ORIGINAL ARTICLE

Combining ability analysis for traits related to N_2-fixation and agronomic traits in peanut (*Arachis hypogaea* L.)

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Abstract

Phudenpa, A., Jogloy, S., Toomsan B., Wongkaew S., Kesmala, T., and Patanothai, A.
Combining ability analysis for traits related to N_2-fixation and agronomic traits in peanut (*Arachis hypogaea* L.)
Songklanakarin J. Sci. Technol., 2006, 28(3) : 449-457

Symbiotic nitrogen fixation in peanut offers an alternative way to reduce chemical nitrogen fertilization. The objectives of this study were to estimate general combining ability (GCA) and specific combining ability (SCA) effects for traits related to N_2-fixation and agronomic traits and to identify the best parents for use in peanut breeding programs aimed at improving nitrogen-fixing ability. Full diallel (F_2) crosses of peanut with reciprocals involving five parents were planted in a randomized complete block design with four replications. GCA mean squares were more important than SCA mean squares for plant dry weight, nodule dry weight, leaf color score, seed weight per plant, shelling percentage and harvest index. SCA mean squares

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Received, 15 July 2005 Accepted, 20 November 2005

were significant for pod weight per plant, seed weight per plant and 100 seed weight. SCA mean squares were more important than GCA mean squares for pod weight per plant, and equally important for seed weight per plant. Reciprocal mean squares were significantly important for 100 seed weight, shelling percentage and harvest index. KKU 72-1, (A3-1-1 (Bc 154) (PI 268770) and 42-G-105 (PI 269 109) were identified as good general combiners for traits related to N_2-fixation, plant dry weight, nodule dry weight and leaf color score, whereas A3-1-1 (Bc 154) (PI 268 770) and KKU 72-1 were the best parents for 100 seed weight. A3-1-1 (Bc 154) (PI 268 770) was also the best general combiner for shelling percentage and harvest index.

Key words : diallel cross, additive gene effect, non-additive gene effect, GCA, SCA

บทคัดย่อ

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ความสามารถในการรวมตัวของลักษณะที่เกี่ยวข้องกับการตรึงไนโตรเจน และลักษณะทางการเกษตรในถั่วลิสง

ว. สงขลานครินทร์ วทท. 2549 28(3) : 449-457

การตรึงไนโตรเจนในถั่วลิสงเป็นทางเลือกหนึ่งในการลดการใช้ปุ๋ยเคมีไนโตรเจน การศึกษานี้มีวัตถุประสงค์เพื่อประเมินความสามารถในการรวมตัวทั่วไป และความสามารถในการรวมตัวเฉพาะสำหรับลักษณะที่เกี่ยวข้องกับการตรึงไนโตรเจน และลักษณะทางการเกษตร และเพื่อระบุพันธุ์พ่อแม่ที่ดีเพื่อใช้ในโครงการปรับปรุงพันธุ์ถั่วลิสงเพื่อให้ตรึงไนโตรเจนได้สูง ได้ประเมินลูกผสมในชั่วที่ 2 ที่ได้จากการผสมพันธุ์พ่อแม่ 5 พันธุ์ แบบพบกันหมดรวมทั้งสลับพ่อแม่ โดยใช้แผนการทดลองแบบสุ่มสมบูรณ์ภายในซ้ำ มี 4 ซ้ำ

