K Amarnath
Ph. D Scholar, Department of
Genetics and Plant Breeding,
S.V. Agricultural College,
Tirupati, Andhra Pradesh, India

M Reddisekhar
Professor, Department of
Genetics and Plant Breeding,
S.V. Agricultural College,
Tirupati, Andhra Pradesh, India

K John
Principal Scientist, Department
of Genetics and Plant Breeding,
IFT, Regional Agricultural
Research Station, Tirupati,
Andhra Pradesh, India

P Sudhakar
Principal Scientist, Department
of Crop Physiology, IFT,
Regional Agricultural Research
Station, Tirupati, Andhra
Pradesh, India

K Viswanth
Scientist, Department of Plant
Pathology, IFT, Regional
Agricultural Research Station,
Tirupati, Andhra Pradesh, India

Studies on combining ability and gene action for pod yield and stem rot resistance in groundnut (*Arachis hypogaea* L.)

K Amarnath, M Reddisekhar, K John, P Sudhakar and K Viswanth

Abstract
The present study was carried out with 20 hybrids generated by hybridizing five lines and four testers in a Line x Tester mating fashion to assess the combining ability of five lines and four testers for pod yield and stem rot incidence. Substantial genetic variability was observed among the hybrids due to diverse nature of lines and testers for the two traits studied. The analysis revealed that among parents, Kadiri-6 and ICGV-07262 are identified as good general combiners for both the traits indicating that these parents could be used in breeding programme for development of high pod yield and stem rot resistant genotypes. Among F_1 crosses, Narayani x J-11, ICGV-07262 x TCGS- 1862, ICGV-07262 x TCGS-2149 and ICGV-91114 x TCGS-2149 were considered as good specific combiners for both the traits suggesting that these crosses would be utilized for further selection to develop high yielding segregants with stem rot resistance in the segregating populations.

Keywords: Groundnut, combing ability, gene action, pod yield and stem rot incidence

Introduction

The cultivated groundnut (*Arachis hypogaea* L. 2n = 40) belongs to family *Fabaceae,* subfamily *Papilionaceae* popularly known as 'king of Oil seeds' or "Wonder nut" and "Poor man's cashewnut". Groundnut is also a good source of minerals and vitamins including vitamin E, niacin, phosphorus, falcin, calcium, riboflavin, magnesium, zinc, iron, thiamine, and potassium (Jibrin *et al*., 2016) [6]. It is a premier oilseed crop grown in India, China, Nigeria, Senegal, Sudan, Myanmar and the United States of America. Globally, it is cultivated in an area of 26.4 Mha with annual production of 37.1 Mt and productivity of 1405 kg ha^{-1}. In India, groundnut covers an area of 4.75 Mha with a production of 6.22 Mt and productivity of 1320 kg ha^{-1} (FAO, 2019-2020). In Andhra Pradesh, it is cultivated in an area of 6.61 lakh ha with a production of 8.50 lakh tonnes and productivity of 1285 kg ha^{-1}. (Directorate of Economics and Statistics, Govt. of A.P, India, 2019-2020).
Both abiotic and biotic stress factors limit peanut crop growth and yield in many ways. Among biotic stresses, stem and pod rot disease caused by *Sclerotium rolfsii* Sacc. is one of the significant factors contributing to yield loss. Southern stem rot or Sclerotium wilt caused by the fungus *Sclerotium rolfsii* is one of the most economically important diseases of peanut accounting for 10 to 25 per cent, sometimes even 80 per cent yield loss in severely infected fields annually (Rakholia and Jadeja, 2010; Pujer *et al*., 2013) [12, 11]. Persistence of the pathogen in soil and its wide host range often limit the effectiveness of chemical and cultural control of stem and pod rot signifying the need for evaluation of genetic resistance. It is evident that stem rot disease has significant effect on the yield. Hence, the simultaneous evaluation of the genotypes for the stem rot resistance as well as yield potential shall form the basis and prioritization in peanut breeding programme. By keeping in view of these constrains an attempt was made to evaluate the hybrids along parents in artificially inoculated sick plot to identify the best performing segregants with consistent yield coupled with stem rot resistance.

