Determination of Yield, Yield Components, and Phenotypic Trait Variation Among Niger Crosses

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Introduction

Niger (*Guizotia abyssinica* (L. f.) Cass.) is primarily marketed in the U.S. as birdseed for American goldfinches (*Carduelis tristis*) because of its high oil content. In this study, five niger accessions were crossed to form six different populations that were evaluated for seed yield, seed oil and agronomic traits to determine the feasibility of future breeding efforts in improving these traits.

Fourteen niger accessions of Indian, Ethiopian, and American origin were obtained from USDA-ARS germplasm collection at Pullman, WA and evaluated in summer of 2012 at the East Tennessee Research & Education Center. Populations were created from five parents: PI 422242, PI 511305, PI 508075, PI 508076, and W6 18860.

Objective

To determine differences among parents, F1s, F2s, and BCs in seed yield, seed oil and morphological traits.

Materials and Methods

A RCBD was used for this experiment. Five parents (3 replications/block), six F1's (5 replications/block) and F2's (25 replications/block), and eight BC's (5 replications/block) were planted in each of four blocks at two University of Tennessee Research & Education Centers (East TN and Highland Rim) in 2013 (See Key). Plants were started in a greenhouse and transplanted to space-planted field nurseries (.61 x .76 m spacing) at each location. All data were collected and reported on a per plant basis. Data were collected on number of primary branches and flowers plant^{-1}, seed flower^{-1}, plant height, lodging, and estimated seed yield (g plant^{-1}). Due to a killing frost it was not possible to measure seed yield at maturity, therefore seed yield was estimated by: flowers plant-1 x avg. seed per flower x avg. seed weight. Analysis of variance, mean separation and correlations for the traits measured were conducted using SAS 9.3 (Cary, NC).