จากผลการทดลอง พบว่า ความสามารถในการรวมตัวทั่วไปมีความสำคัญมากกว่าความสามารถในการรวมตัวเฉพาะ ในลักษณะน้ำหนักต้นแห้ง น้ำหนักปมแห้ง คะแนนสีใบ น้ำหนักเมล็ดต่อต้น เปอร์เซ็นต์กะเทาะ และดัชนีเก็บเกี่ยว ความสามารถในการรวมตัวเฉพาะมีนัยสำคัญในลักษณะ น้ำหนักฝักต่อต้น น้ำหนักเมล็ดต่อต้น และน้ำหนัก 100 เมล็ด ความสามารถในการรวมตัวเฉพาะมีความสำคัญมากกว่าความสามารถในการรวมตัวทั่วไป ในลักษณะน้ำหนักฝักต่อต้น และดัชนีเก็บเกี่ยว และมีความสำคัญใกล้เคียงกับความสามารถในการรวมตัวทั่วไป ในลักษณะน้ำหนักเมล็ดต่อต้น คู่ผสมสลับพ่อแม่มีความแตกต่างกัน ในลักษณะน้ำหนัก 100 เมล็ด เปอร์เซ็นต์กะเทาะ และดัชนีเก็บเกี่ยว พันธุ์ KKU 72-1, A3-1-1 (Bc 154 (PI 268770) และ 42-9-105 (PI 269109) มีความสามารถในการรวมตัวดี ในลักษณะที่เกี่ยวข้องกับการตรึงไนโตรเจน เช่น น้ำหนักต้นแห้ง น้ำหนักปมแห้ง และคะแนนสีใบ ส่วนพันธุ์ A3-1-1 (BC 154) (PI 268770) และ KKU 72-1 มีความสามารถในการรวมตัวทั่วไปดี ในลักษณะน้ำหนัก 100 เมล็ด พันธุ์ A3-1-1 (Be 154) (PI 268-770) มีความสามารถในการรวมตัวทั่วไปดีที่สุด ในลักษณะเปอร์เซ็นต์กะเทาะและดัชนีเก็บเกี่ยว

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Modern crop production depends mainly on the application of chemical fertilizers, particularly nitrogen fertilizer. This input increases the total cost of crop production. Symbiotic nitrogen fixation by leguminous species including peanut offers an alternative way to reduce nitrogen fertilization. Peanut residue also provides nitrogen for following crops such as rice, cassava, sugarcane and field maize. Consequently, the cost of crop production is reduced, soil fertility is recovered and sustainable agriculture can be obtained.

Genetic variation in ability of peanuts to fix atmostpheric nitrogen exists in peanut germplasm (Nambiar and Dart, 1983; Elkan *et al.*, 1980). Elkan *et al.* (1980) found that Virginia-type peanuts had greater nitrogenase activity and produced more nodules than Valencia-type peanuts. Nambiar and Dart (1983) also found that Virginia-type peanut, Kadiri-71, had higher nitrogenase activity than Valencia-type peanut variety, MK2. Toomsan *et al.* (1992) reported that Virginia-type peanut, KK 60-3, fixed more atmostpheric nitrogen than did Spanish-type peanut, KK 60-1. Kucey and Toomsan (1988) reported that the differences in nitrogen fixation ability existed in Spanish-type peanut.

Screening procedures for traits related to N_2-fixation in peanut are costly, tedious and time-consuming. Traits related to N_2-fixation can be used effectively in screening good genotypes in early segregating populations of peanut for high N_2-fixation ability. Date (1970) reported that number of nodules, nodule weight and nodule appearance could be used as indicators for N_2-fixation ability in peanut. Wynne *et al.* (1980) suggested the use of plant dry weight and leaf color as traits related to N_2-fixation parameters. Other traits such as plant height, 100-seed weight and pod yield are also useful.

Ability to give good hybrids or general and specific combining ability (GCA and SCA) effects for N_2-fixation and related traits has been studied by many authors (Isleib *et al.*, 1980; Nigam *et al.*, 1995). In a diallel study, Isleib *et al.* (1980) found that some cultivars in the Virginia botanical type peanuts, PI 275708 and NC Ac 1645, had good general combining ability for number of nodules, nodule weight, nitrogenase activity and total dry weight, whereas some Valencia botanical type peanuts were poor general combiners for these traits. Additive, non-additive and reciprocal genetic variances were important but additive genetic variance had a greater contribution to total genetic variance than non-additive and reciprocal genetic variances. Nigam *et al.* (1985) reported that NC Ac 2821 was a good general combiner for nodule number, nodule weight, plant dry weight, nitrogenase activity and total nitrogen content. Additive and non-additive gene effects were important for nitrogenase activity, total nitrogen, nodule weight, leaf area and plant dry weight but additive gene effects were larger than non-additive gene effects. For nodule number, non-additive gene effects were larger than additive gene effects.

