GENERATION MEANS ANALYSIS OF SEED YIELD AND FATTY ACIDS AMONG CROSSES OF NIGER Victoria Benelli and Fred Allen

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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.

Populations can be expressed by the amount and type of genetic variability they contain. The components include: phenotypic, genotypic, additive, dominance, interaction, and environmental variation (Fehr, 1987). Genetic variance among individuals of a population is a function of the additive, dominance, epistatic interaction, and gene frequencies.



Results

Seed Yield: Evaluations of seed yield plant⁻¹ in this study indicate that dominance gene effects tended to be the most important, especially in P2xP5 and its reciprocal P5xP2. Epistatic interactions, especially additive x additive, tended to have a positive effect whereas additive gene effects were often negligible or negative. With the exception of P5xP1, additive gene effects were negative; having a diminishing effect on seed yield; whereas dominance gene effects were positive (Table A). Of all three types of digenic epistasis, additive x additive gene effects were most positive. These findings support those of Gamble (1961) in which dominance > epistatic > additive gene effects for yield in corn. P5xP2 resulted in greater gene effects than the other crosses for m, a, d, aa, ad, and **Linoleic Acid:** Relative to fatty acid composition, the cross, P1xP5, resulted in the greatest mean effects of all crosses for linoleic fatty acid (Table B). P2xP5 resulted in the greatest additive effects. Values for d and dd were not estimable. F_1 crosses using P5 as the male parent resulted in greater additive gene effects than their reciprocals. Means for P1xP5 and P5xP2 were greater than P5xP1 and P2xP5, respectively. Contrastingly, additive x additive gene effects were greater in P5xP1 and P2xP5 than P1xP5 and P5xP2, respectively. **<u>Oleic Acid</u>**: The cross, P2xP5, had the greatest mean effects of all crosses for oleic acid (Table C). The reciprocal cross, P5xP2, had the greatest additive effects. Again, values for d and dd were not estimable. Means for P1xP5 were lower than reciprocal P5xP1, and means for P5xP2 were lower than reciprocal P2xP5 with the exception of the Plateau location. Additive x additive gene effects were greater for P1xP5 and P5xP2 than the reciprocals P5xP1 and P2xP5, respectively. **Palmitic Acid**: P1xP5 and P5xP2 had the greatest mean effects of all crosses for palmitic fatty acid (%) (Table D). Values for d and dd were not available. Only as effects for P5xP1.

Objective

To determine gene effects for seed yield and fatty acids (linoleic, oleic, palmitic, and stearic) among selected crosses of 3 niger accessions.

Materials and Methods

A preliminary field study was conducted in 2012 to evaluate the performance of 14 niger accessions obtained from the USDA/ARS germplasm collection at Pullman, WA. Upon maturity, 5 accessions were chosen for further study. Crosses were made among 3 of the 5 to produce six F_1 's, F_2 's, and eight BC's. There were four blocks per location. Each parent was replicated three times in each block. Each F_1 and BC was replicated five times in each block, and each F_2 was replicated twenty-five times per block. This study was conducted at two University of Tennessee Research & Education Centers (East TN and Highland Rim) in 2013 and three (East TN, Highland Rim, and Plateau) in 2014.

Tables A-D. Mean estimates of gene effects for four crosses for seed yield plant⁻¹ (g) (A), linoleic acid (%) (B), oleic acid (C), and palmitic acid (D) at the East Tennessee (E) (2013 and 2014), Highland Rim (H) (2013), and Plateau (P) (2014) Research and Education Centers.

+ Significant at P≤0.01 and P≤0.05 is indicated by ** and *, respectively.
‡ P1, P2, and P5 code for the following accessions: PI 422242, PI 511305, and W6 18860, respectively.

§ m= mean effects, a= additive, d= dominance, aa= additive x additive, ad= additive x dominance, and dd= dominance x dominance

¶ n/a indicates the value was not computable due to missing generations

Gene Effects Seed Yield †§¶										
Year	Loc	Cross ‡	m	a	d	aa	ad	dd		
2013	E+H	P1xP5	7.79	-14.07	18.88	16.00	-13.08	-31.15		
		P5xP1	7.99*	-8.30	13.78	2.47	-9.30	9.41		
		P2xP5	7.31	-6.84	52.62**	38.20**	-9.42	-38.77		

Plants were started in a greenhouse and transplanted to spaceplanted field nurseries (.61 x .76 m spacing) at each location. A RCBD was used for this experiment. PI 422242 (P1), PI 511305 (P2), and W6 18860 (P5) were used to make initial and reciprocal crosses. 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 for the traits measured were conducted using SAS 9.3 (Cary, NC).

