Research Article
Volume 06:05, 2022

Journal of Genetics and Genomes

ISSN: 2684-4567

Open Access

Quantitative Trait Inheritance and Genetic Variability on Pod and Seed-Related Traits in Peanut Recombinant Inbred Line Population

Liu Li-feng[1], Yang Xin-Lei[1], Liu Kaige[1], He Mei-Jing[1], Cui Shun-Li[1], Mu Guo-Jun[1],Wang Liang[1], Li Li[1], Yan Congcong[1], Zhao Nannan[1], Chen Yingjie[1] and Addisu Getahun[1,2,3*]

[1]Laboratory for Crop Germplasm Resources of Hebei, College of Agronomy, Hebei Agricultural University, Baoding, Hebei, P.R China

[2]Ethiopian Institute of Agricultural Research, Pawe Agricultural Research Center, Pawe, Ethopia

[3]Department of Plant Science, College of Agriculture, Food and Climate Science, Injibara University, Pawe, Ethopia

Abstract

The present study was conducted to predict genotypic variability, phenotypic variability, heritability, and genetic advance on pod and seed-related traits in cultivated peanut RIL population. Genetic variability is an important prerequisite for selection using certain genetic parameters *viz*: genotypic variation, heritability and genetic advance.

The trait pod length, number of pods per plant, pod weight per plant, multi-seedpods per plant had high genotypic coefficient of variation. The highest narrow sense heritability was recorded in seed length, pod length by width, and pod thickness traits, meanwhile, seed length, seed length by width, number of pods per plant, shelling percentage, pod thickness, thickness of pod shells, seed weight per plant, seed thickness, seed width, multiple seedpods per plant, and pod weight per plant traits had high broad sense heritability. The highest genetic advance as percent of mean had occurred in multiple seedpods per plant, number of pods per plant, pod weight per plant, seed weight per plant, thickness of pod shells, pod length by width, seed length by width, and seed length quantitative traits. The highest broad sense heritability values coupled with high genetic gain were estimated in multiple seedpods per plant, number of pods per plant, pod weight plant, seed weight per plant, thickness of pod shells, pod length by width, seed length by width. Therefore, relatively the present study used more pod and seed-related traits than the previous investigations. The present experiment had tried to estimate a good quantitative trait inheritance and genetic variability between recombinant inbred line populations; so far, our result suggested that superior breeding line selection was confidential for next breeding programs.

Keywords: Peanut • Heritability • Variability • Genetic advance • Gene effect

Introduction

Peanut (*Arachis hypogaea* L.) is one of the kings of oilseeds and multi-functional legume crop grown and highly consuming in tropical and subtropical regions of the world. It is an economically important and versatile crop for resource-poor farmers in Asia and Africa that offers a rich source of oil, protein, minerals (Ca, Mg, P, and K), and vitamins (E, K, and B1) [1]. Yield and yield contributing parameters are the most widely targeted traits of peanut improvement program across the globe. Peanut pod yield is a function of crop growth rate, duration of reproductive growth, and the fraction of crop growth rate partitioned toward pod yields. Therefore, understanding of physiology of yield is also essential for better target yield increase in crop including peanut. The main important yield contributing attributed traits are pod yield per plant, number of pods per plant, and 100-seed weight [2].

In peanut genetic variability is very low due to the origin of a single hybridization event between two different diploid species followed by a chromosome doubling and crossing barriers with wild diploid species due to the variation of ploidy nature. The low genetic variability for the traits of interest and polyploidy nature is a major bottleneck for peanut improvement strategies. The cultivated accession of Arachis hypogaea in the gene banks and the advanced breeding lines are frequently used as sources of variability used as a parent in hybridization program [2]. Segregating populations derived from crossing are most common in peanut breeding programs. In peanut improvement program, segregating populations derived from hybridization through pedigree and bulk-pedigree methods of breeding are the most common. Pedigree selection method allows breeders to practice selection of the best traits with high heritability values such as plant type, pod and seed-related traits and the testa color in early generations. Selection of quantitative traits such as yield and seed composition characters made in later generations. The bulk-pedigree method is a modified method of bulk aimed at improving traits with low heritability traits [3]. The single seed decent method is becoming popular and it has an advantage to save space and resources. G×E has a considerable influence on the progress of crop improvement. In peanut, majorities of important agronomic trait are polygenic and highly influenced by the environment that hinders the achievable genetic gains in breeding program. Genetic analysis of yield has revealed by the high influence of the environment on pod yield traits [4]. High yielding cultivars with the least G×E interactions are normally desirable. However, when a cultivar is to be selected for a specific environment the G×E interaction is ideal for maximizing production efficiency [2].

Heritability is an idea of how much of the variation is available in a trait due to genetic factors. High heritability indicates a strong similarity between parents and their respective offspring with regard to a specific trait, while low heritability implies that low level of resemblance between them. The combined effect of all loci, including possible allelic interactions within each locus (dominance) and between loci (epistasis) is the effect of genotypic value. The effect of a particular allele on a trait depends on the allele's frequency in the population and the effect of each genotype that includes all the allele. The additive genetic value of an individual population called the breeding value is the sum of the average effects of all the alleles [5]. According to the principles of the Mendelian law of segregation one allele from each locus is present in each gamete cell, and in this way, additive genetic information is transferred from parents to offspring. Certainly, in the reason of each offspring receives a different set of alleles from its parents, half of the additive genetic variance in the population occurs within families.

Narrow sense heritability is the proportion of phenotypic variance among an individual population that is due to heritable genetic effects (additive). Broad sense heritability can estimate the proportion of phenotypic variances

---

***Address for Correspondence:** Addisu Getahun, Department of Plant Science, College of Agriculture, Food and Climate Science, Injibara University, Pawe, Ethopia; E-mail: addisu.getahun@inu.edu.et; mailto:addisu.getahun@aastu.edu.et*

Received: 05-Sept-2019, Manuscript No. JGGE-19-001-PreQc-22; **Editor assigned:** 09-Sept-2019, PreQC No. JGGE-19-001-PreQc-22 (PQ); **Reviewed:** 23-Sept-2019, QC No. JGGE-19-001-PreQc-22; **Revised:** 01-Jul-2022, Manuscript No. JGGE-19-001-PreQc-22 (R); **Published:** 01-Sept-2022, DOI: 10.37421/ 2684-4958.2022.6.021.

directly attributable to the effect of the whole genotype, it comprising the sum total of additive, dominance and epistatic variance components [5]. Heritability is a key parameter for quantitative genetics because it determines the response to selection. In the field of plant breeding there are many different selection principles, and mating designs and the possibility of observational units are quite diverse, which is ranging from individual plant population to a means of genotypes tested across multiple environments.