The use of leguminous crops to improve soil fertility is increasingly important because of high population pressure and the intensive use of arable land. Although some species such as *Sesbania* spp. are often used as green manure, they are not well accepted by farmers because they need a long period for growing and also need stover incorporation into soils. Moreover, they do not provide direct economic return to the farmers. Peanut has advantage because it can be used as a dual purpose crop which provides both immediate cash after harvest and peanut residues as green manure for following crops. However, symbiotic nitrogen fixation in peanut is dependent on many factors including soil types, indigenous rhizobuim, peanut genotypes and interaction of these factors. Thus, screening and selection of peanut genotypes should be done in target areas. The objectives of this study were to evaluate general combining ability (GCA) and specific combining ability (SCA) effects, to investigate types of gene actions governing the inheritance of traits related to N_2-fixation and agronomic traits and to identify best genotypes as parents to be used in improving N_2-fixation and agronomic traits in peanut.

Materials and Methods

Plant Materials and Experimental Procedures

Three peanut lines, A3-1-1 (Bc 154) (PI 268 770), 42-G-105 (PI 269 109) and Virginia Bunch (PI 152 133), selected for plant dry weight, number of nodules and nodule weight from previous evaluation (Toomsan *et al.*, 1991), and two high yielding cultivars, KKU 1 and KKU 72-1, were crossed in a diallel fashion with reciprocals to generate 20 F_1 hybrids at the agronomy farm of Khon Kaen University in 1999. KKU 1 is a Spanish-type cultivar released in Thailand by Khon Kaen University and KKU 72-1 is a Virginia-type Cultivar released by Khon Kaen University.

For convenience, A3-1-1 (Bc 154) (PI 268 770), 42-G-105 (PI 269 109) and Virginia Bunch (PI 152 133) were hereafter designated as PI 268 770, PI 269 109 and PI 152 133, respectively. F_1 hybrids of 20 crosses were allowed to self-pollinate to produce sufficient F_2 seeds for evaluation.

F_2 seeds of 20 crosses and their 5 parent lines were evaluated under field conditions in a farmer's farm following rice in Kalasin province in Northeast, Thailand from January to May 2000. Twenty-five entries were assigned in a randomized complete block design with 4 replications. Filter cake (waste sugar mill) at the rate of 2 tons rai^{-1} (0.16 ha) was incorporated into the top layer of raised beds which were raised by a two-wheel tractor during soil preparation to reduce soil nitrogen availability. Seeds were planted on raised beds 5 m long and 0.8 m wide, which could accommodate 2 peanut rows with the spacing of 50 cm between rows and 20 cm between plants within each row. Plot size was 4-row plot, which was laid on 2 raised beds. Seeds were treated with ethephon 0.02% to break possible dormancy. Soil was inoculated soon after planting with mixed strains of cowpea-type rhizobium to ensure uniform nodulation of peanut plants. Soil inoculation was accomplished by spraying the inoculum (1:10 w/v of rhizobuim and water) on the raised beds.

Seeds were over-planted and then peanut plants were thinned to retain 1 plant per hill at 15 days after planting. Mechanical weeding was done at 20 days after planting. Chemical fertilizers at the rate of 0-9-6 kg rai^{-1} of N-P_2O_5-K_2O were applied soon after weeding. Gypsum ($CaSO_4$) at the rate of 50 kg rai^{-1} was applied at 40 days after planting (peak flowering). At the same time, granular carbofuran 3 % G at the rate of 5 kg rai^{-1} was used to prevent pod damage from subterranean ants (*Dorylus oreintallis* West). Furrow irrigation was supplied as needed. Harvesting time was determined by pod scrape technique as suggested by Williams and Drexler (1981).

