



Genetic variability of leaf caterpillar resistance traits among groundnut (*Arachis hypogea* L.) germplasm

Manikandan P^{1*}, V Selvanarayanan², T Sabesan³

^{1,2}Department of Entomology, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India

³Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India

Abstract

Two hundred and ten accessions of groundnut (*Arachis hypogea* L.) were evaluated for leaf caterpillar (*Spodoptera litura* F.) resistance and yield potential during *Rabi* season, 2018- 2019 at Thandavankulam, Nagapattinam, Tamil Nadu, India. Observations were recorded on mean larval population, per cent damage caused by leaf caterpillar and biometrical traits such as plant height, pod yield, number of mature pods, immature pods, primary branches, secondary branches and plant biomass. The mean larval population per plant was significant but negatively correlated with pod yield and number of secondary branches per plant whereas it was positively correlated with the number of matured pods and primary branches per plant. Per cent leaf damage exerted a significant negative correlation with secondary branches per plant and had a non-significant association with pod yield and plant biomass. A significant positive association was observed between the mean larval population and per cent leaf damage. For the characters *viz.*, plant height, pod yield, number of matured pods, plant biomass and per cent leaf damage, high GCV, PCV, heritability and genetic advance were recorded indicating the role of additive gene action in controlling these characters and hence, selection for improvement of these characters in early generation itself might be effective.

Keywords: Groundnut, genetic diversity, leaf caterpillar, resistance

Introduction

Groundnut *Arachis hypogea* L. is the important legume oilseed crop rich in protein, starch, soluble sugar, crude fibre, vitamins and minerals (Doyle and Luckow, 2003; Heywood *et al.*, 2007) [12, 16]. It is cultivated in tropical and sub-tropical regions of the world in 22.2 million hectares. India is the leading producer which occupies 41 % of the total world production (APEDA, 2018) [3]. Yield reduction in groundnut is caused by many biotic and abiotic factors. Among the biotic factors, insect pests are the major yield affecting factors leading up to 50 % reduction in yield by the direct feeding and also by vectoring diseases. Leaf caterpillar, *Spodoptera litura* (F.) is an important defoliator of groundnut throughout India especially in Tamil Nadu, Andhra Pradesh, Gujarat, Maharashtra and Karnataka. It causes more than 30 per cent yield loss (Sahayaraj and Raju, 2003; Atwal and Dhaliwal, 2008) [30, 4]. Use of resistant crop varieties against insect pests is an important eco-friendly approach that will reduce the use of insecticides in the agroecosystem. Groundnut is a highly self-pollinated crop with narrow genetic variability. Many attempts were made on the genetic study in groundnut for yield-related attributes and disease resistance (John *et al.* 2005; Dolma *et al.* 2010; Channayya *et al.* 2011; Choudhary *et al.* 2013) [17, 11, 17, 9] but comparatively fewer attempts were made on the assessment of groundnut genotypes for leaf caterpillar resistance (Dharne and Patel, 2000) [10].

For any resistance breeding program, germplasm collection and assessment of genetic variability is an important step. Hence, it is very essential to partition the observed variability into heritable and nonheritable components

measured as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (BS)%, and genetic advance expressed as per cent mean (GAM%). Screening of available groundnut germplasm is the important step in the development of leaf caterpillar resistant variety. Keeping this in view, this experiment was conducted to evaluate the genetic variability in different morphological traits and their association with leaf caterpillar resistance.

Materials and methods

The field screening was conducted at Thandavankulam village, Nagapattinam district of Tamil Nadu, India during *Rabi* season 2018 –2019. Groundnut germplasm comprising 210 accessions collected from various sources and the accessions were sown in the field with forty plants per accession, maintained in 30 cm row –row spacing and 20 cm plant-plant spacing. All packages of practices were followed (Ntare *et al.* 2008) [24] except pest management activities.