Naturally, variation is classified into three main types such as phenotypic, genotypic, and environmental; Mather and Jinks stated that phenotypic variation is dividing into three main features *viz*; (1) heritable fixable (additive variance), (2) heritable non-fixable (dominance and epistasis variance) and (3) non-heritable non-fixable (environmental variance). Heritable fixable component of phenotypic variance will be included in additive x additive fraction of the epistasis variances. The genetic variances are consists of additive, dominance and epistasis components. In advance, the total phenotypic variations might be divided into (1) fixable (additive and additive x additive), (2) non-fixable (dominance, additive x dominance, dominance x dominance types of epistasis, and environmental fraction) components [6].

Genetic variation is very important to maintain the level of high productivity crops including peanut [7]. The occurrence and continuation of genetic variability is an important tool for crop improvement strategies however, the loss the locally available landrace and adapted germplasm resources have rapid and high, which needs to keep in sustainable conditions [8]. A critical estimation of genetic variability is a precondition for promoting crop improvement strategy and adopting appropriate selection systems [9]. The genetic variability is determined with the help of certain genetic parameters *viz*: genotypic coefficient of variation, phenotypic coefficient of variation and heritability, but for to do selection, heritability integrated with high genetic advance is more useful than heritability estimates alone [10-13].

The effectiveness of selection is depending on the nature, extent, and magnitude of genetic variability that present in the given population with the existence of inheritance between parents and offsprings. Genetic variability within the population is should be larger than environmental influences; the possibility of selecting superior genotypes is a prerequisite for obtaining high yielding genotypes, which is the ultimate expression of various yield-association characters. Therefore, sometimes-direct selection based on high yielding potential could not effective [14] because of uncontrolled environmental variation. The process of breeding in the population is primarily conditioned by the magnitude and the nature of interactions between genotypes and environments in the given plant characters. Inbred line population development, selection, and release new promising cultivars are one of the strategies of crop improvement programs that have been contributed to increasing yield and sustainable agricultural technology innovation and development. Many economically important agronomic traits are quantitative in nature. Quantitative genetic studies are usually based on a simplified model that defines the phenotypic value because of the genotypic plus the environmental effect [15]). Therefore the present study variance components such as phenotypic and genetic, broad sense heritability (H^2), narrow sense heritability (h^2), and estimated genetic advance as percent of mean have computed on pod and seed-related traits [16]. The objectives of this experiment were to estimate heritability, genetic variance components, genetic advance, and gene effects from 251 single cross inbred line populations, which has not been report before.

Materials and Methods

Field experiment and data collection

The present experiment was carried out using 251 RIL populations derived from the cross-made between silihong (female parent) and black peanut (male parent). The field trial was conducted in Baoding and Handan environments for two consecutive cropping years in a randomized complete block design. All pod and see related phenotypic data were collected after harvesting in three replications.

Statistical analysis

All pod and seed-related phenotypic data were subjected to system analysis software (SAS ver. 9.0, SAS Institute, USA) using PROC GLM and PROC MIXED model applied for phenotypic variance component analysis in the 251 RIL populations with the included of two parents. The genetic variance component statistical analysis was computed using Plant Breeding Tools (PBTools ver. 1.4 IRRI, 2014), using single environment analysis system in the Restricted Maximum Likelihood (REML) model and North Carolina one (NC-I) mating design.

Estimation of phenotypic and genotypic variability

Parents and offspring phenotypic and genotypic variances were estimated using the statistical formula developed by Singh, R.K. and Chaudhary, B.D [17] and the expected mean squares under the assumption of random and fixed effect model was calculated from linear combinations of phenotypic and genotypic coefficient of variations, which were computed as per the methods suggested by Burton, and Devane [18].

Genotypic variance

$$(\sigma 2g) = Msg - Mse / r$$

Environmental variance $(\sigma 2e) = Mse$

Phenotypic variance $\sigma 2p = \sigma 2g + V2e$

Where; Msg and Mse are the mean sum squares of the genotypes and error in the analysis of variances respectively r is the number of replications.

Estimation of genotypic and phenotypic coefficient of Variability:

Genotypic and phenotypic coefficient of variability was computed as per the methods given by Burton and Devane [18].

Genotypic Coefficient of Variability (GCV):

$$GCV = (\sigma 2g) / x * 100$$

Phenotypic Coefficient of Variability (PCV):

$$\text{PCV} = \sigma 2p / X * 100$$

Where,

sg = Genotypic standard deviation

sp = Phenotypic standard deviation

`X = Grand mean of the traits

GCV and PCV values were categorized as low, moderate and high as indicated by Siva Subramanian and Menon [19]. It categorized as follows: 0-10 % low, 10-20 % moderate, and = 20% high.

a. Broad Sense Heritability (H^2)

Broad sense heritability was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson et al. [20] and expressed as in percentage.

$$H^2 = \sigma 2g / \sigma 2p * 100$$

Where σ2g = Genotypic variance and σ2p = Phenotypic variance. The heritability percentage have been categorized as low (0-30%), moderate (30-60%), and high (≥ 60%) as developed and given by Robinson et al. [21].

b. Narrow Sense Heritability (h^2)

Narrow sense heritability (h^2) was estimated from parent offspring regression analysis according to the methods of Anderson et al. [22].

Where σxy=covariance of parent-offspring analysis and σ2x = total variance of parental measurements. Genetic correlation between offspring's or RIL population with parental traits determined according to the method suggested and given by Kwon and Torrie [23].

$$H^2 = \sigma 2g / \sigma 2p * 100$$

Where $\sigma 2g$ = Additive variances, and $\sigma 2p$ = Phenotypic variances

Estimated genetic advance

Genetic advance under selection was suggested and estimated using the formula given by Johnson et al. [10].

$$EGA = H^2 \, k\sigma p$$

Where, H^2 = Heritability in broad sense

k = Selection differential which is equal to 2.06 at 5% selection intensity [24].

σp = Phenotypic standard deviation.

Genetic advance as percent of mean

Genetic advance as percent of mean has calculated according to the formula given by Johnson et al. [10].

Genetic advance as percent of mean was categorized as low, moderate and high as given by Johnson et al. [10]. It described, as 0-10% low; 10-20% moderate and ≥ 20% high.