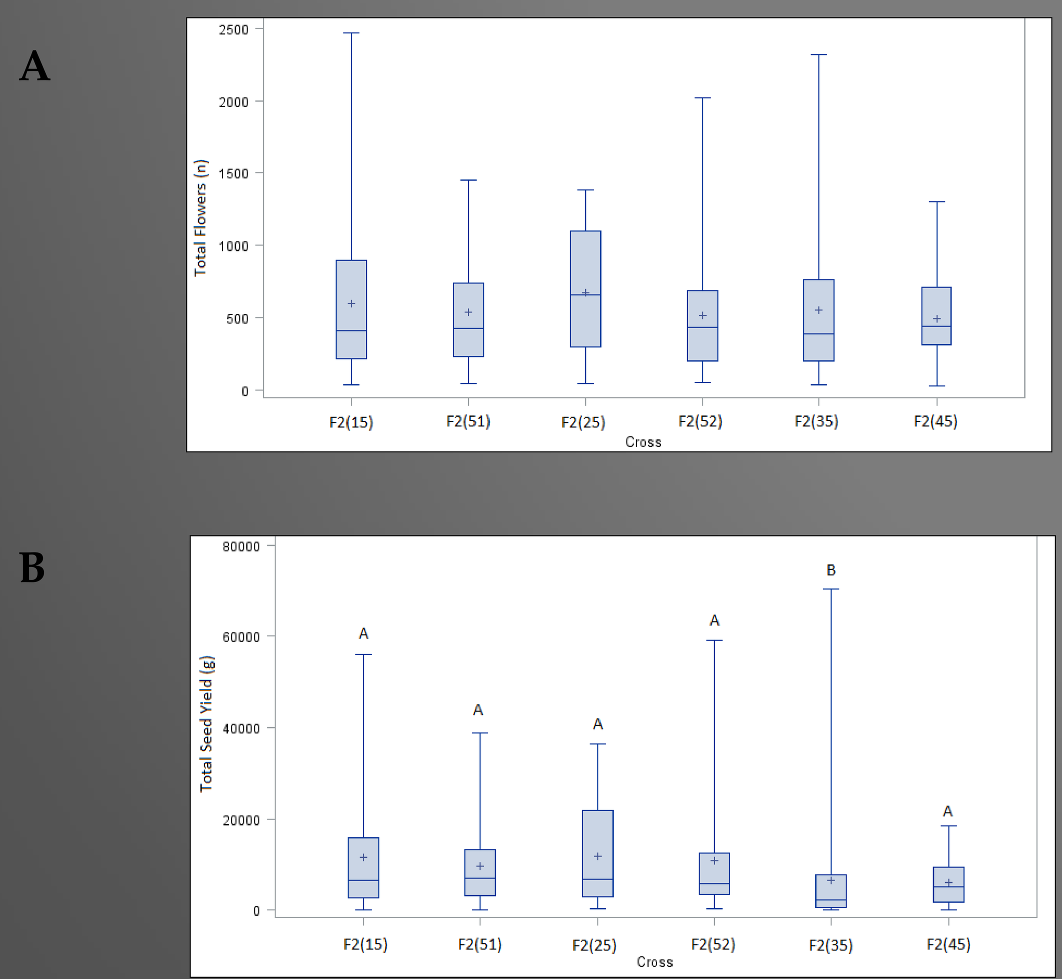
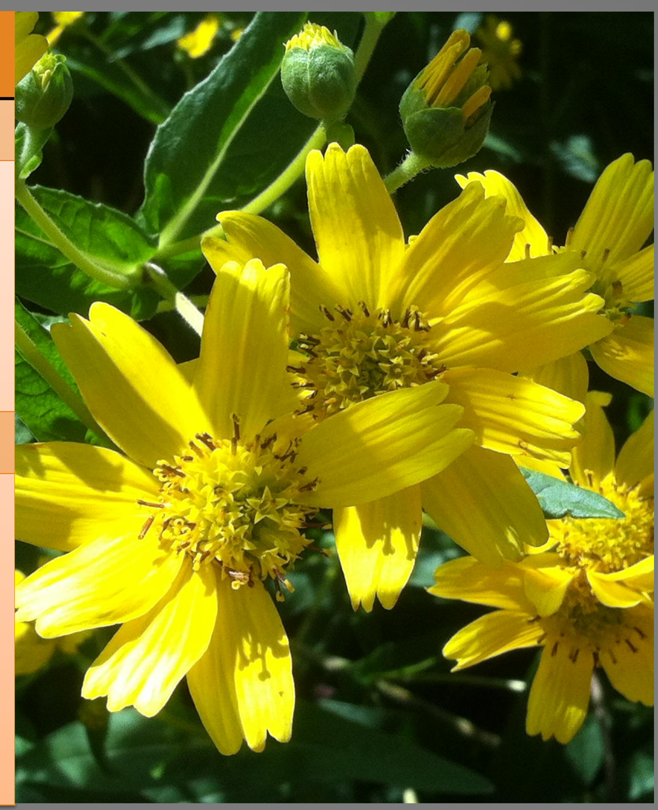


Fig. 1. Boxplots for estimated total flowers plant^{-1} and seed yield (g plant^{-1}) showing variation of F_2 populations. Data were combined across the East Tennessee and Highland Rim Research and Education Centers, 2013.

†Values significantly different based on Fisher's Least Significant Difference (P< 0.05). Populations from Fig. 4B were not significantly different.
‡ Similar letters indicate values do not differ significantly
§ P1, P2, P3, P4, and P5 are parent accessions (PI 422242, PI 511305, PI 508075, PI 508076, and W6 18860, respectively). F15 and F51, for example, are the reciprocal F1 crosses. F15 shows that P1 was the maternal parent plant and P5 was the paternal parent plant. F2 crosses follow the same format. F2(15), for example, is an F2 created from crossing F1(15) with F1(15).

Key

P	F1s
• P1 = PI 422242 • P2 = PI 511305 • P3 = PI 508075 • P4 = PI 508076 • P5 = W6 18860	• P1/P5 = F1(15) • P5/P1 = F1(51) • P2/P5 = F1(25) • P5/P2 = F1(52) • P3/P5 = F1(35) • P4/P5 = F1(45)
F2s	**BCs**
• P1/P5//P1/P5 = F2(15) • P5/P1//P5/P1 = F2(51) • P2/P5//P2/P5 = F2(25) • P5/P2//P5/P2 = F2(52) • P3/P5//P3/P5 = F2(35) • P4/P5//P4/P5 = F2(45)	• P5/P2//P5 = BC525 • P5/P2//P2 = BC522 • P2/P5//P2 = BC252 • P2/P5//P5 = BC255 • P5/P1//P5 = BC515 • P5/P1//P1 = BC511 • P1/P5//P1 = BC151 • P1/P5//P5 = BC155



