ORIGINAL ARTICLE

Heritability and correlation for nitrogen fixation and agronomic traits of peanut (*Arachis hypogaea* L.)

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Abstract

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Heritability and correlation for nitrogen fixation and agronomic traits of peanut (*Arachis hypogaea* L.)
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Heritability and correlation of agronomically important traits are useful information for plant breeders to formulate effective breeding strategies. The objective of this study was to estimate broad-sense heritability, phenotypic and genotypic correlation for nitrogen fixation and agronomic traits in 6 crosses of the F_4 generation of peanut. The experiment was conducted at Khon Kaen University's agronomy farm during rainy season of 2002. Six crosses with 20 families each, their five parents and a non-nodulating line were assigned in a randomized complete block design with 4 replications. Heritability estimates varied depending on crosses and traits. The crosses KKU 1 x PI 269109 and KKU 1 x KKU 72-1 had high heritability estimates for shoot dry weight, total dry weight, fixed nitrogen and total nitrogen, indicating that superior genotypes for these traits can be easily identified in this population. For the crosses having low

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heritability estimates for nitrogen fixation parameters, selection should be emphasized on agronomic traits. High heritability estimates were found for pod number/plant, pod weight/plant, seed weight/plant, 100-seed weight, shelling percentage and harvest index in most crosses. Means of crosses were also close to means of mid-parent for most traits, indicating that gene action controlling the inheritance of most traits were additive. Phenotypic and genotypic correlations among nitrogen fixation traits were positively correlated with each other. The traits were also positively correlated with pod weight/plant, seed weight/plant and 100-seed weight, but were not correlated with pod number/plant, seed number/plant and seed number/pod. Nitrogen fixation parameters were negatively correlated with shelling percentage and harvest index.

Key words : nitrogen fixation parameters

บทคัดย่อ

สำราญ พิมราช สนั่น จอกลอย บรรยง ทุมแสน ประสิทธิ์ ใจศิล ถวัลย์ เกษมาลา
และ อารันต์ พัฒโนทัย

อัตราพันธุกรรมและสหสัมพันธ์ของลักษณะการตรึงไนโตรเจนและลักษณะทางการเกษตรของถั่วลิสง