C

D

Generation means analysis was used to estimate gene effects based on the work of Gamble (1961). Estimates were taken from contrast statements using mixed model analysis of variance in SAS 9.3, and recorded for each F1 and related generations (P1, P2, F2, P1F1, and P2F1) to obtain estimates of gene effects of the mean (m), additive (a), dominance (d), and epistasis (aa, ad, dd). Estimates of the above effects were computed for each cross as follows: m= F2

a=P1F1-P2F1 d=-1/2P1-1/2P2+F1-4F2+2P1F1+2P2F1

	P5xP2	8.17*	-15.69**	57.87**	54.86**	-13.12**	-98.39**
)14 E+P	P1xP5	4.79**	-2.57	n/a	10.53	n/a	n/a
	P5xP1	7.40**	8.42**	n/a	16.55**	n/a	n/a
	P2xP5	11.04**	-10.68**	n/a	15.52	n/a	n/a
	P5xP2	11.57**	-5.45	n/a	-11.65	n/a	n/a

Gene Effects Linoleic Acid †§¶										
lear	Loc	Cross ‡	m	a	d	aa	ad	dd		
2014	E+P	P1xP5	60.94**	2.06	n/a	-16.35	n/a	n/a		
		P5xP1	56.71**	-0.32	n/a	5.26	n/a	n/a		
		P2xP5	51.84**	13.31	n/a	-13.28	n/a	n/a		
		P5xP2	56.99**	-7.38*	n/a	-25.12	n/a	n/a		

Gene Effects Oleic Acid †§¶									
Year	Loc	Cross ‡	m	a	d	aa	ad	dd	
2014	E+P	P1xP5	12.80**	-1.99	n/a	15.35	n/a	n/a	
		P5xP1	18.76**	-3.40	n/a	-15.18	n/a	n/a	
		P2xP5	22.80**	-3.17	n/a	-6.85	n/a	n/a	
		P5xP2	22.59**	2.20	n/a	1.21	n/a	n/a	

Gene Effects Palmitic Acid †§¶									
Year	Loc.	Cross ‡	m	a	d	aa	ad	dd	
2014	E+P	P1xP5	13.46**	1.13	n/a	-2.99	n/a	n/a	

Conclusion

- Based on the results of this study, breeding efforts are encouraged for increased seed yield.
- P5xP2 had the greatest mean performance for seed yield (Table A), linoleic acid (Table B), oleic acid (Table C), and palmitic acid (Table D).
- P1xP5 and P5xP2 cross means were greater than the respective reciprocal crosses for linoleic acid, but lower for oleic acid.
 Reciprocal effects are evident where F₁ crosses using P5 as a male
- parent result in greater additive effects than when the other parents were used as the male parent.

Literature Cited

Gamble, E.E. 1961. Gene effects in corn (Zea Mays L.)- II. Relative importance of gene effects for plant height and certain component attributes of yield. Canadian J. of Plant Sci. 42:349-358.



aa=-4F2+2P1F1+2P2F1 ad=-1/2P1+1/2P2+P1F1-P2F1 dd=P1+P2+2F1+4F2-4P1F1-P2F1

where: $F2=F_2$ mean P1= Female parent one mean P2= Male parent two mean $F1=F_1$ mean P1F1= Backcross mean (backcross F_1 to female parent)

P2F1= Backcross mean (backcross F_1 to remate parent)

P5xP111.81**1.56n/a9.78*n/an/aP2xP511.57**2.76n/a-7.28n/an/aP5xP212.12**1.53n/a-0.12n/an/a

† Significant at P≤0.01 and P≤0.05 is indicated by ** and *, respectively.
‡ P1, P2, P3, P4, and P5 code for the following accessions: PI 422242, PI 511305, PI 508075, PI 508076, and W6 18860, respectively.

§ m= mean effects, a= additive, d= dominance, aa= additive x additive, ad= additive x dominance, and dd= dominance x dominance

 \P n/a indicates the value was not computable due to missing generations comprising the equation

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