

Interspecific Derivatives for Widening the Genetic Base of Groundnut

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One hundred and fifteen interspecific derivatives of groundnut developed at National Research Centre for Groundnut, Junagadh (Gujarat) were evaluated along with checks in augmented design for yield and yield related traits under field conditions. The analysis of variance for quantitative traits revealed wide genetic diversity for biological yield, pod yield, kernel yield, hundred-kernel mass, harvest index and shelling out-turn. Two genotypes NRCGCS 268 and NRCGCS 269 recorded significantly higher hundred-kernel mass than the check variety, TKG 19A. Genotypes NRCGCS 257 and NRCGCS 277 were tolerant to multiple foliar diseases recording less than 4.0 disease severity of early leaf spot, late leaf spot and rust on a modified 9-point scale. Eight genotypes were found promising for oil content with more than 50% oil. The promising interspecific derivatives identified for various quantitative traits would help in broadening the genetic base of groundnut.

Key Words: *Arachis hypogaea*, Foliar disease, Groundnut, Interspecific derivative, Oil content

Introduction

Groundnut (*Arachis hypogaea* L.) is the principal oilseed crop in India accounting for more than 25% of the total area under oilseeds. Though India accounts for the largest area under groundnut, it does not contribute much to the global production and trade due to low productivity, which is further compounded by fluctuations resulting from abiotic and biotic stresses in the rainfed production system. Development of the genotypes endowed with tolerance to different abiotic and biotic stresses along with high reproductive potential continues to be the major objective in groundnut improvement programmes. The success of improvement programme depends on the extent of variability available for desirable traits. Hence, to create wide genetic variability, interspecific crosses were made and they were evaluated for yield attributes, resistance to major foliar diseases like leaf spots and rust, and the oil content.

Materials and Methods

One hundred and fifteen groundnut interspecific derivatives were used in the experiment. Derivatives are progenies of crosses between J11 × *A. cardenasii*, J11 × *A. duranensis*, J11 × *A. kretschmeri*, J11 × *A. correntina*, J11 × *A. oteroi*, J11 × *A. stenosperma* and J11 × *A. diogoi* at National Research Centre for Groundnut (NRCG), Gujarat. Cultivar J11 is a Spanish bunch (erect type) groundnut (*A. hypogaea*) and used as ovule parent in all cross combinations. J11 produces higher number of cross pods than other cultivars while used in interspecific crosses (unpublished data generated by the author) and

are resistant to *Aspergillus flavus*, the causal organism of aflatoxin contamination in groundnut. These were evaluated along with two Virginia bunch (TKG 19A and GG 20) and three Spanish bunch (TAG 24, GG 2 and JL 24) groundnut (*A. hypogaea*) varieties used as checks in Augmented Block Design distributed in five blocks in experimental farm of NRCG during rainy season 2006. Each entry was sown in three lines of five meters bed following standard crop management practices. The data were recorded on various qualitative traits namely biological yield/10 plant (BY), pod weight/10 plant, kernel weight/10 plant, harvest index (HI), shelling out-turn, hundred kernel mass (HKM) and the oil content. The severity of major foliar diseases, viz., early leaf spot (ELS), late leaf spot (LLS) and rust, arising from natural inoculums sources was recorded from 80-90 days old crop using modified 9-point scale (Subrahmanyam *et al.*, 1995). Data were analysed using augmented design II. Range, mean and standard deviation were calculated for quantitative traits following standard statistical procedures.

Results and Discussion

Interspecific derivatives are generally characterized based on distinguishable phenological and agro-morphological traits. Derivatives comprising both Spanish (erect) and Virginia bunch (semi-spreading) habit group showed good early plant vigour. The analysis of variance for quantitative traits revealed good amount of genetic diversity in the population for biological yield/10 plants, pod yield/10 plants, kernel yield/10 plants, hundred-