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อัตราพันธุกรรมและสหสัมพันธ์ของลักษณะที่มีความสำคัญทางการเกษตรเป็นข้อมูลที่มีประโยชน์สำหรับนักปรับปรุงพันธุ์พืชในการกำหนดวิธีการปรับปรุงพันธุ์ที่มีประสิทธิภาพ การวิจัยนี้มีวัตถุประสงค์เพื่อประมาณค่าอัตราพันธุกรรมแบบกว้างและสัมประสิทธิ์สหสัมพันธ์ของลักษณะที่ปรากฏและลักษณะทางพันธุกรรมระหว่างการตรึงไนโตรเจนและลักษณะทางการเกษตรในคู่ผสม 6 คู่ ของประชากรชั่วที่ 4 ของถั่วลิสง โดยทำการทดลองที่หมวดพืชไร่ คณะเกษตรศาสตร์ มหาวิทยาลัยขอนแก่น ในฤดูฝนปี 2545 สิ่งทดลองประกอบด้วยคู่ผสม 6 คู่ แต่ละคู่มี 20 ตระกูล (family) , พันธุ์พ่อแม่ 5 พันธุ์ และพันธุ์ไร้ปม 1 พันธุ์ ใช้แผนการทดลองแบบสุ่มสมบูรณ์ภายในกลุ่มมี 4 ซ้ำ ผลการทดลองพบว่า ค่าอัตราพันธุกรรมแตกต่างกันขึ้นอยู่กับคู่ผสมและลักษณะที่ศึกษา คู่ผสม KKU 1 x PI 269109 และ KKU 1 x KKU 72-1 มีค่าอัตราพันธุกรรมสูงในลักษณะน้ำหนักต้นแห้ง, น้ำหนักรวม, ไนโตรเจนที่ตรึงได้ และ ไนโตรเจนทั้งหมด แสดงว่า การระบุสายพันธุ์ที่ตรึงไนโตรเจนสูงในประชากรนี้ทำได้ง่าย คู่ผสมที่มีอัตราพันธุกรรมของลักษณะการตรึงไนโตรเจนต่ำควรเน้นการคัดเลือกลักษณะทางการเกษตร ซึ่งพบว่าหลายคู่ผสมมีค่าอัตราพันธุกรรมสูงในลักษณะจำนวนฝัก/ต้น, น้ำหนักฝัก/ต้น, น้ำหนักเมล็ด/ต้น, น้ำหนัก 100 เมล็ด, เปอร์เซ็นต์กะเทาะ และ ดัชนีเก็บเกี่ยว ค่าเฉลี่ยของคู่ผสมส่วนใหญ่ไม่แตกต่างจากค่าเฉลี่ยของพ่อแม่ในเกือบทุกลักษณะ แสดงว่ายีนควบคุมลักษณะแสดงออกแบบบวก ค่าสหสัมพันธ์ของลักษณะที่ปรากฏและลักษณะทางพันธุกรรมระหว่างการตรึงไนโตรเจน มีความสัมพันธ์ในทางบวกซึ่งกันและกัน และมีความสัมพันธ์ในทางบวกกับลักษณะน้ำหนักฝัก/ต้น, น้ำหนักเมล็ด/ต้น และน้ำหนัก 100 เมล็ด แต่มีความสัมพันธ์ในทางลบกับลักษณะจำนวนฝัก/ต้น, จำนวนเมล็ด/ต้น และจำนวนเมล็ด/ฝัก ลักษณะการตรึงไนโตรเจนมีสหสัมพันธ์เป็นลบกับลักษณะเปอร์เซ็นต์กะเทาะและดัชนีเก็บเกี่ยว

ภาควิชาพืชไร่ คณะเกษตรศาสตร์ มหาวิทยาลัยขอนแก่น อำเภอเมือง จังหวัดขอนแก่น 40002

Peanut (*Arachis hypogaea* L.) is grown mainly in semi-arid tropic regions which are characterized by low soil fertility and unpredictable rainfalls. The limitation in soil available nitrogen causes low productivity of several crops in these areas. High input of nitrogen fertilizer to maintain acceptable productivity level also causes heavy burden for poor and small-scale farmers. Yet nitrate leaching is of great effect on environmental deterioration. Peanut not only provides nutritional value for human diet but it also adds nitrogen to soils that is beneficial to following crops.

Like many other leguminous species that can fix nitrogen, peanut yield is dependent on nitrogen derived from atmostphere by symbiotic relationship between peanut host and rhizobium. Improvement of peanut lines for their ability to fix more nitrogen may improve yield of peanut. Genotypic variability for nitrogen fixation and related traits in peanut germplasm have been well documented (Toomsan *et al.*, 1991; Elkan *et al.*, 1980; Nambiar and Dart, 1983; Phillips *et al.*, 1989) and genetic basis for these traits has also been studied in some extent (Phillips *et al.*, 1989). However, the discrepancy of the results requires further investigations to draw a sound conclusion.

Many authors have studied genetic variation and heritability for nitrogen fixation and related traits in peanut breeding populations (Isleib *et al.*, 1980; Arrendell *et al.*, 1986; Phudenpa, 2002). Correlation among traits is also available in literature (Toomsan *et al.*, 1991; Nigam *et al.*, 1985; Arrendell *et al.*, 1985;1986). The information is important for breeders to formulate effective and efficient breeding strategies. However, genetic variation and heritability estimates are unique to a particular population. In addition, these genetic properties are dependent on variation due to environment and genetic background of breeding population. Although the information provides useful guidelines for peanut breeders, the extrapolation of the results to other populations is limited.

This study was conducted to estimate broad sense heritability, phenotypic and genotypic correlation among traits related to nitrogen fixation and agronomic traits.