Results

Genetic and phenotypic variability

The two basic requirements of plant breeding are the presence of genetic variation and utilization of the existed variation through the method of selection. The presence of genetic variation in a character is necessary for any crop improvement in that specified character. Selection is the second basic step in crop improvement breeding programs. Selection involves the identification and isolation of desirable plants from vast and variable populations. The progeny from selected plants may be released as a new variety if they are found suitable and superior to the existing cultivars and controls in yield and other important parameters to full fill the requirements of consumers or ultimate users. Selection of plants from a population is usually based on their phenotypic performance. Phenotypic variation has comprised both heritable and non-heritable components with the inclusive of environmental effects. Moreover, the heritable component is due to the genes present in the existed plant population. One or groups of economically important gene(s) mainly control the development of quantitative and qualitative traits. However, the genes cannot able to produce characters directly. In the present study, the highest genetic variability was found in the traits of pod length (7.4), pod weight per plant (3.79), number of pods per plant (3.33), and seed weight per plant (1.64). In this table 1 experiment, the environmental influence was slightly low in the traits of pod weight per plant, pod length and seed weight per plant. The highest experimental error has been recorded in the traits of pod weight per plant, a number of pods per plant, pod length; seed weight per plant, seed length, pod thickness and pod width, the rest traits had a low experimental error.

Quantitative trait inheritance and genetic gain

The quantitative trait inheritance or heritability can be estimated from the given phenotypic data on the observed and expected relationship between relatives. The expected resemblance between relatives of the population depends on the assumptions regarding the characters under the environmental condition and genetic causes. Robinson et al. [21] suggested that the estimated percentage of heritability values of both narrow sense and broad sense have been categorized as low (0-30%), moderate (30-60%), and high (≥ 60%).

In the present study the highest narrow sense heritability values existed in the traits of seed length (66%), pod length by width (87%), and pod thickness (93%), meanwhile moderate narrow sense heritability values have been scored in multi-seedpods per plant (36%), pod length (47%), and seed length by width (55%), but the rest pod and seed-related traits showed low narrow sense resemblance relations within the populations. In table 2 as we mentioned many of pod and seed seed-related traits showed low narrow sense heritability values, in our understanding the iffy causes of these low narrow sense resemblance relations were; (1) additive gene effect was very low, (2) non-additive gene action in the RIL population was very high, (3) many of pod and seed-related traits were highly subjected to environmental influence and genotype by environmental interaction might be high, and (4) perhaps high experimental error with the inclusive of soil factors and unstable weather conditions. The highest broad sense heritability values had been shown in the traits of seed length (99%), seed length by width (99%), number of pods per plant (95%), shelling percentage (94%), pod thickness (93%), thickness of pod shells (92), seed weight per plant (89%), seed thickness (87%), seed width (83%), multi-seedpods per plant (79%), and pod weight per plant (75%) besides, moderate broad sense heritability values found in pod length (47%), but the traits of pod width (2%) had shown very low broad sense and narrow sense heritability values. Some pod traits such as; pod length (47%), pod width (2%), pod length by width (87%), and pod thickness (93) had shown similar narrow sense and broad sense heritability values, this indicates except additive gene effect other gene effects were masked and genotype by environment interaction had no significant effect.

Genotypic variances and environmental effects

Many researchers have been attempting to identify genetic variability and environmental influences that would be existed in the given population; nevertheless, they may not be in a position to accurate prediction of variations either directly or indirectly only using phenotypic data. However, this situation cannot hamper to evaluate and estimate the relative gene effects and environmental variation in the phenotype variance components. The efficiency of genetic variability can be exploited through selection and it depends upon the heritability of individual characters in the population [25] and it can gives an indication of how a given traits would respond to selection [5].

Padmaja et al. [26] had reported the estimation of observed genetic variability is very difficult because it is subjected to environmental variation due to this reason variance component has heritable and non-heritable. The process of breeding in the existed population is primarily conditioned by the magnitude and nature of interactions of genotypic and environmental variations from a given agronomic characters/traits. Moreover, it is important to partition the observed variability into its heritable and non-heritable components and to have an understanding of parameters like genetic coefficient of variation, heritability, and genetic advance or genetic gains. Fisher was categorized the genetic variance components into additive, dominance, and epistasis effect, with the inclusive of interactions, additive x additive, additive x dominance, and dominance x dominance. Interactions and gene effects other than additive are also referred to as non-additive gene effect. Additive gene effect is high the character is subjected for simple selection procedures. Therefore, this indicates that selection in early generations with desirable traits could be possible. Dominance or over dominance gene effects are predominant the best way to use F1 seeds as commercial hybrids but this opportunity is not applicable for peanut breeders because peanut is categorized under cleistogamous seen in Table 3 [27].

In the present study, the highest additive gene effect have existed in the traits of pod length (21.48), pod weight per plant (8.04), shelling percentage (6.39), pod thickness (5.76), seed weight per plant (4.39), seed length (2.52), and pod number per plant (2.02). The highest dominant gene effect was found in shelling percentage (63.11), number of pod per plant (31.70), pod weight per plant (22.84), seed weight per plant (10.08), and seed length (1.32). Additive gene effect interact with the existed environment that had high influence on pod weight per plant (10.39), shelling percentage (4.79), number of pods per plant (1.87), and seed weight per plant (1.32); besides the effect of dominance gene action with the interaction of the given environment had not shown significance change in all pod and seed traits (Table 3).

Table 1. GxE Combined estimation of, genotypic and phenotypic variability, genotypic and phenotypic coefficient of variability, and genetic advance under selection.

Traits	σ2g	σ2e	σ2er	σ2yr	σ2p	σ2GxE	GCV	PCV	GA
PL	7.4	0.97	29.38	0.92	8.37	0	22.47	25.4	10.71
PWD	0.35	0.16	2.5	0.11	0.51	0	2.77	4.05	2.31
PT	0.43	0.2	2.85	0.14	0.63	0	3.17	4.65	2.49
PLW	0.05	0	0.18	0	0.05	0	2.09	2.09	0.96
SL	0.69	0.12	3.59	0.2	0.8	0	4.54	5.3	3.52
SWD	0.08	0.05	0.64	0.17	0.13	0	1.08	1.73	1.13
ST	0.06	0.06	0.59	0.04	0.12	0	0.78	1.6	0.81
SLW	0.01	0	0.09	0	0.01	0	0.61	0.62	0.63
TPS	0.02	0	0.08	0.03	0.02	0	2.05	2.53	0.54
PNPP	3.33	0.05	32.91	1.03	3.38	0	23.66	23.99	12.02
MSNP	0.4	0	1.51	0.08	0.4	0	30.44	30.44	2.81
PWP	3.79	1.71	33.13	1.35	5.51	0	28.43	41.29	8.66
SWP	1.64	0.92	15.07	1.29	2.57	0	19.04	29.75	5.48

Note: Σ2g: Genetic Variance; Σ2e: Environmental Variance; Σ2er: Error Variance; Σ2yr: Year Variance; Σ2p: Phenotypic Variance; Σ2gxe: Genotype by Environment Interaction Variance; GCV: Genotypic Coeficient of Variability; PCV: Phenotypic Coeficient of Variability; GA: Genetic Advance/Genetic Gain; and Gam Genetic Advance as Percent of Mean; PL: Pod Length; PWD: Pod Width; PT: Pod Thickness; PLW: Pod Length by Width; SL: Seed Length; SWD: Seed Width; ST: Seed Thickness; SLW: Seed Length by Width; TPS: Thickness of Pod Shells; PNPP: Pod Number per Plant; MSNP: Multiple Seed Number of Pods per Plant; PWP: Pod Weight per Plant; SWP: Seed Weight per Plant.