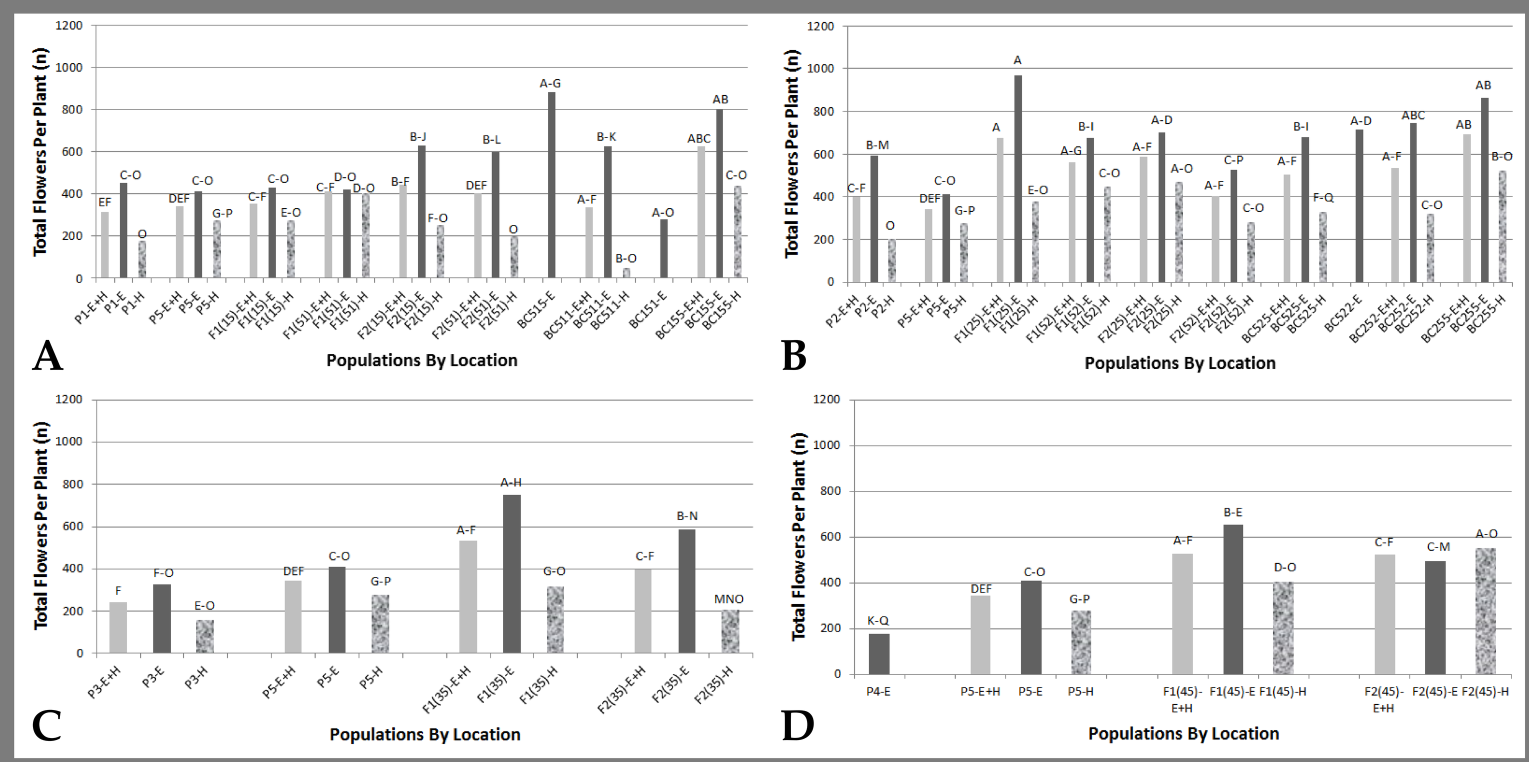


Fig. 2. Mean number of flowers plant^{-1} of niger parents (P's), F1's, F2's, and BC's at the East Tennessee (E) and Highland Rim (H) Research and Education Centers , and locations combined (E+H). P1 and P5 (A), P2 and P5 (B), P3 and P5 (C), and P4 and P5 (D).