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kernel mass, harvest index and shelling out-turn (Table 1). A wide range of variation in HKM, pod weight, kernel weight, shelling out-turn, oil content, resistance to leaf spot and rust diseases in cultivated groundnut was also reported by Reddy and Gupta (1992), Khurram *et al.* (1998) and Salara and Gowda (1998). This indicates wide variation existing in cultivated groundnut for these traits. Block effect was significant and adjusted statistically as per augmented design. Checks used in the experiment differed significantly for biological yield/10 plant, pod yield/10 plants, kernel yield/10 plant, HKM, harvest index and shelling out-turn. Variability estimates indicated that a wide range of variations was available in the population confirming the positive transgression for trait of interest and the entries out yielded for various traits beyond the best check (Table 2). Biological yield/10 plants of the population ranged from 92-529 g with an average of 280 g. Segregants with higher biological yield/10 plants indicated the introgression of traits from wild parent having perennial creeping habit with large volume of foliage. Though twelve genotypes recorded biological yield more than 400 g, only NRCGCS-241 recorded significantly higher biological yield over the best check (505.2 g) (Table 2 and 5). Pod weight varied from 27-162 g with an average of 76.2 g. Frequency distribution showed that majority of genotypes could be grouped into the class of 51-100 g for pod weight. A few positive extreme segregants were available in the population, may be due to introgression of less pod

bearing and smaller pod size characters of both wild pollen parent as well as pistil parent, J-11. However, two genotypes NRCGCS-241 and 242 significantly out-yielded than the best check (147.5 g) for pod yield. Singh and Singh (1998) also observed high variation for pod yield per plant and HKM. Kernel weight varied from 12-93.2 g with an average of 45 g. Unlike the pod weight, majority of the genotypes of population could be grouped into three classes (16-35, 36-45, and 46-55) for kernel weight with a continuous variation distributed in 8 classes. The genotypes, NRCGCS-241, 242, 253 and 296 produced significantly higher kernel weight than the check. HKM of the population varied from 11.5-61.2 g with a mean of 31.0 g. HKM of the majority of the entries grouped into four classes (21-25, 26-30, 31-35, 36-40). Unlike the kernel weight, HKM of the population showed continuous variation and distributed in 8 classes with few promising transgressive segregants. Two of which (NRCGCS-268 and 269) recorded significantly higher HKM than the best check (49.2 g). The continuous variation observed for biological yield, kernel weight and HKM could be due to the introgressive hybridisation of both wild and cultivated forms and subsequent selection under varying intensities of selection pressure (Oka *et al.*, 1959).

Harvest index of the population ranged from 5.7-27 % with comparatively low mean value (16.0%). Harvest index of the population distributed in 5 classes of which, class 16-20 accommodated maximum numbers

Table 1. Analysis of variance for different traits of groundnut

Source	df	Mean sum of squares					
		BY/10 plants (g)	Pod wt./10 plants (g)	Kernelwt./10 plants (g)	HKM (g)	HI (%)	Shellingout-turn (%)
Blocks (b)	4	21842.00**	3326.05**	588.98**	80.48**	25.86**	270.16**
Genotypes (e)	119	10452.77**	1044.59**	340.35**	91.54**	20.28**	67.37**
Checks (c)	4	101878.9**	6999.16**	1655.06**	403.27**	13.35**	169.25**
Varieties (v)	114	7649.19**	892.62**	296.47**	72.14**	21.70**	77.41**
Check vs. varieties	1	35643.34**	5449.25**	83.78	1056.09**	113.55**	1484.73**
Error	28	394.37	50.90	26.72	7.54	2.43	11.39

df = degree of freedom; ** =significant at 1%

Table 2. Variability in quantitative characters of test genotypes

	Range	Mean	Best value	SE of the varieties in the same block	SE of the varieties in the different block	SE of the check varieties and & check
BY/10 plant (g)	92.0 -529.0	280.8	505.2	30.76	28.08	23.07
Pod wt./10 plant (g)	27.0 -162.0	76.2	147.5	11.05	10.09	8.28
Kernel wt./10 plant (g)	12.0 - 93.2	45.0	76.2	8.00	7.31	6.00
HKM (g)	11.5 - 61.2	31.1	49.2	4.25	3.88	3.19
HI (%)	5.7 - 27.0	16.0	18.8	2.41	2.20	1.81
Shelling out-turn (%)	31.0 - 75.0	60.0	61.6	5.22	4.77	3.92

