny plots in Portageville, MO.**New crosses in 2022 summer**A total of 12 new crosses were successfully made in 2022 summer. The hybridized F1 seeds were harvested and shipped to off-season nursery in Costa Rica for generation advancement. Roughly 100 F4:5 lines per population will be planted in 2024 progeny plots in Portageville, MO. ***Molecular analysis***The purpose of molecular analysis is to dissect unknown 2 Mbp deletion in extremely high stearic soybean lines by identifying any structural variations in the deletion. The whole genome sequencing process has been completed by Novogene Co. for 17 selected lines, including six high stearic and six low stearic RILs, two mutant lines in the pedigree, one historical high stearic mutant line, and two wild-type parental lines. We estimated the quality of raw data and we have performed the quality control of data by removing the adapter sequences and trimming the low-quality bases from the reads. Currently, we are aligning the high-quality reads to Williams 82 version 4 genome to generate alignment files for each line in BAM format. |
| **Summary and Highlights:*** **A total of 45 high stearic soybean lines were selected based on the fatty acid profiles and overall agronomic traits.**
* **A total of 12 new high stearic crosses were successfully made.**
* **Bioinformatic analysis is on-going.**
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