Table 2. Estimated genetic variance components based on REML model using North Carolina one (NC-I) mating design and parent offspring regression analysis.

Traits	σ2A	σ2AxE	σ2D	σ2DxE	h^2	H^2	Dr
SL	2.52	0	1.32	0.003	66	99	1.02
SWD	0.12	0.13	0.49	0	16	83	2.85
SLW	0.05	0	0.04	0	55	99	1.27
ST	0.15	0.08	0.43	0	23	87	2.39
SWP	4.39	1.32	10.08	0.56	27	89	2.14
PL	21.48	0	0	0	47	47	0
PWD	0.04	0	0.01	0	2	2	0.63
PLW	0.24	0.01	0	0.02	87	87	0
PT	5.76	0.01	0	0.39	93	93	0
TPS	0.01	0.01	0.08	0	8	92	4.62
MSNP	0.72	0.42	0.87	0	36	79	1.55
PWP	8.04	10.39	22.84	0	19	75	2.38
PNPP	2.02	1.87	31.7	0	6	95	5.61

Note: σ2A:Additive variance; σ2AxE:Additive by environment interaction variance; σ2D:Dominance variance; σ2DxE:Dominance by environment interaction variance; h^2:Narrow Sense Heritability; H^2:Broad Sense Heritability; Dr:Dominance Ratio; SL: Seed Length; SWD: Seed Width; SLW: Seed Length by Width; ST: Seed Thickness; SWP: Seed Weight per Plant; PL: Pod Length; PWD: Pod Width; PLW: Pod Length by Width; PT: Pod Thickness; TPS: Thickness of Pod Shells; MSNP: Multiple Seedpods per Plant; PWP: Pod Weight per Plant; PNPP: Pod Number per Plant; SP: Shelling Percentage.

Table 3. The level of inheritance, gene effect, and environmental influences onto the RIL populations.

Traits	h^2	H^2	Gene effect		Genetic gain	Env. influence	GxE effect
SL	High	High	Additive	Dominance	High	Low	Very low
SWD	Low	High	Non-additive	Non-dominance	Moderate	Low	Very low
SLW	High	High	Additive	Non-dominance	High	Low	Very low
ST	Low	High	No-additive	Non-dominance	Moderate	Low	Very low
SWP	Low	High	Non-additive	Dominance	High	Moderate	Very low
PL	Moderate	Moderate	Additive	Non-dominance	High	Moderate	Very low
PWD	Low	Low	Additive	Non-dominance	Moderate	Low	Very low
PLW	High	High	Additive	Non-dominance	High	Low	Very low
PT	High	High	Additive	Non-dominance	Moderate	Low	Very low
TPS	Low	High	No-additive	Non-dominance	High	Low	Very low
MSNP	Moderate	High	Additive	Dominance	High	Low	Very low
PWP	Low	High	Non-additive	Dominance	High	Moderate	Very low
PNPP	Low	High	Non-additive	Dominance	High	Low	Very low

Note: SL: Seed Length; SWD: Seed Width; SLW: Seed Length by Width; ST: Seed Thickness;, SWP: Seed Weight per Plant; PL: Pod Length; PWD: Pod Width; PLW: Pod Length by Width; PT: Pod Thickness; TPS: Thickness of Pod Shells; MSNP: Multiple Seedpods per Plant; PWP: Pod Weight per Plant; PNPP: Pod Number per Plant.

Discussion

Phenotypic and genotypic coefficient of variation

The highest genotypic coefficient of variation (>10%) was found in the traits of pod length (22.47), number of pods per plant (23.66), pod weight per plant (28.43), multiple seedpods per plant (30.44), and moderate genetic variation was recorded in the traits of seed weight per plant (19.04). The highest phenotypic coefficient of variation (>10%) had been scored in a number of pods per plant (23.99), pod length (25.40), seed weight per plant (29.75), multiple seedpods per plant (30.44), pod weight per plant (41.29) in Tables 3 and 4. In the previous studies, similar findings have been reported on genotypic and phenotypic coefficient of variability in pod and seed related traits such as Shashikumara et al. [16] reported that high GCV and PCV found in pod and seed yield traits, such as pod yield, kernel yield, matured pods and oil yield per plant [28-30]. The trait of pod length, pod number per plant, and multiple seedpods per plant genotypic and phenotypic coefficient of variability almost had similar value and no significance difference the two variations that mean the environmental influence did not affect these traits, so in these pod-related traits genetic variability was higher than environmental variation. Therefore, selection based on those traits will be confidential and successful. Meanwhile the traits pod weight per plant and seed weight per plant had high phenotypic and genotypic coefficient of variation and the variation between them had significant difference, that environmental influence and/or experimental error was higher than genetic effects. Therefore, selection based on this value will not be suggested and feasible. In the present study high genetic variability were indicated that those RIL populations had good genetic variability between them, thus the current variability had similarity with the previous works in traits of pod yield per plant [6,16,31-34].

Table 4. The comparative statement of previously investigated Phenotypic Coeficient of Variation (PCV) and Genotypic Coeficient of Variation (GCV) on pod and seed-related traits.