The larval population on ten randomly selected plants from each row was recorded. The mean number of larvae per plant was recorded from 15 days after sowing (DAS) onwards up to 92 DAS at weekly intervals in all the accessions and the mean larval population per plant was calculated. Per cent damage caused by leaf caterpillar in ten randomly selected plants per accession was observed at 45 DAS. Per cent damage was calculated using the following formula.

$$\text{Per cent damage} = \frac{\text{Number of damaged leaflets}}{\text{Total number of leaflets}} \times 100$$

Seven characters such as plant height, pod yield, number of matured pods, number of immature pods, number of primary branches, number of secondary branches and plant biomass were observed in ten plants from each accession and mean value was worked out for each parameter. The simple correlation coefficient was calculated based on the procedure given by Panse and Sukhatme (1995) [26]. Phenotypic (PCV) and genotypic coefficient of variation

(GCV) was worked out as per the procedure given by Burton and Dewane (1953) [6] while, heritability was calculated based on the method suggested by Falconer (1981) [13] and the genetic advance was calculated based on the formula given by Johnson *et al.* (1955) [18]. Analysis of variance was computed for all the traits evaluated, using SPSS 16.00 for Windows 16.0 computer software system (SPSS Inc., 2007).

Table 1: Analysis of variance for *Spodoptera litura* resistance and other traits in groundnut genotypes (*Arachis hypogaea* L.)

Source of Variation	Mean sum of square								
	Degrees of freedom	Plant Height (cm)	Pod Yield (g)	Number of matured pods	Number of immature pods	Primary branches per plant	Secondary branches per plant	Plant Biomass	Per cent leaf damage
Genotypes	209	302.8026**	459.7797**	137.9098**	124.1762**	3.640018**	28.6109**	2762.25**	376.5308**
Replications	1	0.0607	0.02933	3.5494	0.0644	1.1840	2.4259	0.5379	1.2118
Error	209	0.2899	0.3139	0.6080	87.5690	0.1519	0.1175	4.6127	1.3639

** Significant at 1% level of probability

Table 2: Correlation coefficient among the different plant traits and leaf caterpillar incidence and per cent damage

Plant Traits	Mean Larval population	Per cent leaf damage	Plant Height (cm)	Pod Yield (g)	Number of matured pods	Number of immature pods	Primary branches per plant	Secondary branches per plant	Plant Biomass
Mean Larval population	1								
Per cent leaf damage	0.6935**	1							
Plant Height (cm)	-0.0022	0.1146**	1						
Pod Yield (g)	-0.1484*	-0.0106	0.3365**	1					
Number of matured pods	0.0942*	0.2066**	0.1655**	0.5660**	1				
Number of immature pods	-0.0027	0.0645	0.1219**	0.5214**	0.7715**	1			
Primary branches per plant	0.0262	0.0992*	0.0942*	0.1751**	0.1833**	0.2054**	1		
Secondary branches per plant	-0.2802**	-0.2551**	0.0764	0.2028**	0.0995*	0.2245**	0.1451*	1	
Plant Biomass	-0.0733	-0.0278	0.4051**	0.5816**	0.4513**	0.4535**	0.2003**	0.4040**	1

* -Significant at 0.05%, ** -Significant at 0.01% level of probability

Table 3: Genetic components of variation for *Spodoptera litura* resistance and other traits

	Plant Height (cm)	Pod Yield (g)	Number of matured pods	Number of immature pods	Primary branches per plant	Secondary branches per plant	Plant Biomass	Per cent leaf damage
GV	151.26	229.73	68.65	18.30	1.74	14.25	1378.82	187.58
EV	0.29	0.31	0.61	87.57	0.15	0.12	4.61	1.36
PV	151.55	230.05	69.26	105.87	1.90	14.36	1383.43	188.95
GCV	28.97	34.52	43.29	13.52	29.93	77.70	60.31	45.05
ECV	1.27	1.28	4.07	29.56	8.84	7.06	3.49	3.84
PCV	29.00	34.55	43.48	32.50	31.21	78.02	60.41	45.21
h ² _{BS}	99.81	99.86	99.12	17.29	91.98	99.18	99.67	99.28
GA	25.35	31.25	17.02	3.67	2.61	7.75	76.48	28.15