Materials and Methods

Plant materials and experimental procedures

The experiment was conducted at Khon - Kaen University's agronomy farm during May to December in 2001. Twenty families from each of 6 peanut crosses of the F_4 generation were used in this study. The F_3 seeds were planted in dry season 2002 for seed increase and the F_4 seeds were used in this experiment. The crosses were KKU 1 x Virginia Bunch (PI 152133), A_3-1-1 (BC 154) (PI 268770) x 42-G-105 (PI 269109), KKU 1 x KKU 72-1, A_3-1-1 (BC 154) (PI 268770) x KKU 72-1, KKU 1 x 42-G-105 (PI 269109) and KKU 72-1 x 42-G-105 (PI 269109). For convenience, Virginia Bunch (PI 152133), A_3-1-1 (BC 154) (PI 268770) and 42-G-105 (PI 269109) are hereafter designated as PI 152 133, PI 268770 and PI 269109, respectively. Descriptions of their parents, cross regeneration and evaluation of the F_2 generation were reported by Phudenpa (2002). A non-nodulating line was used as reference plant for leaf color score evaluation and nitrogen determination.

One hundred and twenty six entries consisting of 6 crosses with 20 families each, their five parents and a non-noduating line were arranged in a randomized complete block design with 4 replications. Plot size was a single row plot with 3 m long. Spacing was 20 cm between plants within row and 50 cm between rows. Lime (CaO) at the rate of 100 kg rai^{-1} (0.16 ha) was incorporated into soil during soil preparation. Seeds were treated with fungicide (Captan) at rate of 5 g kg^{-1} (seed). Seeds were over-planted and then thinned to obtain 1 plant per hill. Gap filling was also done at 7 days after planting because of poor germination. No rhizobium inoculation was applied because the experimental site had history of peanut cultivation in previous years and peanut did not respond to rhizobium inoculation (Toomsan *et al.*, 1988). Pre-emergence herbicide (Alachlor) at rate of 500 cm^3 rai^{-1} was sprayed soon after planting and hand weeding was done at 15 and 35 days after planting. Inorganic fertilizers (N-P_2O_5-K_2O) at the rate of 0-9-6 kg rai^{-1} were applied at 15 days after planting. Gypsum ($CaSO_4$) at rate of 100 kg rai^{-1} and Cabofuran 3% G at rate of 5 kg rai^{-1} were applied at 35 days after planting by side dressing. Fungicides, insecticides and supplemental irrigation were applied as necessary to obtain optimum growth and yield.

Data collection

Data were recorded on each plot for nitrogen fixation parameters, viz. leaf color score, nodule dry weight, shoot dry weight, total nitrogen and fixed nitrogen and agronomic traits. Leaf color score was recorded at 50 days after planting by scoring 1-4 on each plot where 1= pale yellow and 4= dark green (Srisaowakonthorn, 1989; Phudenpa, 2002). The rest of traits were recorded at harvest. Plant at the two ends of each row were discarded and only competitive plants were taken as samples. Samples in each plot were dug and separated into parts. Nodules, stems and leaves were oven-dried at 80 ° C for 48 hr and nodule dry weight, shoot dry weight and total dry weight were determined. Pods were air-dried to obtain approximately 8% moisture content and shelled. Then, pod number per plant, seed number per plant, pod weight per plant, seed weight per plant, 100-seed weight, shelling percentage and harvest index were determined.

To measure nitrogen fixation, samples were ground and crude protein content was obtained according to micro-Kjeldahl method (Black, 1965). Nitrogen content was measured by automated indophenol method (Schuman *et al.*, 1973) and were read on flow injection analyzer (FIA), model 5012 ANALYZER, TECATOR 5207.

Fixed nitrogen content was calculated as difference between total nitrogen content and taken up nitrogen content based on the assumption that the fixing cultivars took up the same amount of soil nitrogen as the non-fixing cultivar and the remainder was fixed.

Total fixed N = Total N of each genotype –
Total N of nonnod

Data analysis

Mean comparison: The data were subjected to analysis of variance according to a randomized complete block design. Mean comparision was performed by Duncan's multiple range test (Gomez and Gomez, 1984).