Traits	Components	References
Pod yield	High (PCV)	[35,38]
	Moderate (PCV)	[39,40]
	High (GCV)	[35,37]
	Moderate (GCV)	[38]
Mature pods per plant	High (PCV)	[16,26,35-37,41-44]
	Moderate (PCV)	[45]
	High (GCV)	[16,26,35-37,41-44]
	Moderate (GCV)	[45,26]
Immature pods per plant	High (PCV)	[35,43]
	High (GCV)	[35,43]
100-pod weight (g)	Moderate (PCV)	[38,42,45,46]
	Moderate (GCV)	[38,42,45,46]
100-seed weight (g)	High (PCV)	[26,41,43]
	Moderate (PCV)	[36,44-46]
	High (GCV)	[26,41,43]
	Moderate (GCV)	[41]
Pod length	High (PCV)	[41]
	Moderate (PCV)	[41]
	High (GCV)	[41]
Pod width	Moderate (PCV)	[41]
	Moderate (GCV)	[41]
Pod yield per plant	High (PCV)	[37,41-43,46]
	Moderate (PCV)	[44,45,47];
	High (GCV)	[37,41-43,46]
	Moderate (GCV)	[44,45]
Seed yield per plant (g)	High (PCV)	[33,37-39,41,46,47]
	Moderate (PCV)	[44,45]
	High (GCV)	[35,37,41,46]
	Moderate (GCV)	[38,44,45]
Sound mature seeds/ plant (%)	High (PCV)	[26,43]
	Moderate (PCV)	[38,46]
	High (GCV)	[26,43]
	Moderate (GCV)	[38]
Shelling (%)	High (PCV)	[35]
	Moderate (PCV)	
	High (GCV)	[35]
	Moderate (GCV)	[16,35,42,46]
Immature seeds per plant	High (PCV)	[43]
	High (GCV)	[43]
Seed uniformity	High (PCV)	[37]
	High (GCV)	[37]

Heritability and genetic advance as percent of mean

Estimation of heritability in the given populations depends on the partition and association of observed phenotypic variation components into the reflection of unobserved genetic and environmental effects. High heritability values coupled with high genetic advance as percent of mean is an important method of individual plant selection [46]. The genetic gain that can be obtained from a particular trait through selection is the product of its heritability, phenotypic standard deviation and selection differential [18]. High heritability value combined with high genetic advance is considered as an indication of additive genetic variance. Many reports indicated that several crops including peanut heritability values were highly influenced by environmental variations [27]. According to Johnson et al. [10] stated that, the highest expected genetic advance selection values or high genetic gain were existed in the traits of pod length, seed length, pod thickness, pod width, multi-seedpods per plant, number of pods per plant, pod weight per plant, seed weight per plant, pod length by width, and seed thickness.

In this study the highest broad sense heritability values coupled with high genetic gain were estimated and identified in the traits of multi-seedpods per plant, number pods per plant, pod weight plant, seed weight per plant, thickness of pod shells, pod length by width, seed length by width, seed length, and some traits had moderate genetic advance as percent of means coupled with high broad sense heritability such as seed width, seed thickness, and pod thickness; similarly in the past other scientists estimated and reported that high heritability and genetic advance as percent of mean values from pod and seed-related traits had existed in peanut, for instance; Shashikumara et al. [16] were stated in the three inbred line cross that had high heritability values coupled with high genetic advance as percent of mean, were existed in pod yield, that would be indicated direct selection applied for pod yield and seed-related traits that were more effective in the given populations [29, 46]. Table 5 used us a crosscheck comparison of our new findings with the past investigations.

Table 5. The comparative statement of the past finding reports of heritability (H-broad and h-narrow sense) and genetic advance as percent of mean (G) or genetic gain values on pod and seed traits.

Traits	components	References
Pod yield	High (H)	[16,26,35-37,42-43,46,48-57]
	Moderate (H)	[16,57]
	High (h)	[58]
	Moderate (h)	[59]
	High (G)	[16,36-38,40]
Mature pods per plant	High (H)	[35-37,41-46,48,50,54,60,61-63]
	High (G)	[16, 35-37,41-45,52,62,64,65]
	Moderate (G)	[25]
Immature pods per plant	High (H)	[35,43,46]
	High (H and G)	[52,62,64,65]
	Moderate (h)	[46,47]
	High (G)	[43]
100-pod weight (g)	High (H)	[42,45,51,61]
	Moderate (H)	[38,46]
	High (G)	[42,45,46]
	Moderate (G)	[38]
100-seed weight (g)	High (H)	[43-46,51,52,57,61]
	Moderate (H)	[36,37,41,57,62]
	High (G)	[26,36,41,43-45,52,64,65]
	Moderate (G)	[37,41,46,62]
Pod length	High (H)	[41,65]
	High (h)	[58]
	High (G)	[41]
Pod width	High (H)	[41]
	Moderate (H)	[41]
	High (G)	[41]
	Moderate (G)	[41]
Pod breadth	High (H)	[65]
Seeds per pod	High (H)	[42]
Pod yield per plant	High (H)	[44,45,46]
	Moderate (H)	[41]
	High (G)	[37,41-46]
Seed yield per plant	High (H)	[35, 43-46]
	Moderate (H)	[38,41]
	High (G)	[16,37,38,41,44-46]
	Moderate (G)	[37]
Sound mature seeds/ plant (%)	High (H)	[37,46]
	Moderate (H)	[45]
	High (G)	[26,43]
	Moderate (G)	[16,38,46]
Shelling percentage	High (H)	[38,42,44-46]
	Moderate (H)	[35,37]
	High (G)	[16,42]
	Moderate (G)	[37,38,44-46]
Immature seeds per plant	High (H)	[43]
	High (G)	[43]
Seed uniformity	High (H)	[37]
	High (G)	[37]

Similarly, Narasimhulu et al. [66] had reported high broad sense heritability coupled with high genetic advance, as percent of the mean was existed in pod yield, seed yield per plant and shelling percentage traits. Veeramani et al. [31] also stated high broad sense heritability and genetic advance values existed in the number of pods per plant and seed yield characters. John et al. [47] were reported high broad sense heritability and genetic advance for harvest index. This indicated that additive gene action plays a vital role in controlling pod and seed-related traits hence individual plant selection would be effective for these pod and seed-related traits. In pod-related traits high genetic gain or genetic advance as percent of mean values reported in number of mature pods per plant, number of immature pods per plant, hundred pod yield, pod yield per plant Padmaja et al. [43] and Shashikumara et al. [16] they have been also reported that the highest genetic gain was observed in pod traits from three peanuts recombinant inbred line population. Therefore, in the present study the highest genetic advance as percent of mean values scored in the traits of multi-seedpods per plant (215.44), number of pods per plant (85.28), pod weight per plant (64.90), seed weight per plant (63.49), thickness of pod shells (56.87), pod length by width (36.55), seed length by width (30.98), seed length (23.26), and moderate genetic advance as percent of mean have been explained in pod thickness (18.29), pod width (18.17), seed width (14.88), and seed thickness (11.23) traits. None of pod and seed-related traits had low genetic advance values, so the present study had high genetic gain values.

