Phenotypic Variation in Fruit and Seed Characteristics of Buffalo Gourd[1]

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ABSTRACT

Eighty-five accessions of Buffalo gourd, *Cucurbita foetidissima* HBK., were assayed for variation in seven fruit and seed characteristics: fruit diameter ($\bar{x}$ = 65 mm); seed weight per 100 seeds ($\bar{x}$ = 3.8 g); seed weight per fruit ($\bar{x}$ = 8.4 g); seed number per fruit ($\bar{x}$ = 225); percentage embryo in seed ($\bar{x}$ = 67.3%); percent crude fat of whole seed ($\bar{x}$ = 32.9%); and percent crude protein of defatted embryo ($\bar{x}$ = 69.5%). The variation in amino acid distribution (12) accessions) and in oil composition (15 accessions) was obtained. Relationships among traits were explored. Agronomic improvement through breeding was also discussed.

INTRODUCTION

The Buffalo gourd, *Cucurbita foetidissima* HBK., exhibits agronomic potential as a arid adapted crop (1-4). This feral, xerophytic cucurbit produces seeds rich in protein (32.9%) and oil (33.0%) (5). Hensarling et al. (6) evaluated the nutritive value of Buffalo gourd seed globins. Weber et al. (7) studied defatted seed meal as a protein source using weanling mice. Bemis et al. (1) discussed the composition of the seed oil. The perennial plants also develop large tuberous roots which contain 55% starch on a moisture equilibrated basis (8). The distribution of the species, growth habits, morphology, and mode of reproduction were described by Bemis et al. (1).

Variation within the species remains virtually unexplored. This study measured the phenotypic variation in fruit and seed characteristics among accessions collected from diverse germplasm sources. Possible relationships between these characteristics were also evaluated. As superior phenotypes are identified in later studies, selection procedures will be employed to improve the agronomic potential of the species.

MATERIALS AND METHODS

Collection

Accessions of *C. foetidissima* were obtained from 33 Arizona collection sites in autumn 1975 (Fig. 1). Fifty-two additional accessions were collected in autumn 1976 from the southern Rocky Mountains and the Great Plains regions of the U.S. At each collection site, 10 to 40 pepos were harvested from individual plants. Visual observations concerning fruit and leaf characteristics were recorded at the site.

Sample Preparation

Data concerning fruit diameter and carpel number were obtained from cleaved fruit of each accession. Seeds were extracted by submerging fruits in water until fermentation disintegrated the placental tissue. The seeds of each lot were washed, air-dried, and weighed. A weight per 100 seeds was also recorded. Estimates of the seed weight per fruit and the seed number per fruit were calculated from the following equations:

seed weight per fruit =
total seed weight/number of fruit collected

seed number per fruit =
100 (seed weight per fruit/weight per 100 seeds)

To determine the proportion of seed parts, the hulls and embryos of 20 seeds per accession were manually separated, dried overnight in a 100 C oven, and weighed. For laboratory analysis, approximately 20 g of each seed lot were ground to a 10 mesh maximum particle size.

Laboratory Analysis

The crude fat content of each accession was determined for triplicate 5 g samples by Soxhlet extraction with hexane. Fatty acid distributions of 15 accessions chosen at random were obtained. Triglycerides were cold extracted

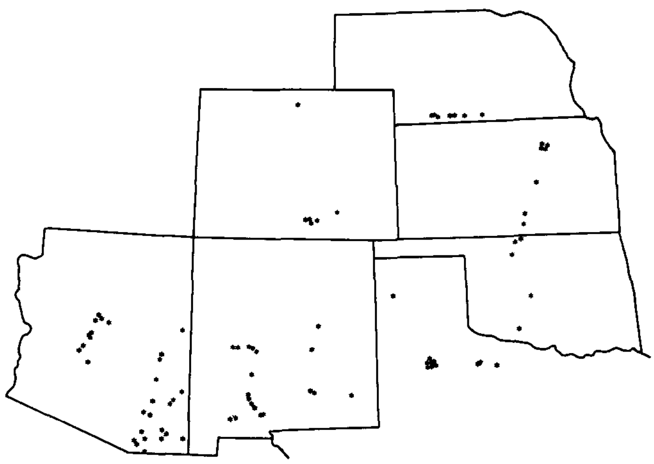

Fig. 1. Location of *C. foetidissima* collection sites.