Heritability: Broad sense heritability estimates were calculated by using the expected means squares following analysis of variance of a randomized complete block design (Table 1).

Table 1. Mean squares and expected mean squares for analysis of variance according to a randomized complete block design.

Sources of variation	df.	MS	EMS
Replications	r-1	M_r	
Families of each cross	f-1	M_f	$\sigma^2_E + r\sigma^2_F$
Error	(r-1)(f-1)	M_e	σ^2_E

M_e = error variance, M_f/r = phenotypic variance based on progeny means and σ^2_F = genotypic variance (σ^2_G)

Phenotypic variance of each cross was partitioned to obtain genotypic variance and error variance (σ^2_E). Error variance was further divided by number of replications to obtain environmental variance, and then broad sense heritability estimate (h^2_b) based on family means for each cross was calculated as $\sigma^2_G/(\sigma^2_G + \sigma^2_E/r)$.

Phenotypic and genotypic correlation: Phenotypic and genotypic correlation coefficients were calculated based on family means by the method described by Srinives (1982) (Table 2).

Results and Discussion

Mean comparison

Selection scheme for quantitative traits in segregating population of autogamous species is dependent on means, genetic variance and types of gene action controlling the inheritance of traits. Selection will be effective only when additive genetic effect is substantial. Mean comparisons showed that the crosses PI 268770 x KKU 72-1 and KKU 72-1 x PI 269109 had means for total nitrogen, fixed nitrogen, shoot dry weight and total dry weight higher than those of other crosses, whereas the cross KKU 1 x PI 152133 had the low means for all nitrogen fixation parameters (Table 3). Toomsan *et al.* (1991) reported that high nitrogen fixing lines generally gave high values for weight and number of nodules and shoot dry weight. In contrast, low nitrogen fixing lines gave

Table 2. Mean squares and expected mean squares for X and Y traits according to a randomized complete block design.

Sources of variation	df	MS character		MCP	EMS	EMCP
		X	Y			
Replications	r-1					
Families of all crosses	f-1	M_2*	M_2	M_2* M_2	$\sigma^2_E + r\sigma^2_F$	$\sigma_{E*E} + r\sigma_{F*F}$
Error	(r-1)(f-1)	M_1*	M_1	M_1* M_1	σ^2_E	σ_{E*E}

Where:

$\sigma^2_{E*} = M_1*$ and $\sigma^2_E = M_1$

$\sigma^2_{E*E} = M_1* M_1$

$\sigma^2_{F*} = (M_2* - M_1*)/r$ and $\sigma^2_F = (M_2 - M_1)/r$

$\sigma^2_{F*F} = (M_2*M_2 - M_1* M_1)/r$

Therefore:

Phenotypic variance $\sigma^2_{P*} = \sigma^2_{F*} + (\sigma^2_{E*}/r)$ and $\sigma^2_P = \sigma^2_F + (\sigma^2_E/r)$

Phenotypic covariance $\sigma_{P*P} = \sigma_{F*F} + (\sigma_{E*E}/r)$

Phenotypic correlation, $r_P = (M_2*M_2)/[(M_2*)(M_2)]^{1/2}$

Environmental correlation, $r_E = (M_1*M_1)/[(M_1*)(M_1)]^{1/2}$

Genotypic correlation, $r_G = \sigma_{F*F}/(\sigma^2_{F*} \times \sigma^2_F)^{1/2}$

$= (M_2*M_2 - M_1*M_1)/ [(M_2* - M_1*)(M_2 - M_1)]^{1/2}$

low values for these traits. Wynne *et al.* (1983) and Phillips *et al.* (1989) reported that high nitrogen fixing lines gave high leaf color score, shoot dry weight, and nitrogenase activity. Considering association among traits, leaf color score, nodule dry weight, shoot dry weight and total dry weight should be useful as selection criteria for nitrogen fixation.