Gene effect components

In the concept of quantitative genetics, the population structure was understood through the estimation of genetic variance components in the outcomes of allelic and non-allelic gene effects with the included of interaction effects called epistasis. Fisher (1918) was attempting to partition the genetic variances components as additive (average effects of genetic alleles), dominant (interaction between alleles of the same locus) and epistatic (interactions between alleles at different loci), of which the latter considered the most complex for trait inheritance studies (Fisher 1984). Epistatic effects can exist when the sum of the individual effects of the loci are larger or smaller than the overall effects, therefore; besides in the absence of epistatic effects, a single additive-dominant model would fully explain the expression of traits; on the other hand, when epistasis is present, it can bias the estimates of additive and dominant genetic variance components, resulting in inaccurate estimates of important genetic parameters, such as heritability and expected response to selection [15]. For more discussion and comparison, the following table 6 showed the statement of comparison our findings with previously investigated outcomes by different researchers in different time.

Table 6. Genetic variance components and gene effects on pod and seed-related traits.

Traits	Components	Gene effect	Envt. influence	References
Total pods/ plant	High (G)	Additive	Low to moderate	[16]
Matured pods/ plant	High (G)	Additive	Low	[16]
Seed yield/plant	High (G)	Additive	Low	[16]
Sound mature seed (%)	Low to high (G)	Additive +Non-additive	Low	[16]
Pod yield/plant (g)	High (G)	Additive	Low	[16,67,68]
		Non-additive		[54,69]
Shelling (%)	High (G)	Additive	Low	[16]
Pod number/ plant		Non-additive		[54,70]
100 pod weight		Non-additive		[69]

100 seed weight	Additive	[67]
	Additive +Non-additive	[71]
	Non-additive	[54]
Number of seeds/pod	Non-additive	[69]
Pod length	Additive	[70]
	Non-additive	[69]
	Non-additive	[69]

In the present study high narrow sense heritability value coupled with high additive gene variance was recorded in pod thickness and seed length traits, pod length by width trait had high narrow sense heritability but it had low additive genetic variance, moderate narrow sense heritability coupled with high additive genetic variance existed in the trait of pod length, this indicate this pod trait had additive gene effect, however sometimes this assumption affected by several uncertainty reasons, for instance, the variation of the given environment, and experimental error, but the remaining pod, and seed traits showed low narrow sense heritability value. Therefore, for promising line selection, we have recommended the traits that should have high heritability values coupled with high genetic advance, besides high additive genetic variances.

Conclusion

The highest genetic variability was existed in pod number per plant and multi-seedpods per plant. Except pod length and pod width traits, all quantitative traits showed high broad sense heritability. The highest additive gene effect was found in seed length, seed length by width, pod thickness, and pod length by width. The present study will be important and helpful for peanut improvement program to harnessing heritability and genetic variability within and between individual RIL populations. Therefore, from overall results of this study our selection prospective had focused on superior inbred line populations based on their genotypic variability, phenotypic variation, heritability, and genetic advance values.

Additional File

No additional file

Abbreviations

Not applicable

Authors' Contributions

The following authors had equal contribution: LIU Li-feng, YANG Xin-lei, LIU Kaige, HE Mei-jing, Addisu Getahun

Competing Interests

Not applicable

Availability of Data and Materials

Not applicable

Consent to Publish

Not applicable

Ethics Approval and Consent to Participate

Not applicable

Funding

The field research was funded by Chinese Ministry of Commerce.

Acknowledgements

This study was supported by Hebei Agricultural University, College of Agronomy, peanut research project, P.R. China

Competing interests:

The authors declared that no competing interests

References

1. Prabhu, R, Divyadharsini R and Manivannan N. "Genetic Variability Analysis in F3 Populations of Groundnut (Arachis hypogaea L.)." *Int J Agri Envi Biot* 8 (2015): 819-825.
2. Janila, Pasupuleti, Nigam SN, Pandey Manish K and Nagesh P, et al. "Groundnut Improvement: Use of Genetic and Genomic Tools." *Fron plant sci* 4 (2013):23.
3. Wynne, JC, and Gregory WC. "Peanut Breeding." *Adv Agron* 34 (1981): 39–72.
4. Zhang, X, Han S, Tang F and Xu J, et al. "Genetic Analysis of Yield in Peanut (Arachis Hypogaea L.) Using Mixed Model of Major Gene Plus Polygene." *Afr J Biotechnol* 10 (2011): 7126–7130.
5. Falconer, DS, and Mackay TFC. "Introduction to Quantitative Genetics." 4th Ed., Benjamin Cummings. England. (1996)
6. Singh, SB and Singh JP. "Estimation of Variability Parameters for Some Quantitative Characters in Groundnut." *Ind J Agri Sci* 69 (1999): 800-801.
7. Tripathi, A, Rajani B, Ahirwal RP and Paroha S, et al. "Study on Genetic Divergence in Sesame (Sesamum indicum L.) Germplasm Based on Morphological and Quality Traits." *The Bioscan* 8 (2013): 1387-1391.
8. Harlan, JR. "Our vanishing genetic resources." *Sci New York* 188 (1975): 618-621.
9. Dhanwani, RK, Sarawgi AK, Solanki A and Tiwari JK. "Genetic Variability Analysis for Various Yield Attributing and Quality Traits in Rice (O. Sativa L.)" *The Bioscan* 8(2013): 1403-1407.
10. Johnson, HW, Robinson HF and Comstock RE. "Estimation of Genetic and Environmental Variability in Soybeans." *Agronomy J* 47 (1955): 314–318.
11. Cholin, Sarvamangala, Gowda MVC, and Nadaf HL. "Genetic Variability and Association Pattern among Nutritional Traits in Recombinant Inbred Lines of Groundnut (Arachis Hypogaea L.)" *Indian J Genet* 70(2010): 39-43.
12. Shinde, PP, Khanpara MD, Vachhani JH and Jivani LL, et al. "Genetic Variability in Virginia Bunch Groundnut (Arachis Hypogaea L.)." *Pl Archives* 10(2010): 703-706.
13. Meshram, MP, Ali RI, Patil AN, and Meena S. "Variability Studies in M3 Generation in Blackgram (Vigna Mungo (L.) Hepper)." *The Bioscan* 8(2013), 1357-1361.
14. Islam, MS and Rasul MG. "Genetic Parameters, Correlations and Path Coefficient Analysis in Groundnut." *Bangla J Sci Ind Res* 33 (1998): 250-254.
15. Antonio, M, Acevedo B, José M and Colombari F, et al. "Epistatic Effects on Grain Yield of Soybean [Glycine Max(L.)Merrill]." *Crop Breed App Biot Brazil Scity of Plant Breed* 12 (2012): 231–236.
16. Shashikumara, P, Sanjeev BG, and Venkataravana P. "Assessment of Genetic Variability and Identification of Transgressive Segregants for Pod Yield and its Component Traits in F2 Segregating Generation of Groundnut (Arachis Hypogea L)." *Int J Farm Sci* 6 (2016): 53–60.
17. Singh, RK and Chaudhary BD. (1979) "Biometrical Methods in Quantitative Genetic Analysis, Kalyani Publications, Ludhiana."
18. Burton, GW, and Devane EM. "Estimating Heritability in Tall Fescue (Festuca Circunclinaceae) from Replicated Clonal Material." *Agronomy* J 45 (1953):478-481.