Data Collection

Data were recorded based on individual plants in the plot for leaf color, plant dry weight, nodule dry weight, pod number per plant, pod weight per plant, seed weight per plant, seed number per plant, 100 seed weight, shelling percentage and harvest index. Leaf color score was observed at 50 days after planting by scoring 1 = pale yellow, 2 = yellow, 3 = light green, 4 = green and 5 = dark green on each plant in the plot. Other traits were recorded at harvest. At maturity, plants were dug by hoe for whole plants. Shoot, nodules and pods were taken from each plant and kept in separate paper bags. Nodules were oven-dried at 75ºC for 48 hours and weighed to obtain nodule dry weight. Shoots were oven-dried at 75ºC for 48 hours and weighed to obtain plant dry weight. Pods were air-dried to obtain approximately 8% moisture content, shelled and weighed. Then, pod number per plant, pod weight per plant, seed weight per plant, seed number per plant, 100 seed weight, shelling percentage and harvest index were determined.

Data Analysis

Data based on plant mean of parents and crosses were subjected to analysis of variance according to a randomized complete block design and Duncan's multiple range test (DMRT) was used to compare means (Gomez and Gomez, 1984).

Combining ability analysis was performed, according to Model I, Method III of Griffing (1956), e.g. one set of F_2's and reciprocals, excluding parents. Parental lines were deliberately chosen. Entries were considered to be fixed effect and replications were regarded as random effect, using the genetic model:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_{ij} + b_k + E_{ijkl} \qquad \text{[Eq. 1]}$$

where:

Y_{ijk} = the observation on (i x j)th genotype in kth block
μ = the population mean
g_i or g_j = the GCA effect for the ith or jth parents
s_{ij} = the SCA effect for the cross between ith and jth parents
r_{ij} = the reciprocal effect of the crosses between the ith and jth parents

b_k = the effect of k^{th} block
and E_{ijkl} = the error effect associated with the ijk^{th} observation.

Differences among crosses were partitioned into general combining ability (GCA), specific combining ability (SCA) and reciprocal mean squares. Standard error calculated from pooled error mean squares was used to test the significance of the genetic components. Diallel analysis of combining ability was conducted on the plant mean F_2 data. GCA and SCA effects of individual parents were calculated using the method of Singh and Chaudhary (1976) as follows:

$$g_i = \frac{1}{2n(n-2)}\left[n(Y_{i.} + Y_{.i}) - 2Y_{..}\right] \quad \text{[Eq. 2]}$$

$$S_{ij} = \frac{1}{2}(Y_{ij} + Y_{ji}) - \frac{1}{2n(n-2)}(Y_{i.} + Y_{.i} + Y_{j.} + Y_{.j}) + \frac{1}{(n-1)(n-2)}Y_{..} \quad \text{[Eq. 3]}$$

where:
Y_{ji} = the mean of genotype ji^{th}
Y_{ij} = the mean of genotype ij^{th}
$Y_{i.}$ = the sum of genotypes having female parent i^{th} in common
$Y_{.i}$ = the sum of genotypes having male parent i^{th} in common
$Y_{j.}$ = the sum of genotypes having female parent j^{th} in common
$Y_{.j}$ = the sum of genotypes having male parent j^{th} in common
$Y_{..}$ = the total of all genotypes
n = the number of parents involved

Estimation of standard errors was calculated as follows:
$SE(g_i) = [(n-1)\,\delta^2 e/2n\,(n-2)]^{1/2}$ [Eq. 4]
$SE(g_i - g_j) = [\delta^2 e/(n-2)]^{1/2}$ [Eq. 5]
$SE(s_{ij}) = [(n-3)\,\delta^2 e/(2n-2)]^{1/2}$ [Eq. 6]
$SE(sij - s_{ik}) = [(n-3)\,\delta^2 e/(n-2)]^{1/2}$ [Eq. 7]
$SE(s_{ij} - s_{kl}) = [(n-4)\,\delta^2 e/(n-2)]^{1/2}$ [Eq. 8]

where:
$\delta^2 e$ = the pooled error mean square.

