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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: | Pengyin Chen |
| Other investigators: | Caio Canella, Dongho Lee |
| Report Period: | June 15 to September 15, 2022 |
| **Research updates**:  ***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 breeding populations in 2022 progeny plot***  A total of nine high stearic breeding populations (F4:5) have been planted in progeny rows in Portageville, MO in 2022. Promising lines will be selected during the season based on fatty acid profiles and overall agronomic traits, including uniformity, pod load, plant structure, etc. The desirable fatty acid profiles (high stearic/high oleic/low linolenic) have been screened among the populations (Table 1).  **Table 1. New breeding populations for high stearic project in 2022 progeny plot.**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | **Traitsa** | **Population** | **Pedigree** | **# lines** | **Stearic acid (%)** | | **Oleic acid (%)**  **(average)** | | **Range** | **Average** | | UHS | CR20-132 | S19-19710 x S16-11644C | 2 | 20.2 - 20.9 | 20.6 | 23.8 | | UHS | CR20-133 | S19-19712 x S16-7922C | 7 | 21.0 - 34.3 | 27.1 | 12.1 | | HSHO | CR20-131 | S19-19715 x S17PR-481 | 11 | 6.3 - 14.9 | 9.9 | 75.1 | | HS | CR20-131 | S19-19715 x S17PR-481 | 16 | 6.4 - 19.3 | 10.4 | 27.3 | | HS | CR20-132 | S19-19710 x S16-11644C | 39 | 6.5 - 19.0 | 12.7 | 20.7 | | HS | CR20-133 | S19-19712 x S16-7922C | 44 | 6.0 - 18.8 | 10.9 | 19.5 | | UHS | PR20-038 | S19-19710 x S17CR-172 | 2 | 20.0 - 23.6 | 21.8 | 23.3 | | UHS | PR20-039 | S19-19181 x S16-5540R | 4 | 20.8 - 25.1 | 22.3 | 22.5 | | UHS | PR20-040 | S19-19181 x S17CR-189 | 18 | 20.1 - 33.4 | 22.1 | 21.2 | | UHS | PR20-042 | S19-19196 x S17CR-172 | 2 | 21.7 - 21.8 | 21.8 | 23.9 | | UHS | PR20-043 | S19-19188 x S11-20337 | 6 | 20.0 - 27.4 | 22.5 | 20.4 | | UHS | PR20-044 | S19-19188 x S17PR-482R | 2 | 21.3 | 21.3 | 34.9 | | HSHOLL | PR20-038 | S19-19710 x S17CR-172 | 1 | 11.7 | -b | 74.0 / 3.2 (18:3) | | HSHOLL | PR20-042 | S19-19196 x S17CR-172 | 1 | 7.4 | - | 79.2 / 3.1 (18:3) | | HSHOLL | PR20-043 | S19-19188 x S11-20337 | 1 | 8.4 | - | 81.5 / 3.0 (18:3) | | HSHO | PR20-038 | S19-19710 x S17CR-172 | 1 | 9.6 | - | 68.3 | | HSHO | PR20-039 | S19-19181 x S16-5540R | 1 | 6.8 | - | 76.8 | | HSHO | PR20-042 | S19-19196 x S17CR-172 | 7 | 7.0 - 17.2 | 11.2 | 72.1 | | HSHO | PR20-044 | S19-19188 x S17PR-482R | 4 | 8.8 - 18.4 | 12.9 | 70.9 | | HS | PR20-038 | S19-19710 x S17CR-172 | 20 | 6.6 - 18.6 | 12.0 | 31.9 | | HS | PR20-039 | S19-19181 x S16-5540R | 38 | 6.3 - 19.9 | 13.6 | 22.3 | | HS | PR20-040 | S19-19181 x S17CR-189 | 53 | 6.2 - 19.8 | 14.9 | 23.9 | | HS | PR20-042 | S19-19196 x S17CR-172 | 35 | 6.0 - 19.4 | 12.8 | 32.2 | | HS | PR20-043 | S19-19188 x S11-20337 | 34 | 6.2 - 19.6 | 12.5 | 22.2 | | HS | PR20-044 | S19-19188 x S17PR-482R | 24 | 6.2 - 19.9 | 13.4 | 32.8 |   aUHS, ultra-high stearic; HSHO, high stearic & high oleic; HSHOLL, high stearic & high oleic & low linolenic; HS, high stearic.  bdata not available.  ***New crosses made in 2022 summer***  A total of 13 new crosses were made in 2022 summer. The hybridized F1 seeds will be harvested in October and shipped to winter nursery for advancement in November.  ***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. The bioinformatic analysis is on-going. Targeted sequencing analysis of two known high stearic genes on chromosome 2 (SACPD-B) and 14 (SACPD-C) for the selected 12 RILs is on-going. | |
| **Summary and Highlights:**   * **New breeding populations planted in 2022 progeny plots contain some interesting lines with the most desirable fatty acid profiles (high stearic/high oleic/low linolenic) and will be focused for selection.** * **The whole-genome sequencing process is done and analysis for structural variation is on-going.** * **Targeted-sequencing analysis is on-going.** | |