GV-Genetic variation, EV- Environment variation, PV- Phenotypic variation, GCV- Genetic coefficient variation (%), ECV- Environment coefficient variation (%), PCV- Phenotypic coefficient variation (%), h²_{BS}- Heritability (Broad Sense) (%), GA- Genetic advance (%)

Result and Discussion

Analysis of variance for various characters confirmed the existence of significant variation among the genotypes taken for the study (Table 1). The results revealed that leaf caterpillar population was significantly correlated with traits such as plant height, pod yield, number of pods per plant, number of primary and secondary branches per plant (Table 2). Gangadhara *et al.* (2016) [14] also reported association of plant traits with *S.litura* damage and foliar disease incidence. Mean larval population per plant was negatively correlated with pod yield and number of secondary branches per plant whereas it was positively correlated with the number of primary branches and plant height. Per cent leaf damage was negatively correlated but non-significant with pod yield. Mohammad Saleem *et al.* (2018) [23] also reported the non-significant correlation between *S. litura* damage and pod yield per plant. Mean larval population per plant and

per cent leaf damage showed a highly significant and positive correlation. Pod yield and number of matured pods per plant, primary branches, secondary branches, plant height and plant biomass were strongly correlated with a positive association (Table 1). The positive correlation between pod yield and number of pods per plant corroborates with earlier reports of Meta and Monpara (2010) [22]; Raut *et al.* (2010) [29] and Vekariya *et al.* (2010) [34].

The highest genetic variation (GV) was observed with regard to plant biomass and the lowest in case of number of primary plant branches per plant. Moderate to low GV was recorded for pod yield, per cent leaf damage, plant height, number of mature pods, immature pods and number of primary branches. Environment variation (EV) was the maximum in case of number of immature pods per plant in contrast to the minimum in case of number of secondary

branches per plant (Table 3).

In general, higher phenotypic coefficient of variability values than that of genotypic coefficient of variability values indicate the influence of environment on traits. But, minimal differences between PCV and GCV values were observed for all the characters, as they are less influenced by the environment indicating the reliability of selection based on these traits. The PCV and GCV values were ranked as low, medium and high as follows: 0-10%-Low; 10-20%-Moderate; >20%-High. High genetic coefficient variation (GCV) was observed for almost all the characters with the exception of the number of immature pods. Many authors estimate high GCV in various plant traits such as kernel yield and branch numbers (Chavadhari *et al.* 2017)^[8], number of branches per plant (Gupta *et al.* 2015; Vasanthi *et al.* 2016)^[15, 17], biological yield per plant (Gupta *et al.* 2015)^[15]. In the present study, high level of GCV estimates for per cent leaf damage, number of matured pods, pod yield, primary branches and plant height were observed as like the earlier findings of Rao *et al.* (2014)^[5], Maurya *et al.* (2014)^[21] and Ramana *et al.* (2015)^[27].

The higher level of heritability was recorded for almost all the traits except the number of immature pods per plant which suggests that the selection based on the phenotypic performance of these traits would be more effective. High heritability for biological yield per plant was recorded by Korat *et al.* (2009)^[20]; pod yield by Chavadhari *et al.* (2017)^[8]; plant height, biological yield branches per plant and biological yield per plant by Gupta *et al.* (2015)^[15] and Bhargavi *et al.* (2016)^[5]; kernel yield per plant by Ramana *et al.* (2015)^[27] and Rao *et al.* (2015)^[5]; plant height by Kadam *et al.* (2016)^[19] and the number of branches per plant by Yadlapalli (2014)^[35].

Since high heritability does not always indicate a high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect of selecting superior varieties (Ali *et al.* 2002)^[2]. High genetic advance (GA) was recorded in most of the traits except immature pods per plant, the number of primary branches per plant and number of secondary branches per plant (Table 3).

High heritability coupled with high genetic advance as per cent of mean indicates that such traits are under the strong influence of additive gene action and hence simple selection based on the phenotypic performance of these traits would be more effective. High heritability and moderate genetic advance as per cent of mean values indicate the influence of non-additive gene action and considerable influence of environment on the expression of these traits. This trait could be exploited through the manifestation of dominance and epistatic components through heterosis.