Results and Discussion

The traits related to N_2-fixation, e.g. plant dry weight, nodule dry weight and leaf color score, and agronomic traits were evaluated in the F_2 diallel cross populations and their parents. Significant differences were found among parental lines in plant dry weight, leaf color score, pod dry weight, seed dry weight, 100-seed weight, shelling percentage and harvest index, but the differences for nodule weight, pod number per plant and seed number per plant were not significant (Table 1). Analysis of variance of crosses indicated that there were significant differences in most traits under the study except for pod number per plant and seed number per plant (data were not reported). The non-significant differences found for pod number per plant and seed number per plant may be caused by the lack of genetic variability in the tested materials. Although parent lines were not significantly different for nodule weight, significant differences were found in their cross progenies. Genes controlling this trait may disperse among parental lines then recombine to create a complementary effect and cause differences in their cross progenies because parent lines were deliberately selected, based on agronomic performance and their ability to fix nitrogen.

Variance due to difference among cross means was partitioned into general combining ability (GCA), specific combining ability (SCA) and reciprocal means of squares, which are attributable to additive gene action, non-additive gene action and cytoplasmic difference, respectively. GCA mean squares were highly significant for most traits except for pod weight per plant (Table 2), whereas SCA mean squares were significant only for pod weight per plant, seed weight per plant and 100-seed weight. Reciprocal mean squares were also significant for 100-seed weight, shelling percentage and harvest index. GCA mean squares were larger than SCA mean squares for

Table 1. Mean comparison of parental lines of peanut from a 5 x 5 diallel cross for traits related to N_2-fixation and agronomic traits[1/]

Parent	Plant Dry weight(g)	Nodule Dry weight(g)	Leaf color score[2/]	Pod weight /plant(g)	Seed weight /plant(g)	Pod number /plant	Seed number /plant	100 seed weight(g)	Shelling percentage	Harvest index
PI 268 770	24.19a	0.64	2.23a	15.33a	7.02a	7.48	16.79	39.35a	43.97b	0.14b
PI 269 109	20.72ab	0.48	2.24a	13.19ab	7.13a	9.66	17.10	38.28a	48.87b	0.17b
PI 152 133	7.31c	0.38	1.53b	5.85d	3.84b	7.72	15.20	25.69b	61.75a	0.29a
KKU 1	11.52bc	0.43	2.00ab	7.96cd	4.56b	9.99	17.58	31.68ab	54.28ab	0.19ab
KKU 72-1	23.01a	0.56	2.44a	10.02bc	5.79ab	7.55	17.09	36.97a	53.32ab	0.16b
F-test[3/]	**	ns	*	**	**	ns	ns	*	*	**
CV (%)	26	23	15	17	15	23	14	15	13	23

[1/]Means in the same column followed by a common letter are not significantly different ($p<0.05$) by DMRT

[2/] Score 1-5:1 = pale yellow, 5 = dark green

[3/]ns ,*, Not significant, significant at 0.05 and 0.01 probability levels, respectively**

Table 2. Mean squares for general combining ability (GCA), specific combining ability (SCA) and reciprocal effects of parental lines of peanut from a 5 x 5 dialell analysis for traits related to N_2-fixation and agronomic traits

Sources of variation	df	Plant dry weight	Nodule Dry weight	Leaf Color Score[1/]	Pod weight /plant	Seed weight /plant	100-seed weight	Shelling percentage	Harvest index
GCA	4	111.36**	0.016**	0.34**	5.94	0.74**	59.91**	81.56**	0.003**
SCA	5	8.95	0.004	0.02	20.44**	0.50*	11.97**	6.45	0.001
Reciprocal	10	4.67	0.004	0.02	2.53	0.18	7.99**	12.09**	0.001**
Error	57	12.94	0.003	0.01	1.91	0.20	5.44	4.52	0.001
GCA/SCA		12.4:1	4.0:1	24.1:1	0.3:1	1.5:1	5.0:1	12.6:1	3.0:1