Significant difference among crosses was found for 100-seed weight. PI 268770 x KKU 72-1 was the best cross for seed size having 100-seed weight of 49.52 g, while KKU 1 x PI 152133 was the poorest having 100-seed weight of 38.80 g. The rest of the traits, such as pod number per plant, seed weight per plant, shelling percentage and harvest index, were not statistically different among these crosses.

Heritability

Heritability estimates for shoot dry weight, total dry weight, total nitrogen and fixed nitrogen were high in the crosses KKU 1 x PI 269109 and KKU 1 x KKU 72-1, ranging from 0.80 to 0.88. However, heritability estimates in these crosses were low for nodule dry weight and leaf color score. Moderate heritability estimates, ranging from 0.37 to 0.62, for shoot dry weight, total dry weight, total nitrogen and fixed nitrogen were found in the crosses KKU 1 x PI 152133 and PI 268770 x PI 269109. Similarly, heritability estimates in these crosses were low for nodule dry weight and leaf color score. The cross KKU 72-1 x PI 269109 had very low heritability estimates for all traits (Table 4).

The low heritability estimates for nodule dry weight and leaf color score in most crosses indicate that the improvement for these traits will be difficult. In contrast, the moderate to high heritbility estimates for shoot dry weight, total dry weight, total nitrogen and fixed nitrogen in

Table 3. Mean comparison for traits related to nitrogen fixation and agronomic traits of six crosses of peanut.

Cross	Traits related to nitrogen fixation					
	Nodule weight (g/plant)	Shoot weight (g/plant)	Total weight (g/plant)	Leaf color score[1/]	Total N (mg/plant)	Fixed N (mg/plant)
KKU 1 x PI 152133	0.40c	32.34c	40.39c	2.80d	56.73c	27.08c
PI 268770 x PI 269109	0.48a	51.91b	59.33b	4.00a	112.80a	82.85b
KKU 1 X KKU 72-1	0.39c	50.31b	57.95b	3.49b	108.00b	78.03b
PI 268770 x KKU 72-1	0.43bc	64.93a	73.26a	4.00a	152.10a	122.10a
KKU 1 x PI 269109	0.40c	45.26b	55.37b	3.25c	91.86b	62.17b
KKU 72-1 x PI 269109	0.47ab	64.19a	75.05a	4.00a	150.10a	120.20a
F-ratio	4.2*	33.3**	40.8**	118.5**	40.2**	40.5**
C.V. (%)	8.5	8.2	6.3	2.6	10.2	13.8

Cross	Agronomic traits							
	Pod number/ plant	Pod weight/ plant (g)	Seed number/ plant	Seed number/ pod	Seed weight/ plant (g)	100-seed weight (g)	Shelling percentage	Harvest index
KKU 1 x PI 152133	7.8	7.50	11.49	1.55	4.48	38.80c	57.57	0.21
PI 268770 x PI 269109	7.8	9.44	11.41	1.44	5.24	46.75ab	53.36	0.19
KKU 1 X KKU 72-1	9.6	9.50	14.27	1.48	6.00	43.46bc	61.80	0.20
PI 268770 x KKU 72-1	8.9	10.75	13.31	1.48	6.35	49.52a	57.28	0.18
KKU 1 x PI 269109	9.2	9.07	13.50	1.60	5.23	41.52c	56.05	0.20
KKU 72-1 x PI 269109	9.1	10.64	13.61	1.51	6.15	47.03ab	56.22	0.18
F-ratio	0.7	1.4	0.5	0.6	1.0	12.2**	1.8	1.4
C.V. (%)	19.8	20.9	22.8	9.6	25.8	5.1	7.2	22.2

Means in the same column with the same letter(s) are not statistically different at 0.01 probability level by DMRT.
***,** Significant at 0.05 and 0.01 probability levels, respectively.**
[1/] Rating 1-4 where 1= yellowish, 4= dark green.

most crosses, except in the cross KKU 72-1 x PI 269109 indicated high possibility to improve these traits. However, the success of selection scheme is highly dependent on the magnitude of additive genetic variance in the population.