† Bars sharing a letter in common are not significantly different based on Fisher's Least Significant Difference (P< 0.05).
‡ All P's, F_1's, F_2's, and BC's in graphs were run the same analysis. BC515, BC151, BC522, and P4.were only present at location E.
§ P1, P2, P3, P4, and P5 are parent accessions (PI 422242, PI 511305, PI 508075, PI 508076, and W6 18860, respectively). F_1(15) and F_1(51), for example, are the reciprocal F_1 crosses. F_1(15) shows that P1 was the maternal parent plant and P5 was the paternal parent plant. F_2 and BC crosses follow the same format. F_2(15), for example, is an F_2 created from crossing F_1(15) with F_1(15). BC515, for example shows that F_1(51) was backcrossed to P5.

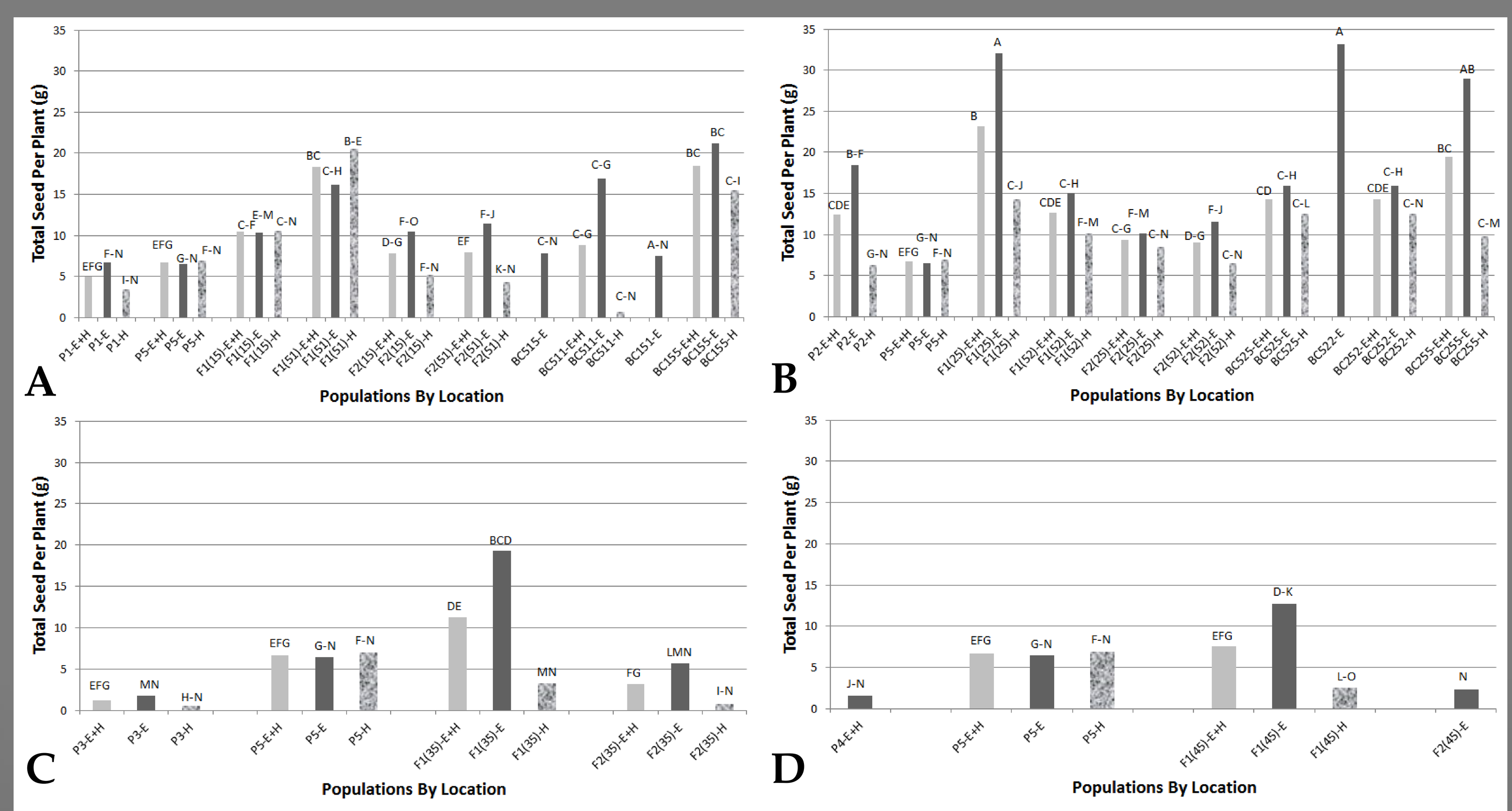


Fig. 3. Estimated seed yield plant^{-1} for niger parents (P's), F1's, F2's, and BC's at the East Tennessee (E) and Highland Rim (H) Research and Education Centers, and locations combined(E+H). P1 and P5 (A), P2 and P5 (B), P3 and P5 (C), and P4 and P5 (D).

† Bars sharing a letter in common are not significantly different based on Fisher's Least Significant Difference (P< 0.05).
‡. All P's, F_1's, F_2's, and BC's in graphs were run the same analysis. BC515, BC151, BC522, P4, and F2(45) were only present at location E.
§ P1, P2, P3, P4, and P5 are parent accessions (PI 422242, PI 511305, PI 508075, PI 508076, and W6 18860, respectively). F_1(15) and F_1(51), for example, are the reciprocal F_1 crosses. F_1(15) shows that P1 was the maternal parent plant and P5 was the paternal parent plant. F_2 and BC crosses follow the same format. F_2(15), for example, is an F_2 created from crossing F_1(15) with F_1(15). BC515, for example shows that F_1(51) was backcrossed to P5.

Results

Results indicate significant differences among crosses for total flowers, estimated seed yield, total branches, height and days to full bloom (P<0.01). Lodging showed insignificant differences among crosses. Locations were significantly different for total flowers and seed yield (Figs. 1 and 2).