***,** Significant at 0.05 and 0.01 probability levels, respectively**

[1/] Score 1-5 : 1 = pale yellow, 5 = dark green

most traits except for pod weight per plant in which GCA mean square was not significant. For seed weight per plant, GCA and SCA mean squares seemed to be equally important.

The results indicated that additive gene effects were important for all traits under study, whereas non-additive gene effects were important for pod weight per plant, seed weight per plant, and 100-seed weight. Cytoplasmic difference was present only in 100-seed weight, shelling percentage, and harvest index. Our results are in agreement with those of Islieb *et al.* (1980) and Nigam *et al.* (1985), who independently reported that additive gene effects were more important for nodule number, nodule weight, plant dry weight, nitrogenase activity and total nitrogen than non-additive gene effects. In contrast, Miller *et al.* (1986) found that non-additive gene effects were important for nodule weight, plant dry weight, seed yield and 100-seed weight, whereas additive and non-additive gene effects were equally important for seed weight per plant. Dwivedi *et al.* (1989) and Swe and Branch (1986) reported independently that pod weight per plant was conditioned by genes with non-additive effects, while Anderson *et al.* (1993) found that additive genes controlled pod weight and seed weight. The discrepancy of the results may be caused by differences in materials used and environments evaluated.

Considering gene effects involving the inheritance of the traits related to N_2-fixation, selection for plant dry weigh, nodule dry weight and leaf color score would be possible because the additive gene effect was more important for these traits, whereas non-additive gene effect was not significant. However, selection would be difficult for pod weight per plant, seed weight per plant and 100-seed weight because non-additive gene effects were predominant for these traits. For 100-seed weight, shelling percentage and harvest index in which reciprocal effects were important, reciprocal cross should be made to generate breeding materials in selection for those traits.

High positive GCA effects were more favorable for all traits under the study (Table 3). GCA effects for individual parents could identify the superior parents for plant dry weight (PI 268 770, PI 269 109 and KKU 72-1), nodule dry weight (KKU 72-1), leaf color score (PI 268 770, PI 269 109 and KKU 72-1), 100-seed weight (PI 268 770 and KKU 72-1), shelling percentage (PI 152 133) and harvest index (PI 152 133). GCA effects failed to identify the best parent for pod weight per plant. However, GCA effect of KKU 72-1 was much larger than the standard error for pod weight per plant. PI 268 770 was a good parent for plant dry weight, leaf color score and 100-seed weight but it was a poor parent for shelling percentage. PI 269 109 was the best parent for leaf color score but it was a poor parent for shelling percentage and harvest index. PI 152 133 was a poor parent for most traits but it was superior for shelling percentage and harvest index. KKU 1 did not perform well in hybrid combinations for all traits, and KKU 72-1 was the best parent for leaf color score and 100-seed weight. Significant positive correlation coefficients between *per se* performance of parents and their respective GCA effects were found for plant dry weight and shelling percentage, indicating that *per se* performance of parents can be used to predict performance of cross progeny and further confirms the importance of additive gene effect for these traits. The rest of the traits also had high correlation coefficients but not significant, possibly due to small number of samples (5 parents).

For the traits related to N_2-fixation, the best parent could be clearly identified for plant dry weight, nodule dry weight and leaf color score, A3-1-1 (Bc 154 (PI 268 770), 42-G-105 (PI 269 109), and KKU 72-1 are the best parents for these traits.