19. Siva, Subramanian SM. (1973). "Heterosis and in Breeding Depression in Rice." *Madras AgricJ* 60, 1139-1149.
20. Hanson, GH, Robinson HF and Comstock RE. "Biometrical Studies of Yield in Segregating Population of Korean Lespedeza." *Agron J* 48 (1956): 268-272.
21. Robinson, HF, Comstock RE, and Harvey VH. "Estimates of Heritability and Degree of Dominance in Corn." *Agron J* 41 (1949): 353-359.
22. Anderson, SM, Brown MR, and McDonald JF. "Tissue-Specific Expression of the Drosophila Adh Gene: A Comparison of in Situ Hybridization and Immunocytochemistry." *Genetica* 84 (1991): 95-100.
23. Kwon SH, and Torrie JH. "Heritability and Inter-Relationship of Traits of Two Soybean Populations." *Crop Sci* 4(1964): 196-198.
24. Lush, JL. "Intro-Site Correlation and Regression of Offspring on Corn as a Method of Estimating Heritability of Characters." *Proc Am Soc Anim Prod* 33 (1949): 293-301.
25. Bilgin, O, Korkut KZ, Baser ID and Ozturk O, et al. "Variation and Heritability for Some Semolina Characteristics and Grain Yield and their Relations in Durum Wheat (Triticum Durum Desf.)." *Wrld J Agri Sci* 6(2010): 301-308.
26. Padmaja, D, Brahmeswara R, Eswari KB, and Madhusudhan Reddy S. "Genetic Variability, Heritability for Late Leaf Spot Tolerance and Productivity Traits in a Recombinant Inbred Line Population of Groundnut (Arachis Hypogaea L.)." *J Agri Vet Sci* 5(2013): 36–41.
27. Singh, F, and Oswalt DL. "Genetics and Breeding of Groundnut. Skill Development Series No. 4" International Crops Research Institute for the Semi-Arid Tropics Patancheru, Andhra Pradesh, 502 324, India.
28. Lal, M, Roy D, and Ojha OP. "Genetic Variability and Selection Response for Root and Other Characters in Groundnut (Arachis Hypogaea L.)." *Legume Research* 26(2003): 128-130.
29. Golakia, PR, Makne VG and Monpara BA. (2005) "Heritable Variation and Association in Virginia Runner and Spanish Bunch Group of Groundnut." *Natnl J Plant Imp* 7 (1), 50-53.
30. Veeramani, BB, Prakash M, Jagdeeshan S and Kavimani S, et al. "Variability Studies in M2 Generation of Groundnut (Arachis Hypogaea L.)." *Legume Research* 28 (2005): 68-70.
31. Naazar, A, Mallik SN, Bashir K, and Mirza MY. "Genetic Variability, Heritability and Correlation Studies in Groundnut." *J Agri* 16 (2000): 533-536.
32. John, K, Vasanthi RP, and Venkateswarlu O. "Variability and Heritability Studies in Groundnut (Arachis Hypogaea L.)." *Legume Res* 29 (2006): 225-227.
33. Kadam, PS, Desai DT, Jagdish U and Chauhan DA. "Variability, Heritability and Genetic Advance in Groundnut." *J Maharashtra Agric Univ* 32 (2007), 71-73.
34. Khote, AC, Bendale VW, Bhave SG and Patil PP. "Genetic Variability, Heritability and Genetic Advance in Exotic Genotypes of Groundnut (Arachis Hypogaea L.)." *Crop Res* 37 (2009): 186-191.
35. Raut, RD, Dhaduk LK, and Vachhani JH. "Studies on Genetic Variability and Direct Selections for Important Traits in Segregating Materials of Groundnut (Arachis Hypogaea L.)." *Int J Agri Sci* 6 (2010): 234–237.
36. Satish, Y. "Genetic Variability and Character Association Studies in Groundnut (Arachis Hypogaea L.)." *Int J plant animal and envi sci* 4 (2014): 298–300.
37. Patidar, S, Rai PK, and Kumar A. "Evaluation of Groundnut (Arachis Hypogaea L.) Genotypes for Quantitative Character & Yield Contributing Traits." *Int J Emerg Tech Advan Eng* 4 (2014): 500–504.
38. Darvhankar, MS, Bera SK, Balakrishna N and Patel SV. "Evaluation of Genotypic Variations and Stability Analysis for Pod Yield in Recombinant Inbred Lines of Groundnut (Arachis Hypogaea L.)." *Green farm* 7 (2016):1321-1325.
39. John, K, Raghava Reddy P, Haripraad Reddy K and Sudhakar P, et al. "Studies on Genetic Variability for Morphological, Water Use Efficiency, Yield and Yield Traits in Early Segregating Generation of Groundnut (Arachis Hypogaea L.)." *Int J Bio and Consrv* 4 (2012), 446–452.
40. Sabiel, Salih A, Mohamed I, Ismail I and Elgailani Abdalla, et al. "Genetic Variation of Groundnut (Arachis Hypogaea L.) Genotypes in Semi-Arid Zone Sudan." *Int J Envi 3 Osman* (2014): 16–23.
41. Shoba, D, Manivannan N, and Vindhiyavarman P. "Studies on Variability, Heritability and Genetic Advance in Groundnut (Arachis hypogaeae L .)." *Elect J Plant Breed* 1 (2009): 74–77.
42. Nath, UK and Alam MS. "Genetic Variability, Heritability and Genetic Advance for Yield and Related Traits in Groundnut (Arachis Hypogeae L.)." *Online J of biol sci 2* (2002), 762–764.
43. Padmaja, D, Eswari KB, Brahmeswara Rao MV and Madhusudhan Reddy S. "Genetic Variability Parameters for Yield Components and Late Leaf Spot Tolerance in Bc1f2 Population of Groundnut (Arachis Hypogeaea L.)." *Int J inno Res & Dev* 2 (2013): 348-354.
44. Rao, V, Thirumala Venkanna V, Bhadru D, and Bharathi D. "Studies on Variability, Character Association and Path Analysis on Groundnut (Arachis Hypogaea L.)." *Int J Pure and appli Biosci* 2 (2014), 194–197.
45. Patil, AS, Punewar AA, Nandanwar HR, and Shah KP. "Estimation of Variability Parameters for Yield and its Component Traits in Groundnut (Arachis Hypogaea L.)." *Suppl Gent Plant Breed* 9 (2014), 749–754.
46. John, K, Vasanthi RP, Sireesha K and Giridhara Krishna T. "Genetic Variability Studies in Different Advanced Breeding Genotypes of Spanish Bunch Groundnut (Arachis Hypogaea L)." *Int J Appli Bio Pharma Tech* 4 (2013): 185-187.
47. John, K, Reddy PR, Reddy PH and Sudhakar P, et al. "Genetic Variability for Morphological, Physiological, Yield and Yield Traits in F2 Populations of Groundnut (Arachis Hypogae*a L)." Int J Appl Bio Pharma Tech* 2 (2011), 463-469.
48. Lin, H, Chan CC, and Lin CY. "Studies of the Effect of Selection for Yield of Pod at Different Planting Densities. In F5 Bulk Population of Peanut." *J Agri Ass China* 67 (1971): 27-35.
49. Reddy, PS. "Genetics Breeding and Varieties of Groundnut." New Delhi, India: *Ind Cncil Agri Res* (1988): 200-317.
50. Majumdar, PK, Ram Prakash, and Haque MF. "Genotypic and Phenotypic Variability in Quantitative Characters in Groundnut." *Ind J Genet Plant Breed* 29 (1969): 291-296.
51. Dixit, PK, Bhargava PD, Saxena DK, and Bhatia L.K. "Estimates of Genotypic Variability of Some Quantitative Characters in Groundnut (Arachis Hypoqaea L.)." *Ind J Agri Sci* 40 (1970): 197-202.
52. Sangha, AS. "Genetic Diversity in Spreading Groundnut." *Madras Agri J* 60 (1973): 1380-1387.
53. Patra, GJ. "Heritability and Genetic Advance of Some Quantitative Characters in Groundnut Hybrids in F8 Generation." *Ind J Agri Sci* 45 (1975): 308-311.]
54. Sandhu, BS and Khera AS. "The Role of Epistasis in the Inheritance of Yield and its Components in Groundnut." *Crop Imp* 3 (1976): 9-17.
55. Lakshmaiah, B. "Studies on the Relationship between Yield and its Components in Groundnut (Arachis Hypogaea L.)." M.Sc. thesis, Andhra Pradesh Agricultural University, Bapatla, Andhra Pradesh, India. (1978).
56. Gibori, A, Hillel J, Cahaner A, and Ashri A. "A 9x9 Diallel Analysis of Peanuts (A. Hvpoqaea L.)." *Theoretical and Applied Genetics* 53 (1978): 169-179.
57. Jogloy, C, Jaisil P, Akkasaeng C and Kesmala T, et al. "Heritability and Correlation for Maturity and Pod Yield in Peanut." *Jrnl of Appl Sci Res* 7(2011), 134–140.
58. Wynne, JC, and Rawling JO. "Genetic Variability and Heritability for an Inter Cultivar Cross of Peanut." *Peanut Sci* 5 (1978): 23-26.
59. Basu, MS, Singh NP, Vaddoria MA, and Raddy, PS. "Genetic Architecture of Yield and its Components in Groundnut (Arachis. Hypogaea L.)." *Annls Agri Res* 7 (1986): 144-148.
60. Kulkarni, GN, and Albuquerqua SDS. "Study of Variation in Some Quantitative Characters of Nine Strains of Groundnut Evolved at Raichur." *Mysore Jrnl Agri Sci* 1 (1967): 53-59.
61. Basu, AK, and Ashokraj PCA. "Genotypic Variability in Some Quantitative Characters of Groundnut." *Sci Cult* 35 (1969): 408-409.
62. Alam, MS, Begum D, and Khair ABMA. "Study of Genetic Parameters and Character Interrelationship in Groundnut." *Bangla Jrnl Agri Res* 10 (1985): 111-117.
63. Siva, Subramanian P, Ramanathan T, Mahalingam R and Prasad KNS, et al. "Genetic variability in certain metric traits of (Arachis hypogaea L.)." *Madras Agri Jrnl* 64 (1977), 447-450.
64. Dholaria, SJ, and Joshi SN. "Effect of High and Low Fertilization on Variability in Groundnut (Arachis Hypoqaea L.)." *Ind Jrnl Agri Sci* 42 (1972): 467-470.