Isleib *et al.* (1980) and Nigam *et al.* (1985) reported that additive genetic variance was more important than non-additive genetic variance for nodule number, nodule weight, nitrogenase activity (acetelene reduction), and total nitrogen. In contrast, Miller *et al.* (1986) found that the importance of non-additive genetic variance was greater than that of additive genetic variance for nodule weight and shoot dry weight. Phudenpa, (2002) also found that additive genetic variance was greater than non-additive genetic variance for nodule weight, shoot dry weight and leaf color score, and the heritability estimates in the F_2 generation were generally low.

Although the cross KKU 72-1 x PI 269109 had low heritability estimates for all nitrogen fixation traits, its performance for these traits was high (Table 3). This might be due to high performance for these traits of both parents (high x high). Improvement for agronomic traits might be possible in this cross if heritability estimates were high.

Heritability estimates for agronomic traits,

Table 4. Broad-sense heritability estimates for traits related to nitrogen fixation and agronomic traits of six crosses of peanut.

Cross	**Traits related to nitrogen fixation**					
	Nodule weight	**Shoot weight**	**Total weight**	**Leaf color score**[1/]	**Total nitrogen**	**Fixed N**
KKU 1 x PI 152133	0.00	0.44	0.49	0.20	0.40	0.37
PI 268770 x PI 269109	0.00	0.62	0.56	0.00	0.56	0.56
KKU 1 X KKU 72-1	0.33	0.83	0.85	0.22	0.80	0.80
PI 268770 x KKU 72-1	0.00	0.00	0.22	0.00	0.22	0.22
KKU 1 x PI 269109	0.40	0.86	0.85	0.27	0.88	0.88
KKU 72-1 x PI 269109	0.20	0.00	0.00	0.00	0.00	0.00

Cross	**Agronomic traits**							
	Pod number/ plant	**Pod weight /plant**	**Seed number/ plant**	**Seed number/ pod**	**Seed weight/ plant**	**100-seed weight**	**Shelling percentage**	**Harvest index**
KKU 1 x PI 152133	0.42	0.47	0.26	0.10	0.41	0.47	0.17	0.50
PI 268770 x PI 269109	0.36	0.27	0.27	0.00	0.23	0.05	0.53	0.00
KKU 1 X KKU 72-1	0.74	0.84	0.78	0.63	0.84	0.92	0.71	0.75
PI 268770 x KKU 72-1	0.40	0.56	0.52	0.40	0.55	0.73	0.26	0.50
KKU 1 x PI 269109	0.88	0.77	0.87	0.61	0.72	0.61	0.37	0.80
KKU 72-1 x PI 269109	0.54	0.46	0.49	0.23	0.51	0.21	0.64	1.00

Negative heritability estimates were assumed to be zero and expressed as zero.

[1/] **Rating 1-4 where 1= yellowish, 4= dark green.**

viz. pod number per plant, seed number per plant, pod weight per plant, seed weight per plant, 100-seed weight, shelling percentage and harvest index, varied depending on crosses and traits. The crosses KKU 1 x PI 152133 and PI 268770 x PI 269109 had low to moderate heritability estimates for agronomic traits ranging from 0.10 to 0.50 and 0.00 to 0.53, respectively. The cross KKU 1 x KKU 72-1 and KKU 1 x PI 269109 had high heritability estimates for most agronomic traits ranging from 0.61 to 0.92 except for shelling percentage (0.37). The crosses PI 268770 x KKU 72-1 and KKU 72-1 x PI 269109 generally had low to moderate heritability estimates. However, the exceptionally high heritability estimate was found for harvest index in the cross KKU 72-1 x PI 269109.

Because all F_4 families in the six crosses were randomly selected from unselected populations derived from the F_2 generation, the cross means were tested against their respective mid-parent values. The results showed that mid-parent values were not statistically different from the cross means for most traits except for total dry weight and seed number per pod in the cross KKU 1 x KKU 72-1 (results not reported). The additive effects seemed to be predominant for most traits under the study. Therefore, broad sense heritability estimates obtained were assumed to be close to narrow sense heritability estimates. Selection for traits with high heritability estimates in these populations would be possible. For agronomic traits, the crosses KKU 1 x KKU 72-1 and KKU 1 x PI 269109 were more promising than the other crosses.