[1] Arizona Agricultural Experiment Station No. 2805.

TABLE I

Means, Ranges, Standard Deviations, and Coefficients of Variability (C.V.) of Seven Fruit and Seed Characteristics of 85 *C. foetidissima* Accessions

Characteristic	Mean	Range	Std. dev.	C.V.
Fruit diameter	65. mm	52. mm - 77. mm	5.9 mm	9.1%
Seet wt/100 seeds	3.8 g	1.1 g - 5.5 g	0.9 g	20.0%
Seed wt/fruit	8.4 g	2.7 g - 18.8 g	3.1 g	36.9%
Seed number/fruit	225	87 - 386	63.6	28.3%
% Embryo in seed	67.3%	42.1% - 76.3%	6.5%	9.7%
% Crude fat of whole seed	32.9%	21.1% - 43.1%	4.7%	14.3%
% Crude protein of defatted embryo	69.5%	55.5% - 75.8%	3.5%	5.0%

TABLE II

Correlation Coefficients among Seven Fruit and Seed Characteristics of 85 *C. foetidissima* Accessions

Characteristic	Fruit diameter	Seed wt/ 100 seeds	Seed wt/ fruit	Seed number/ fruit	% Embryo in seed	% Crude fat of whole seed
Fruit diameter	----					
Seed wt/100 seeds	+0.45[a]	----				
Seed wt/fruit	+0.43[a]	+0.57[a]	----			
Seed number/fruit	+0.13	-0.09	+0.70[a]	----		
% Embryo in seed	----	+0.48[a]	----	----	----	
% Crude fat of whole seed	----	----	----	----	+0.74[a]	----
% Crude protein of defatted embryo	----	----	----	----	----	+0.41[a]

[a]Significant at 1% level.

TABLE III

Means, Ranges, Standard Deviations, and Coefficients of Variability (C.V.) of Amino Acid Constituents in *C. foetidissima* Defatted Embryos[a]

Amino acid[b]	Mean	Range	Std. dev.	C.V.
Lysine	3.7	3.5 - 4.0	0.2	5.4
Histidine	2.2	2.1 - 2.3	0.1	2.7
NH_3	1.7	1.7 - 1.9	0.1	4.1
Arginine	15.7	15.4 - 16.2	0.3	1.7
Aspartate	9.2	8.5 - 9.4	0.2	2.5
Threonine	2.7	2.7 - 2.9	0.1	2.5
Serine	4.8	4.6 - 5.0	0.1	2.1
Glutamate	19.9	19.7 - 20.2	0.2	0.8
Proline	3.5	3.4 - 3.8	0.1	3.2
Glycine	5.7	5.2 - 6.2	0.3	5.3
Alanine	4.3	4.2 - 4.4	0.1	1.4
Cysteine	0.5	tr. - 0.7	0.2	46.9
Valine	5.0	4.7 - 5.1	0.1	2.0
Methinine	2.1	1.9 - 2.3	0.1	5.2
Isoleucine	4.0	3.9 - 4.2	0.1	2.0
Leucine	7.1	6.9 - 7.2	0.1	1.1
Tyrosine	3.0	2.8 - 3.4	0.2	6.7
Phenylalanine	4.9	4.7 - 5.1	0.1	2.3

[a]12 Accessions chosen at random.
[b]Data expressed as percentages of total amino acid content.

from ground whole seed with hexane, transesterified, and isolated from other hexane-soluble material by thin layer chromatography. The isolated methyl esters were separated by gas liquid chromatography under the following conditions: 6 ft x 1/8 in. stainless steel columns, packed with 15% DEGS on Chromosorb W; isothermal operation at 170 C; injector port temperature at 200 C; nitrogen (carrier gas) flow rate of 20 ml/min.

For each accession, embryo material was obtained by sifting the defatted seed meal through a 150 mesh screen. The crude protein content of this material was determined by the micro-Kjeldahl analysis of triplicate samples. Protein percentages were calculated using a conversion factor of 6.0 2as determined by the amino acid data. Amino acid profiles of 12 accessions chosen at random were determined by ion exchange chromatography of acid hydrolysates on an automatic amino acid analyzer.