65. Kushwaha, JS, and Tawar ML. “Estimates of Genotypic and Phenotypic Variability in Groundnut (Arachis Hypogaea L.).” *Ind J Agri Sci* 43 (1973): 1049-1054.

66. Narasimhulu, R, Kenchanagoudar PV, and Gowda MVC. “Study of Genetic Variability and Correlations in Selected Groundnut Genotypes.” *Int J Applied Bio and Pharma Tech* 3 (2012): 355-358

67. Sridharan, CS, and Marappan PV. “Biometrical Studies on the Hybrids of Bunch Groundnut (Arachis Hypoqaea L.).” Pages 39-42 in National Seminar on the Application of Genetics to Improvement of Groundnut, 16-17 Jul 1980, Coimbatore, Tamil Nadu, India: Tamil Nadu Agricultural University.

68. Basu, MS, Vaddoria MA, Singh NP, and Reddy PS. “Combining Ability for Yield and its Components in Diallel Cross of Groundnut.” *Ind J Agri Sci* 57 (1987): 82-84.

69. Schilling, TT. “Breeding Studies Utilizing Elite Peanut Germplasm.” Ph.D. thesis, North Carolina State University, Raleigh, NC, USA, 73. (1986).

70. Dwivedi, SL, Thondapani K, and Nigam SN. “Heterosis and Combining Ability Studies and Relationship Among Fruit and Seed Characters in Peanut.” *Peanut Sci* 16 (1989): 14-20.

71. Reddy, CR. “Studies for the Formulation of Selection Indices for Yield in Groundnut (Arachis Hypoqaea L.).” M.Sc. thesis, Andhra Pradesh Agricultural University, Hyderabad, Andhra Pradesh, India. (1968)

How to cite this article: Li-feng, L, Xin-Lei Y, Kaige L and Mei-Jing H, et al. “Quantitative Trait Inheritance and Genetic Variability on Pod and Seed-Related Traits in Peanut Recombinant Inbred Line Population” *J Genet Genom* 6 (2022): 021