Green *et al.* (1983) found that additive gene effects and non-additive gene effects were equally important in conditioning yield and pod dry weight in peanut. In contrast, Dwivedi *et al.* (1989) and Swe and Branch (1986) found that non-additive gene effects were more important than additive gene effects for pod dry weight. These studies were in agreement with Jogloy *et al.* (1999) who found that additive gene effects were more important than non-additive gene effects for pod length and seed size, while non-additive gene effects were less important for agronomic traits.

Phenotypic and genotypic correlation

For phenotypic correlation, moderate to high correlation coefficients ranging from 0.40** to 1.00** were found among nitrogen fixation parameters viz., fixed N, total N, nodule dry weight, shoot dry weight, total dry weight and leaf color score. Similarly, for genotypic correlation, these traits also correlated well with each other and the correlation coefficients ranged from 0.70** to 1.00** (Table 5).

Most nitrogen fixation parameters were generally low correlated with pod number per plant, seed number per plant and seed number per pod. The correlation coefficients ranged from –0.14** to 0.32** and –0.07 to 0.30** for phenotypic and genotypic correlations, respectively.

Nitrogen fixation parameters had moderate correlation with pod weight per plant, seed weight per plant and 100-seed weight. The correlation coefficients ranged from 0.15** to 0.62** and 0.25** to 0.76** for phenotypic and genotypic correlations, respectively.

However, nitrogen fixation parameters were negatively correlated with shelling percentage and harvest index. The correlation coefficients ranged from –0.52** to 0.06 and –0.76** to –0.01 for phenotypic and genotypic correlations, respectively. The relationships among agronomic traits were also reported, but we did not emphasize herein.

Among nitrogen fixation traits, genotypic correlations were somewhat higher than phenotypic correlation possibly due to the fact that environmental effects were removed from genotypic variance. Similar results were also reported (Nigam *et al.*, 1985; Arrendell *et al.*, 1985; 1986). Nigam *et al.* (1985) reported that genotypic correlations between nitrogenase activity with other traits such as nodule weight, total nitrogen, root dry weight, shoot dry weight, and nodule number were higher than phenotypic correlations. In addition, total nitrogen was positively correlated with shoot dry weight, nodule dry weight, root dry weight and leaf area. Fixed nitrogen and total nitrogen were also positively correlated with leaf color score and nodule weight. Arrendell *et al.* (1985) found that genotypic correlations between nitrogenase activity and shoot dry weight ranged from 0.66** to 0.89** and phenotypic correlations ranged from 0.35 to 0.60. They also found low correlation between nitrogenase activity and yield. Arrendell *et al.* (1986) found that genotypic correlations of two-year data between pod dry weight and nitrogenase activity were higher than phenotypic correlation.

Fixed nitrogen contributed to pod weight, seed weight and seed size rather than pod number and seed number. This implies that fixed nitrogen might increase seed fill or translocation rate of assimilate rather than increasing sink capacity and thus increase yield. Similarly, Toomsan *et al.* (1991) reported that high nitrogen fixing lines also gave high nodule number, nodule weight and shoot dry weight, whereas low nitrogen fixing lines gave low values for these traits. In addition, fixed nitrogen was correlated with total nitrogen (0.97**) and nodule weight (0.60**). In contrast, Swe and Branch (1986) reported that shoot dry weight was correlated with pod number and seed number. Peanut genotypes might respond differently to increased nitrogen.

Nitrogen fixation parameters were negatively correlated with shelling percentage and harvest index, indicating that fixed nitrogen contributed to vegetative growth rather than to yield. Therefore, indicative traits of nitrogen fixation such as shoot dry weight, total dry weight and leaf color score might be used as selection criteria for high nitrogen fixation, but our results did not strongly support the conclusion that these traits

Table 5. Phenotypic and genotypic correlation among nitrogen fixation parameters and agronomic traits in six crosses of the F_4 generation of peanut based on plot means.

