

Article

Identification of high-yielding soybean lines with exceptional seed composition qualities

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Version April 8, 2022 submitted to Journal Not Specified



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2. Introduction

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6 3. Materials and Methods

3.1. Population development

In 2018, oil mapping populations 201 and 202 were grown at the Central Crops Research Station in 28 Clayton, NC. These populations consisted of 273 and 237 recombinant inbred lines (RILs) respectively. 29 Several agronomic traits were scored in the field for each population. These included height, lodging, 30 maturity date, and a composite agronomic score. Lodging was scored on a scale of 1-5 where 5indicates that all plants in a plot are on the ground, and a score of 1 indicates that all plants are erect[Feh87]. The agronomic score aimed to capture other traits of value such as visual estimation of pod load and plot uniformity to provide a general score of a line's agronomic desirability. Agronomic score was recorded on a scale of 1-5 aswell, with 1 identifying the best lines of a population, and 5 the worst. Maturity was recorded at the R8 maturity date. Height was measured in centimeters from the soil to the top of the plant. Following harvest, yield, seed weight, protein, and oil content were measured after seed was air dried to approximately 7% moisture content in a greenhouse. Protein and oil contents were measured on a dry basis using a Perten DA 7250 NIR®instrument. Yield and seed weight were measured after seed had been sifted and cleaned of debris and cracked seed. To select lines for the 2019 growing season, lines with abnormally low bulk weights or extreme maturity dates from 2018 were first removed from consideration. Two yield trials were then developed for each mapping population. The maturity data of RILs were considered when forming tests such that the lines of each test would have a maturity data range approximately half that of the total mapping population from which it was derived. RILs were selected for each test which were also representative of the distribution of seed protein and seed oil traits for each population. Eighty unique lines were selected from each population 46 which satisfied these criteria, and each yield test was comprised of 40 RILs. Three high-yielding check cultivars and the two parents of the respective population were also included in each test. Yield check cultivars Dunphy, Osage, and Roy were used in tests 1 and 2, while Dunphy, Dilday, and N.C. Raleigh were used for tests 3 and 4. These lines were selected to represent the estimated maturities of the RILs in each test. The parents for tests 1 and 2 were cultivars LMN09-119 and N09-09, and the parents for 51 tests 3 and 4 were LMN09-19 and N13-47.

These four tests were grown in two locations in 2019: the Tidewater Research Station in Plymouth, NC (PLY) and the Caswell Research Farm in Kinston, NC (CAS). The same data was collected for each test in this season that was collected in the previous season. Selections were done using this data by first identifying the lines with a yield within or above a least significant difference (LSD) of the average yield of the checks for each test. Further selection was done using the seed composition traits by identifying the thirty lines with the highest protein + oil content.

These thirty lines were then grouped into two new tests of 15 RILs each which were then grown in both the 2020 and 2021 seasons. These tests were grown in CLA and CAS in 2020 and CAS and PLY in 2021.

3.2. Statistical Analysis

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The data for seed yield, seed oil, and seed protein contents were analyzed using a mixed model with the metan[4] R package. Environment, replication nested with environment, and the interaction of genotype with environment were considered to be random effects while genotype was considered to be a fixed effect.

Materials and Methods should be described with sufficient details to allow others to replicate and build on published results. Please note that publication of your manuscript implicates that you must make all materials, data, computer code, and protocols associated with the publication available to readers. Please disclose at the submission stage any restrictions on the availability of materials or information. New methods and protocols should be described in detail while well-established methods can be briefly described and appropriately cited.

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4. Results

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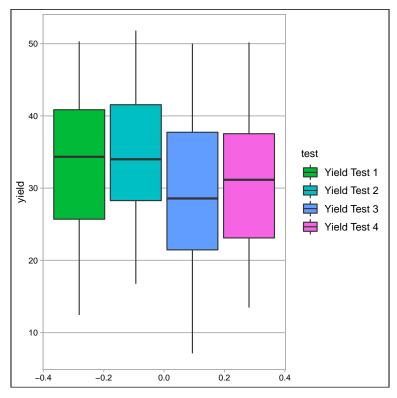


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Title 1	Title 2	Title 3
entry 1	data	data
entry 2	data	data

This is an example of an equation:

$$\mathbb{S}$$
 (1)

- Example of a theorem:
- **Theorem 1.** Example text of a theorem.

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb	
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4	
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4	
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1	
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1	
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2	
Valiant	18.1	6	225	105	2.76	3,460	20.22	1	0	3	1	

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₀₈ 6. Conclusion

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Abbreviations

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The following abbreviations are used in this manuscript:

MDPI Multidisciplinary Digital Publishing Institute

DOAJ Directory of open access journals

TLA Three letter acronym

LD linear dichroism

133 Appendix A

134 Appendix A.1

The appendix is an optional section that can contain details and data supplemental to the main text. For example, explanations of experimental details that would disrupt the flow of the main text, but nonetheless remain crucial to understanding and reproducing the research shown; figures of replicates for experiments of which representative data is shown in the main text can be added here if brief, or as Supplementary data. Mathematical proofs of results not central to the paper can be added as an appendix.

141 Appendix B

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144 References

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