Material and Methods

The experiment was carried out during *rabi-* 2019 in sick plot maintained at Regional Agricultural Research, Tirupati situated at an altitude of 182.9 m above mean sea level (MSL), 32.27°N latitude and 79.36°E longitude, geographically in southern agro climatic zone of Andhra Pradesh. The crop was artificially inoculated with *sclerotium* fungus multiplied in sorghum grains between inter rows followed by mulching with paddy straw to entire field after

Corresponding Author:
K Amarnath
Ph. D Scholar, Department of
Genetics and Plant Breeding,
S.V. Agricultural College,
Tirupati, Andhra Pradesh, India

30 DAS, 60 DAS and irrigation was given frequently through drip pipes to conserve moisture which aggravate the mycelium and aids in further multiplication. The material for the present investigation comprised of nine parents (5 Lines and 4 testers) and their F_1's generated through crossing these parents in a Line x Tester mating fashion were grown in a Randomized Block Design replicated twice. Each entry was grown in two rows of 3 m length and the spacing adopted was 22.5 x 10 cm. Data was recorded in 5 randomly selected plants for pod yield per plant While, Percent Disease Incidence at Maturity was recorded as outlined by Ashok *et al.*, 2004.

Per cent Disease incidence at maturity (%)
At the time of crop maturity, total number of plants per row and number of affected plants in the same row were counted as calculated in the following formula to obtain percent index in terms of percentage.

Per cent disease incidence =

$$\frac{\text{Total number of plants in a row}}{\text{Number of affected plants in a row}} \times 100$$

The data collected for both the traits were subjected to Line x Tester analysis as suggested by Kempthorne (1957) [8] which provides valid information on combining ability effects of lines and testers. The statistical analysis was done using TNAU STAT software.

Results and Discussion
The analysis of variance carried out for twelve traits revealed highly significant differences among nine parents and 20 F_1s for pod yield per plant and Per cent disease incidence at maturity (Table 1) indicating that the presence of ample amount of genetic variation for these traits among the experimental material studied.

The assessment of the mean performance of genotypes is so crucial that decides the real field performance of genotypes. Therefore, analytical scrutiny of *per se* performance is the main element that decides the fate of breeding program. The mean performance of nine parents and 20 crosses for pod yield and stem rot incidence (%) is given in Table 2. The line, ICGV-07262 and tester, J-11 were found to have desirable high mean performance to pod yield coupled with low values for per cent disease incidence. Among the lines, Kadiri-6 and ICGV-07262 had significant and positive *gca* effect for pod yield per plant and negative and significant *gca* effect for percent disease incidence at maturity which is in desirable direction and these parents were considered as good general combiners for their inclusion in breeding programme.

Among crosses (Table 2), ICGV-07262 x TCGS-1862 recorded the highest *per se* performance for pod yield per plant followed by K-6 x CS-19, Narayani x J-11 and ICGV-07262 x TCGS-2149 whereas the cross K-6 x CS-19 registered the lowest value for percent disease incidence at maturity which is desirable for this trait followed by ICGV-07262 x J-11, Narayani x J-11, ICGV-07262 x TCGS-1862 and ICGV-07262 x TCGS-2149 in increasing order of values. Hence, these cross combinations could be utilized for

isolation of high pod yielding varieties with stem rot resistant. Selection of parents with greater mean values alone not advised to fulfil the need of hybridization programs as they are not capable to transmit the superior characters to their off springs. The genotypes which perform well in combinations are of prominent importance to the plant breeder. Hence, there is a need to assess the combining ability of parents and their resulting off springs. The data pertaining to all the hybrids along with parents was subjected to combing ability analysis as suggested by Kempthorne (1957) [8].

Analysis of variance of combining ability using Line × Tester mating design for pod yield per plant and per cent disease incidence at maturity was furnished in Table 3. It revealed that lines and testers exhibited highly significant differences for both characters inferring that there is a existence of certain genetic variability among the parental lines. Estimates of genetic components for pod yield and stem rot resistance is presented in Table 4 and indicated the existence of sufficient variability in the breeding material. The magnitude of *SCA* variance was higher than *GCA* variance for percent disease incidence at maturity and pod yield per plant indicating the preponderance of non-additive gene action in the expression of these traits. This was in the agreement with the research findings of Jayalakshmi *et al.* (2002) [5], Vasanthi *et al.* (2004) [15], Yadav *et al.* (2006), Manivannan *et al.* (2008) [9], Ganesan *et al.* (2010) [4], Savithramma *et al.* (2010) [13], John *et al.* (2011) [7] and Mothilal and Jayaramachandran, (2014) [10], Vaithiyalingan (2015) [14] and Abady *et al* (2021) [1].