	Traits related to nitrogen fixation						Agronomic trait							
	Fixed N	**Total N**	**Nodule weight**	**Shoot weight**	**Total weight**	**Leaf color score**	**Pod number/ plant**	**Seed number/ plant**	**Seed number/ pod**	**Pod weight/ plant**	**Seed weight/ plant**	**100-seed weight**	**Shelling percen-tage**	**Harvest index**
Fixed N		1.00**	0.41**	0.97**	0.96**	0.81**	0.12*	0.15**	-0.03	0.47**	0.40**	0.60**	-0.06	-0.51**
Total N	1.00**		0.41**	0.97**	0.96**	0.81**	0.11*	0.15**	-0.03	0.47**	0.39**	0.60**	-0.06	-0.52**
Nodule weight	0.71**	0.71**		0.40**	0.41**	0.56**	0.00	0.01	-0.05	0.25**	0.15**	0.36**	-0.32**	-0.22**
Shoot weight	0.98**	0.98**	0.70**		0.99**	0.75**	0.16**	0.20**	0.00	0.50**	0.44**	0.60**	-0.01	-0.51**
Total weight	0.97**	0.97**	0.69**	0.99**		0.75**	0.28**	0.32**	0.03	0.62**	0.56**	0.61**	0.06	-0.39**
Leaf color score	0.88**	0.88**	0.84**	0.83**	0.83**		0.04	0.05	-0.14**	0.39**	0.29**	0.62**	-0.19**	-0.42**
Pod number/plant	0.11*	0.11*	-0.07	0.15**	0.24**	0.06		0.95**	0.02	0.81**	0.84**	-0.04	0.55**	0.64**
Seed number/plant	0.16**	0.15**	0.02	0.21**	0.30**	0.08	1.00**		0.30**	0.86**	0.89**	-0.02	0.61**	0.65**
Seed number/pod	-0.09	-0.03	0.18**	-0.04	-0.03	-0.33**	0.13*	0.21**		0.18*	0.21**	-0.15**	0.27**	0.22**
Pod weight /plant	0.59**	0.47**	0.43**	0.63**	0.71**	0.52**	0.77**	0.80**	0.04		0.98**	0.43**	0.42**	0.44**
Seed weight/plant	0.52**	0.39**	0.25**	0.57**	0.65**	0.41**	0.82**	0.85**	0.08	0.98**		0.39**	0.59**	0.51**
100-seed weight	0.74**	0.74**	0.55**	0.75**	0.75**	0.72**	-0.12*	-0.07	-0.32**	0.52**	0.45**		0.01	-0.21**
Shelling percentage	-0.01	-0.09	-0.76	-0.05	-0.01	-0.29**	0.50**	0.55**	0.28**	0.24**	0.43**	-0.21**		0.56**
Harvest index	-0.63**	-0.64**	-0.54**	-0.63**	-0.54**	-0.56**	0.59**	0.57**	0.24**	0.19**	0.27**	-0.44**	0.40**	

Above diagonal is phenotypic correlation and below diagonal is genotypic correlation.
***,** significant at 0.05 and 0.01 probability levels, respectively.**

might be used as selection criteria for yield. However, nitrogen fixation parameters were moderately correlated with pod weight per plant, seed weight per plant and 100-seed weight, indicating that these traits were somewhat useful as selection criteria for yield.

Conclusion

Based on heritability estimates, there would be a possibility to improve nitrogen fixation and agronomic traits in six crosses of the F_4 generation by selecting families in the crosses. Phenotypic and genotypic correlation indicated that nitrogen fixation could contribute to yield but to a lesser extent than to vegetative growth. Shoot dry weight and total dry weight may be useful as selection criteria for high nitrogen fixation and may help reducing research cost, since direct measurement of nitrogen fixation is not necessary.

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