Likewise, high positive SCA effects were more desirable for all traits. SCA effects for individual hybrids could identify at least one specific hybrid for each trait. PI 268770 x KKU 72-1 and PI 269 109 x PI 268 770 were the good specific crosses for pod weight per plant (Table 4). PI 269 109 x PI 268 770 was also a good specific cross for seed weight per plant. PI 269 109 x KKU 72-1 and PI 152 133 x KKU 72-1 were the good specific crosses for 100-seed weight. PI 269 109 x PI 268 770 was a good specific cross for pod weight per plant and seed weight and also a specific cross for 100 seed weight. The good specific combinations were expected to give transgresive segregation in later generations. Our results were restricted to the experiment in one location and the traits related to nitrogen fixation were determined at harvest. The severe infestation of *Peanut bud necrosis virus* (PBNV) could also affect leaf color score assessment.

Conclusion

Inheritance of plant dry weight, nodule dry weight, leaf color score, seed weight per plant, pod number per plant, seed number per plant, 100-seed weight, shelling percentage and harvest index is mainly governed by additive gene action. However, non-additive gene effects and cytoplasmic difference are also importance for some traits, indicating that selection should be practised in later generation (not early generation of segregation) and the reciprocal cross is required to generate breeding population for selection. A3-1-1 (Bc 154) (PI 268 770), 42-G-105 (PI 269 109) and KKU 72-1 tended to be good general combiners for traits related to N_2-fixation, plant dry weight, nodule dry weight and leaf color score.

Table 3. General combining ability (GCA) effects of 5 parental lines of peanut for traits related to N_2-fixation and agronomic traits.

Parent	Plant dry weight	Nodule dry weight	Leaf color score[1/]	Pod weight /plant	Seed weight /plant	100-seed weight	Shelling percentage	Harvest index
PI 268 770	3.26	0.03	0.15	0.50	0.38	2.46	-2.33	-0.01
PI 269 109	2.92	0.03	0.19	0.49	0.08	1.93	-4.41	-0.03
PI 152 133	-6.42	-0.07	-0.25	-1.75	-0.57	-4.08	5.15	0.03
KKU 1	-2.66	-0.04	-0.27	0.16	-0.05	-2.75	1.73	0.01
KKU 72-1	2.90	0.05	0.18	0.60	0.16	2.44	-0.14	-0.01
Parent and GCA correlation	0.984	0.827	0.834	0.733	0.842	0.821	0.885	0.821
SE (g_i)	1.313	0.020	0.036	0.505	0.163	0.852	0.776	0.011
SE (g_i - g_j)	2.077	0.032	0.058	0.798	0.258	1.347	1.227	0.018

[1/] **Score 1-5: 1 = pale yellow, 5 = dark green**

Table 4. Specific combining ability (SCA) effects of 10 crosses of peanut for pod weight/plant, seed weight/plant and 100 seed weight.

Cross	Pod weight/plant	Seed weight/plant	100 seed weight
KKU 1 x PI 268 770	-0.93	-0.15	0.21
PI 268 770 x KKU 72-1	1.52	0.10	-1.99
PI 268 770 x KKU 72-1	-0.78	-0.23	1.82
PI 269 109 x KKU 1	-1.26	-0.44	0.68
PI 269 109 x PI 268 770	1.90	0.72	-3.08
PI 269 109 x KKU 72-1	-0.46	0.01	2.36
PI 152 133 x PI 269 109	-0.19	-0.29	0.04
PI 152 133 x KKU 1	0.66	0.50	1.10
PI 152 133 x PI 269 770	-0.20	-0.33	1.05
PI 152 133 x KKU 72-1	-0.46	0.01	2.36
SE (S_{ij})	0.691	0.224	1.166
SE (S_{ij} - S_{jk})	1.128	0.365	1.904
SE (S_{ij} - S_{kl})	0.798	0.258	1.347

Acknowledgements

This research was funded by the Senior Scholar Research Project of Professor Dr. Aran Patanothai under the Thailand Research Fund and also supported by Peanut Improvement Project, Department of Agronomy, Faculty of Agriculture, Khon Kaen University, Khon Kaen 40002, Thailand.