The GCA:SCA variance were recorded as -0.013 and 0.001 (less than unity) for pod yield per plant and *per cent* disease incidence at maturity respectively confirming the operation of the non-additive gene action for these traits. Hence, selection should be postponed to later generations for these traits. From the estimates of additive and dominance variance, it was observed that dominance variance was predominant for both the characters indicating the major role of non-additive gene action and was highest for percent disease incidence at maturity followed by pod yield per plant.

The *gca* effects of nine parents and *sca* effects of 20 F_1 crosses for pod yield per plant and percent disease incidence at maturity were presented in Table 5. Positive *gca* and *sca* effects are considered for pod yield per plant while negative effects for per cent disease incidence at maturity. Among the parents, Kadiri-6 and ICGV-07262 had significantly positive *gca* effects for pod yield per plant and desirable negatively significant gca effects for percent disease incidence at maturity and were considered as good general combiners for their inclusion in production programme. Out of 20 F_1 crosses, Narayani x J-11, ICGV-07262 x TCGS- 1862 and ICGV-91114 x TCGS-2149 registered significant positive *sca* effects for pod yield per plant and desirable negatively significant *sca* effects for percent disease incidence at maturity suggesting that these crosses were identified as good specific combiners for both the traits. Intermating among the selects followed by selection in advanced generations of these four crosses *viz.*, Narayani x J-11, ICGV-07262 x TCGS- 1862, ICGV-07262 x TCGS- 2149 and ICGV-91114 x TCGS-2149 is advocated as a breeding strategy to isolate high yielding stem rot resistant recombinant lines.

Table 1: Analysis of variance for pod yield per plant and stem rot incidence (%) in groundnut

S. No	Character	Mean Sum of Squares		
		Replications (df:1)	Treatments (df:28)	Error (df:28)
1	Pod yield per plant	2.888	16.844**	0.217
2	Percent disease incidence at maturity	74.082	1310.101**	27.966

Table 2: Mean performance of nine parents and 20 F_1 crosses for pod yield per plant and stem rot incidence (%) in groundnut.

S. No.	Genotypes	Pod yield per plant	Percent Disease Incidence at Maturity
	Lines		
1	K-6	16.46	79.55
2	Narayani	17.00	72.08
3	TAG-24	12.39	66.37
4	ICGV-07262	18.45	65.91
5	ICGV-91114	13.19	84.39
	Mean of Lines	26.13	73.66
	Testers		
6	TCGS-1862	17.30	13.64
7	TCGS-2149	15.20	9.09
8	J-11	14.80	7.05
9	CS-19	16.30	10.87
	Mean of Testers	15.68	45.44
	Crosses		
10	K-6 x TCGS-1862	15.22	27.92
11	K-6 x TCGS-2149	16.10	23.27
12	K-6 x J-11	15.50	21.59
13	K-6 x CS-19	21.40	11.82
14	Narayani x TCGS-1862	13.91	48.92
15	Narayani x TCGS-2149	12.58	64.95
16	Narayani x J-11	21.30	17.50
17	Narayani x CS-19	15.24	26.37
18	TAG-24 x TCGS-1862	14.35	72.50
19	TAG-24 x TCGS-2149	13.25	65.91
20	TAG-24 x J-11	13.79	29.29
21	TAG-24 x CS-19	14.24	21.43
22	ICGV-07262 x TCGS-1862	22.90	17.50
23	ICGV-07262 x TCGS-2149	21.60	19.32
24	ICGV-07262 x J-11	13.95	12.26
25	ICGV-07262 x CS-19	13.70	56.82
26	ICGV-91114 x TCGS-1862	12.44	65.26
27	ICGV-91114 x TCGS-2149	16.55	22.50
28	ICGV-91114 x J-11	15.40	61.37
29	ICGV-91114 x CS-19	12.75	20.89
	Mean of crosses	15.81	35.37
	Max. value	22.90	72.50
	Min. value	12.44	11.82
	General mean	15.77	38.49
	C.D.	0.95	10.84
	C.V.	2.96	13.74