It is concluded that significant differences were observed among the groundnut accessions regarding all the traits studied. The characters namely, plant height, pod yield, number of matured pods, plant biomass and per cent leaf damage recorded higher level of GCV, PCV, heritability and genetic advance indicating the role of additive gene action in controlling these characters. Selection for improvement of these characters in early generation itself might be effective.

Acknowledgement

The authors thank Dr.K.Saravanan, Department of Genetics and Plant breeding, Faculty of Agriculture, Annamalai

University for his help in statistical analysis.

References

1. Agropedia. Nutritional features of groundnut, 2009. <http://agropedia.iitk.ac.in/content/nutritional-features-groundnut>. Accessed on 27.01.2020
2. Ali A, Khan S, Asad MA. Drought tolerance in wheat: Genetic variation and heritability for growth and ion relations. *Asian J Plant Sci*, 2002; 1:420-422.
3. APEDA.2018. Groundnut crop survey. https://apeda.gov.in/apedawebsite/Announcements/2018_Groundnut_Survey_Report.PDF. Accessed on 27.01.2020.
4. Atwal AS, Dhaliwal GS. *Agricultural Pests of South Asia and their Management*, Kalyani Publishers, New Delhi, India, 2008.
5. Bhargavi G, Rao SV, Rao KLN. Genetic variability, heritability and genetic advance of yield and related traits of Spanish bunch groundnut (*Arachis hypogaea* L.). *Agric. Sci. Digest*. 2016; 36(1):60-62.
6. Burton GW, Dewane EM. Estimating heritability from replicated clonal material. *Agron. J*. 1953; 45:478-481.
7. Channayya P, Hiremath Nadaf HL, Keerthi CM. Induced genetic variability and correlation studies for yield and its component traits in groundnut (*Arachis hypogaea* L.). *Electron. J Plant Breed*. 2011; 2(1):135-142.
8. Chavadhari RM, Kachhadia VH, Vachhani JH, Virani MB. Genetic variability studies in groundnut (*Arachis hypogaea* L.). *Electron. J Plant Breed*. 2017; 8(4):1288-1292.
9. Choudhary M, Sharma SP, Dashora A, Maloo SR. Assessment of genetic variability, correlation and path analysis for yield and its components in groundnut (*Arachis hypogaea* L.). *J Oilseeds Res*. 2013; 30(2):163-166.
10. Dharne PK, Patel SK. Screening of promising groundnut genotypes for their reaction to *Spodoptera litura*. *Int. Arach. News*. 2000; 20:67-69.
11. Dolma T, Sekhar MR, Reddy KR. Genetic variability, correlation and path analysis for yield its components in late leaf spot resistance in groundnut (*Arachis hypogaea* L.). *J Oilseeds Res*. 2010; 27(2):154-157.
12. Doyle JJ, Luckow MA. The rest of the iceberg. Legume diversity and evolution in a phylogenetic context. *Plant Physiol*. 2003; 131:900-910.
13. Falconer DS. *Introduction to Quantitative Genetics*. 2nd edition. Oliver and Boyd, Edinburg, London, UK, 1981.
14. Gangadhara K, Nadaf HL, Chetana C. Phenotypic evaluation of backcross population for yield and foliar diseases in groundnut (*Arachis hypogaea* L.). *The bioscan*. 2016; 11(2):1323-1327.
15. Gupta R, Vachhani JH, Kachhadia VH, Vaddoria MA, Reddy P. Genetic variability and heritability studies in Virginia groundnut (*Arachis hypogaea* L.). *Electron. J. Pl. Breed*. 2015; 6(1):253-256.
16. Heywood VH, Brummitt RK, Culham A, Seberg O. *Leguminosae (Fabaceae)*. Pp.185-188. In: *Flowering Plant Families of the World*. New York, Firefly Books, 2007.
17. John K, Vasanthi RP, Venkatewarlu O, Haranath Naidu P. Variability and correlation studies for quantitative traits in Spanish bunch groundnut. *Legume Res*. 2005; 28(3):189-193.

18. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agron. J.* 1955; 47:314-318.
19. Kadam VK, Chavan BH, Rajput HJ, Wakale MB. Genetic diversity in summer groundnut (*Arachis hypogaea* Linn.). *Int. Res. J Multidisciplinary Studies.* 2016; 2(1):1-11.
20. Korat VP, Pithia MS, Savaliya JJ, Pansuriya AG, Sodavadiya PR. Studies on genetic variability in different genotypes of groundnut (*Arachis hypogaea* L.). *Legume Res.* 2009; 32(3):224-226.
21. Maurya MK, Rai PK, Kumar A, Singh BA, Chaurasia AK. Study on genetic variability and seed quality of groundnut (*Arachis hypogaea* L.) genotypes. *Int. J Emerg. Tech. Adv. Engg.* 2014; 4(6):818-823.
22. Meta HR, Monpara BA. Genetic variation and trait relationships in summer groundnut, *Arachis hypogaea* L. *J Oilseeds Res.* 2010; 27(1):8-11.
23. Mohammad Saleem A, Gopalakrishna Naidu K, Mahalaxmi KK, Tippannavar PS, Nadaf HL. Evaluation of recombinant inbred population for *Spodoptera litura* resistance and productivity parameters in groundnut (*Arachis hypogaea* L.). *J Pharm. Phytochem.* 2018; 7(6):987-990.
24. Ntare BR, Diallo AT, Ndjeunga J, Waliyar F. Groundnut Seed production Manual. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), 2008.
25. Panse VG. Genetics of quantitative characters in relation to plant breeding. *Indian J Genet. Pl. Br.* 1957; 28:225-229.
26. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR Publication, New Delhi. India, 1995.
27. Ramana E, Vasanthi RP, Reddy KH, Reddy BVB, Reddy BR. Studies on genetic variability for yield, yield components and resistance to kalahasti malady in groundnut (*Arachis hypogaea* L.). *Int. J App. Bio. Pharm. Tech.* 2015; 6(1):1-4.
28. Rao VT, Venkanna V, Bhadrud D, Bharathi D. Studies on variability, character association and path analysis on groundnut (*Arachis hypogaea* L.). *Int. J Pure. Appl. Biosci.* 2014; 2(2):194-197.
29. Raut RD, Dhaduk LK, Vachhani JH. Character association and path coefficient analysis in F2 generation of groundnut (*Arachis hypogaea* L.). *Int. J Agric. Sci.* 2010; 1:305-310.
30. Sahayaraj K, Raju G. Pest and natural enemy complex of groundnut in Tuticorin and Tirunelveli districts of Tamil Nadu, India. *Int. Arach. Newsl.* 2003; 233:25-29.
31. Savaliya JJ, Pansuriya AG, Sodavadiya PR, Leva RL. Evaluation of inter and intraspecific hybrid derivatives of groundnut (*Arachis hypogaea* L.) for yield and its components. *Legume Res.* 2009; 32(2):129-132.
32. SPSS Inc. SPSS for Windows. Release 16.0. SPSS Inc. Chicago, IL. USA, 2007.
33. Vasanthi RP, Suneetha N, Sudhakar P. Genetic diversity based on physiological attributes among released and pre-release cultures of groundnut (*Arachis hypogaea* L.). *Legume Res.* 2015; 38(1):110-113.
34. Vekariya HB, Khanpara MD, Vachhani JH, Jivani LL, Vagadiya KJ, Revar HJ, *et al.* Correlation and path analysis in bunch groundnut (*Arachis hypogaea* L.). *Intl. J Pl. Sci.* 2010; 6:11-15.
35. Yadlapalli S. Genetic variability and character association studies in groundnut (*Arachis hypogaea* L.). *Int. J Plant Animal and Environ. Sci.* 2014; 4(4):298-300.
36. Ezgi Yazici, Oğuz Bilgin. Heritability estimates for milling quality associations of bread wheat in the northwest turkey. *Int. J Res. Agron.* 2019;2(2):17-22. DOI: 10.33545/2618060X.2019.v2.i2a.18.