BY= Biological yield, HKM= 100 kernel mass, HI= Harvest index

Table 3. Frequency distribution of quantitative characters

BY/10 pl. (g)		PodWt./10 pl. (g)		KernelWt./10 pl. (g)		HKM (g)		HI (%)		Shellingout-turn (%)	
Class	Freq.	Class	Freq.	Class	Freq.	Class	Freq.	Class	Freq.	Class	Freq.
1-100	1	1- 25	0	1-15	1	1-15	2	1- 5	0	1- 15	0
101-150	2	26-50	24	16-35	36	16-20	10	6-10	16	16-35	1
151-200	15	51-100	67	36-45	29	21-25	18	11-15	27	36-45	8
201-250	29	101-125	12	46-55	22	26-30	22	16-20	51	46-55	23
251-300	25	126-150	9	56-65	12	31-35	30	21-25	19	56-65	53
301-350	22	151-200	3	66-75	7	36-40	17	26-30	2	66-75	30
351-400	9	201-225	0	76-85	5	41-45	12	31-35	0	76-85	0
400-529	12	226-250	0	85-93	3	45-61	4	36-40	0	86-95	0

Table 4. Variability estimates of foliar diseases and oil content

Particulars	Disease severity (1-9 scale)			
	Early leaf spots	Late leaf spots	Rust	Oil content (%)
Range	4.17-8.67	3.67-8.67	2.67-8.50	44.0-54.0
Mean	7.76	7.49	7.00	49.95
Check	8.7	8.7	8.5	50.00
SD	0.89	1.01	1.06	1.98
CV %	11.52	13.43	15.16	3.97

of genotypes followed by class 11-15. In spite of lower HI of the population, twenty genotypes significantly surpassed the highest value of check (18.8) and the two genotypes (NRCGCS-297 and 304) were promising. Shelling out-turn of the population ranged from 31-75%, with the population mean of 60%. Majority of the genotypes grouped in the class 56-65 followed by the class 66-75 for shelling out-turn. Twenty-nine genotypes recorded significantly higher shelling out-turn than best check (61.6%), of which NRCGCS-357, 355, 301, 323 and 279 were promising recording more than 73% shelling out turn. Mathur *et al.* (1997) reported that shelling out-turn is most stable character in groundnut and can be used as selection criteria. Scoring of genotypes and checks against major foliar diseases *viz.*, ELS, LLS and rust revealed high disease severity (8.50-8.67) under natural field conditions (Table 4). Singh and Singh (1997) also reported high disease pressure under field conditions among checks. Two genotypes NRCGCS-257 and 277 showed resistance to multiple foliar diseases recording low disease severity (<5) against ELS, LLS and rust (Table 5). These two genotypes could be utilized in developing multiple disease resistant groundnut varieties. Vasanthi and Naidu (1998) has also reported resistance to multiple diseases indicating that these three foliar diseases have fair amount of positive association if they are not tightly linked and can be incorporated in a single background by a single breeding effort.

The oil content of the population ranged from 44-54% with the population mean of 50%. The genotypes,

Table 5. Promising breeding lines of groundnut for various traits

Character	Genotypes
BY/10 plant (g)	NRCGCS-241
Pod wt./10 plant (g)	NRCGCS-241, 242
Kernel wt./10 plant (g)	NRCGCS-241, 242, 245, 253, 264, 268, 280, 296
HKM (g)	NRCGCS-268, 269
HI (%)	NRCGCS-242, 305, 286, 296, 309, 338, 253, 266, 273, 356, 298, 260, 342, 357, 287, 264, 291, 289, 304, 297
Shelling out-turn (%)	NRCGCS-351, 290, 328, 314, 346, 345, 298, 322, 340, 321, 338, 260, 248, 342, 356, 297, 298, 325, 291, 319, 304, 320, 294, 306, 357, 355, 301, 323, 279
ELS (< 5 grade)	NRCGCS-277, 303, 311, 257
LLS (< 5 grade)	NRCGCS-257, 311, 303, 277
Rust (< 5 grade)	NRCGCS-277, 257, 256, 242, 243, 306
Oil content (%)	NRCGCS-269, 254, 273, 297, 237, 243, 251, 266

NRCGCS-269, 254, 273, 297, 237, 243, 251 and 266 recorded more than 52% oil content and can be utilized for developing high oil content cultivars (Table 5). Promising genotypes identified for different quantitative traits can find their way into future breeding programmes.

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