Table 3: Analysis of variance for combining ability in a Line x Tester analysis for pod yield and stem rot incidence (%) in groundnut

Source of variation	df	Mean squares	
		Pod yield per plant	Percent Disease Incidence at Maturity
Replications	1	0.29	74.08
Entries	28	16.84**	1310.10**
Parents	8	7.76**	2312.16**
Lines	4	13.43**	132.77**
Testers	3	2.55**	15.64
L vs T	1	0.73	17919.28**
Crosses	19	21.54**	890.90**
Lines in crosses	4	24.92	981.20
Testers in crosses	3	0.65	825.80
L vs T in crosses	12	25.64**	877.06**
Parents vs Crosses	1	0.21	1258.50**
Error	28	0.22	27.97

Table 4: Estimates of components of genetic variance for pod yield per plant components and stem rot incidence (%) in groundnut.

Character	Pod yield per plant	Percent Disease Incidence at Maturity
GCA variance	-0.170	0.600
SCA variance	12.700	422.690
GCA/SCA	-0.013	0.001
σ^2A	-0.710	2.420
σ^2D	50.830	1690.780
Ratio σ^2A: σ^2D	-0.014	0.001

Table 5: Estimates of general combining ability (*gca*) effects of parents and specific combining ability (*sca*) effects of crosses for pod yield per plant and percent disease incidence (stem rot) in groundnut.

S. No.	Genotypes	Pod yield per plant	Percent Disease Incidence at Maturity
		PARENTS	
1	K-6	1.25**	-14.22**
2	Narayani	-0.05	4.06
3	TAG-24	-1.90**	11.91**
4	ICGV-07262	2.23**	-8.89**
5	ICGV-91114	-1.52**	7.14**
6	TCGS-1862	-0.05	11.05**
7	TCGS-2149	0.21	3.82*
8	J-11	0.18	-6.97**
9	CS-19	-0.34*	-7.90**
	S.E. (g$_i$)	**0.16**	**1.98**
	S.E. (g$_j$)	**0.15**	**1.77**
		CROSSES	
10	K-6 x TCGS-1862	-1.79**	-4.28
11	K-6 x TCGS-2149	-1.16**	-1.70
12	K-6 x J-11	-1.73**	7.41
13	K-6 x CS-19	4.69**	-1.43
14	Narayani x TCGS-1862	-1.81**	-1.57
15	Narayani x TCGS-2149	-3.38**	21.70**
16	Narayani x J-11	5.36**	-14.96**
17	Narayani x CS-19	-0.17	-5.16
18	TAG-24 x TCGS-1862	0.49	14.17**
19	TAG-24 x TCGS-2149	-0.87*	14.81**
20	TAG-24 x J-11	-0.30	-11.03*
21	TAG-24 x CS-19	0.67	-17.95**
22	ICGV-07262 x TCGS-1862	4.91**	-20.03**
23	ICGV-07262 x TCGS-2149	3.35**	-10.98*
24	ICGV-07262 x J-11	-4.27**	-7.25
25	ICGV-07262 x CS-19	-4.00**	38.25**
26	ICGV-91114 x TCGS-1862	-1.80**	11.71**
27	ICGV-91114 x TCGS-2149	2.06**	-23.83**
28	ICGV-91114 x J-11	0.94*	25.83**
29	ICGV-91114 x CS-19	-1.19**	-13.71**
	S.E. (S$_{ij}$)	**0.33**	**3.97**

Conclusion

From the foregoing discussion it is to conclude that based on *per se* and *gca* effects of the genotype *viz.,* ICGV-07262 is adjudged as best general combiner for pod yield per plant and percent disease incidence at maturity. In addition, J-11 was also identified as best general combiner for percent disease incidence at maturity and could be utilized in resistance breeding program of groundnut. The crosses *viz.,* Narayani x J-11, ICGV-07262 x TCGS-1862, ICGV-07262 x TCGS-2149 and ICGV-91114 x TCGS-2149 were found superior for both the traits with respective desirable *sca* effects. Hence, theses crosses could be exploited in future breeding programmes to isolate desirable segregants for yield coupled with stem rot resistance.

Acknowledgements

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