RESULTS AND DISCUSSION

Collection sites ranged in elevation from 1000 ft at Manhattan, KS, to 7000 ft at Mayhill, NM. Visual observations recorded at the collection sites revealed differences in fruit and foliage characteristics. Leaf shapes were entire and predominantly deltoid with few accessions developing chordate or reniform leaves. Most fruit were globose or ovate shaped, with oblong or oblate fruit produced on occasional plants. Fruit yield varied from a few pepos to over 300 pepos per plant.

Fruit and Seed Characteristics

No geographical trends in fruit and seed characteristics were uncovered. The means, ranges, standard deviations, and coefficients of variability for seven fruit and seed characteristics are listed in Table I. The mean fruit diameter of the population was 65 mm. The mean weight per 100 seed and the seed weight per fruit averaged 3.8 g and 8.4 g, respectively. The average seed number per fruit (225) was lower than that of the homogeneous population studied by Ba-Amer and Bemis (9) and by Costa and Bemis (10). The mean percent of embryo in seed lots (67.3%), the mean percent crude fat from whole seed (32.9%), and the mean percent crude protein of defatted embryo (69.5%) were similar to those values obtained from a single germplasm source (5).

Variation within the species for these seven traits suggests the feasibility of agronomic improvement through selection and breeding. The weight per 100 seeds, seed weight per fruit, and seed number per fruit displayed variability coefficients of 20.0%, 36.9%, and 28.3%, respectively. Weight per 100 seeds was not correlated with seed number per fruit (r = -0.09) (Table II), and indicates the possibility of independent improvement in seed size and seed number. Seed weight per fruit was associated with seed weight per 100 seeds (r = +0.57), but more closely with seed number per fruit (r = +0.70). Selection for increased seed number per fruit appears to be a feasible method to improve yield. Two highest yielding first generation progeny of collected seeds lots (1975) produced fruit which averaged 48% more seed (312 seeds per fruit) than those of the whole population (225 seeds per fruit).

Feasibility of improving the crude fat content of whole seed (C.V. 14.3%) through selection and breeding seemed probable. Higher percent crude fat values were associated

TABLE IV

Means, Ranges, Standard Deviations, and Coefficients of Variability (C.V.) of Fatty Acid Constituents in *C. foetidissima* Accessions[a]

Fatty acid[b]	Mean	Range	Std. dev.	C.V.
Palmitate	9.7	7.3 - 12.1	1.4	14.6
Stearate	4.5	3.8 - 6.8	0.8	17.8
Oleate	27.0	17.2 - 36.2	6.4	23.7
Linoleate	58.5	49.5 - 68.8	6.3	10.7

[a]15 Accessions chosen at random.
[b]Data expressed as percentages of total fatty acid content.

TABLE V

Correlation Coefficients among Fatty Acid Constituents in *C. foetidissima* Accessions[a]

Fatty acid	Palmitate	Stearate	Oleate
Palmitate	- - -		
Stearate	+0.46	- - -	
Oleate	-0.09	-0.28	
Linoleate	-0.19	-0.06	-0.95[b]

[a]15 Accessions chosen at random.
[b]Significant at the 1% level.

with a larger embryo percentage (r = +0.74). The crude protein content of defatted embryo was relatively stable among accessions (C.V. 5.0%). The few accessions displaying low protein values may have been immature at the time of collection. The correlation between the crude protein level of the embryo and the crude fat content of the whole seed was +0.41.

Amino Acids

Little variation in amino acid composition was found among seed lots. The mean distribution of amino acid constituents supported previous determinations of this trait (6,7). Glutamate (19.9%) and arginine (15.7%) predominated, while cysteine (0.5%), was present in least amount (Table III). Tryptophan content was not available from acid hydrolysates.

Fatty Acids

The mean fatty acid distribution (Table IV) resembled that reported by Bemis et al. (1). Sufficient variation in oil composition was present to suggest its possible alteration through breeding. Oleate and linoleate, closely associated biochemically (11), displayed a strong negative correlation (r = -0.95) (Table V). Selection for either form of unsaturation appears possible.

ACKNOWLEDGMENTS

This study was supported in part by grants from the USDA-ARS, Plant Germplasm Coordinating Committee and by NSF-RANN No. A ER 76-82387.

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[Received November 21, 1977]