Boxplots of F2 populations show that total flowers (Fig. 1A) and estimated seed yield (Fig.1B) performed similarly, and had similar amounts of variation. No significant differences among F2 populations for total flowers (Fig. 1A). The F2(35) population yields were significantly greater than the other populations (Fig. 1B).

Total flowers plant^{-1} resulted in significant differences between E and H for P2, F1(25), F2(51), and BC155 (Fig. 2). E+H results showed that all BC's from same P's performed similarly, F1(25), F1(52), F1(35), and F1(45) showed high-parent heterosis, and F2(45) showed mid-parent heterosis.

Estimated seed yield resulted in significant differences between E and H for P2, F1(25), F1(35), F1(45), F2(51), and BC255 (Fig. 3). E+H results showed that all BC's from same P's performed similarly. High-parent heterosis was evident in F1(15) and the reciprocal F1(51), F1(25) and the reciprocal F1(52), and F1(35).

A moderate positive correlation was found between height and number of branches (r=0.47). Also, moderate positive correlations were found between flowers and number of branches (r=0.39) as well as height and total flowers (0.31)(P<0.0001)(data not shown).

Conclusion

- Total flowers, estimated seed yield, total branches, height and days to full bloom showed significant differences among cross populations
- Total flowers plant^{-1} and seed yield plant^{-1} were higher at ETREC than HREC
- F1(25) produced the greatest number of flowers and seed yield
- P4 and P3 produced the least number of flowers and seed yield, respectively
- Locations differed significantly for total flowers and seed yield
- Seed yield boxplots showed significant differences between F2 populations
- Based on the results of this study, breeding efforts are encouraged for increased seed yield.

Future Research

A two year study (2013 and 2014) will evaluate:
1) Self-incompatibility within niger accessions
2) 2 yr mean yields and yield components evaluated at 3 locations
3) Genetic variance of yield and yield components
4) Correlations between seed yield and yield component traits as well as seed yield and seed oil and fatty acid traits

Acknowledgments

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