References

Anderson, W.F., Fitzner, M.S., Islieb, T.G., Wynne, J.C. and Phillips, T.D. 1993. Combining ability for large pod and seed traits in peanut. Peanut Sci. 20: 49-52.

Date, R.A. 1970. Microbiological problems in the inoculation and nodulation of legumes. Plant and Soil. 32: 703-725.

Dwivedi, S.L., Thendapani, K. and Nigam, S.N. 1989. Heterosis and combining ability studies and relationships among fruit and seed characters in peanut. Peanut Sci. 16: 14-20.

Elkan, G.H., Wynne, J.C., Schneeweis, T.J. and Islieb, T.G. 1980. Nodulation and nitrogenase activity of peanuts inoculated with single strain isolates of Rhizobium. Peanut Sci. 7: 95-97.

Gomez, K.A. and Gomez, A.A. 1984. Statistical procedures for agricultural research. 2nd ed. John Wiley and Sons, New York.

Griffing, B. 1956. Concepts of general and specific combining ability in relation to diallel crossing system. Aust. J. Biol. Sci. 9: 463-493.

Islieb, T.G., Wynne, J.C., Elkan, G.H. and Schneeweis, T.J. 1980. Quantitative genetics aspects of nitrogen fixation in peanut (*Arachis hypogaea* L.). Peanut Sci. 7: 101-105.

Kucey, R.M.N. and Toomsan, B. 1988. Peanut cultivar responses to *Bradyrhizobium* inoculation in Northeast Thailand. Peanut Sci. 15: 63-69.

Miller, Jr., J.C., Zary, K.W. and Fernandez, G.C.J. 1986. Inheritance of N_2 fixation efficiency in cowpea. Euphytica 35: 551-560.

Nambiar, P.T.C. and Dart, P.J. 1983. Factors influencing nitrogenase activity (acetylene reduction) by root nodules of groundnut, *Arachis hypogaea* L. Peanut Sci. 10: 26-29.

Nigam, S.N., Dwivedi, S.L., Nambiar, P.T.C., Gibbons, R.W. and Dart, P.J. 1985. Combining ability analysis of N_2-fixation and related traits in peanut. Peanut Sci. 12: 55-57.

Singh, R.K. and Choudhary, B.D. 1976. Biometrical techniques in genetics and breeding. International Biosience Publishers, Hissar, India.

Swe, S.T. and Branch, W.D. 1986. Estimates of combining ability and heterosis among peanut cultivars. Peanut Sci. 13: 70-74.

Toomsan, B., Limpinuntana, V., Homchan, J., Sripa, P., Paopuree, P., Srichantawong, M., Manikan, S., Saranun, S., Sanitchon, J., Theerapongthanathorn, S., McDonagh, J.F. and Giller, K.E. 1991. Measurement of nitrogen fixation in some groundnut lines using N-15 isotope dilution technique. Proc. 10th Thailand National Groundnut Research Meeting, Rayong, Thailand, Oct. 16-19, 1991. p. 311-316. (in Thai with English summary)

Toomsan, B., Limpinuntana, V., Homchan, J., Sripa, P., Paopuree, P., Manikan, S., Sanitchon, J., Srichantawong, M., Saranun, S., McDonagh, J.F. and Giller, K.E. 1992. Nitrogen fixation of groundnut and its residual benefits to succeeding cassava. Proc. 11st Thailand National Groundnut Research Meeting, Bangkok, Thailand, May 17-21, 1992. p. 465-475. (in Thai with English summary)

Williams, E. and Drexler, J.S. 1981. A nondestructive method for determining peanut pod maturity. Peanut Sci. 8: 134-141.

Wynne, J.C., Elkan, G,H., Meisner, C.M., Schneeweis, T.J. and Ligon, J.M. 1980. Greenhouse evaluation of *Rhizobium* for peanut. Agron. J. 72: 645-649.