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Heritability and Correlation for Components of Crop Partitioning in Advanced Generations of Peanut Crosses

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Abstract: The rapid accumulation and conversion of the dry matter into harvestable yield under limited crop duration are preferable for peanut (*Arachis hypogaea* L.) grown in various cropping systems where intensified cropping systems are generally practiced. In these cropping systems, peanut genotypes with acceptable yield and shorter crop duration are required. The objectives of this study were to estimate the broad sense heritability for Crop Growth Rate (CGR), Pod Growth Rate (PGR), Partitioning Efficiency (PC) and reproductive duration in an advanced generation of segregating population of large-seeded type peanut and to investigate the relationship among these characters. Two-hundred breeding lines in the F_6 generation of 10 peanut crosses (twenties for each cross) were assigned in a randomized complete block design with two replications. CGR, PGR, PC and RD were recorded at harvest. Heritability estimates for CGR (0.00-0.60) were lower than those for PGR (0.04-0.68), PC (0.00-0.82) and RD (0.17-0.90). Correlation coefficients among CGR, PGR and PC were positive and significant, whereas they were negatively and significantly correlated with RD. The results suggested that improvement of CGR, PGR, PC would be possible among studied materials and would result in lower reproductive duration and early maturity.

Key words: Peanut, crop duration, early maturity, intensified cropping systems

INTRODUCTION

Fitting legume species into crop rotations is highly recommended to reduce the need for an expensive chemical nitrogen fertilizer that adds up to the total cost of crop production (Yusuf *et al.*, 2009; Umrit *et al.*, 2009). The benefits of legume green manures or legume crops to improve soils and provide sufficient nutrients to succeeding crops have been well recognized (Farthofer *et al.*, 2004; Balkcom and Reeves, 2005; Umrit *et al.*, 2009; Becker and Johnson, 1999), knowing that every year the land is becoming more productive than it was before. However, adoption of legume green manures in cropping systems has been low for many reasons, depending on the context of the specific cropping systems and socio-economic factors (Becker *et al.*, 1995). High labor demand, especially, for establishment and timely incorporation of the manure and lack of legume seed, in addition to, technical support were the most important constraints (Odendo *et al.*, 2000; Unscher *et al.*, 2004).

Intensification of crop production needs shorter growing periods of legume crops and they are substituted by early mature high yielding grain legumes (Becker *et al.*, 1995; Kerr *et al.*, 2007). Intensification and diversification of the crops can bring diverse profits, effective resource use and marketing opportunities. Although many green manure legumes meet this criterion, they still needs the application of phosphorus fertilizer and do not provide immediate cash for farmers (Kamanga *et al.*, 2010). For growing large-seeded type peanut (*Arachis hypogaea* L.) in crop rotations, farmers still need earlier maturing varieties to fit into their cropping systems such as cereal-based rainfed systems when peanut is grown after main crops and rice-based systems when peanut is grown during follow period with or without irrigation before rainy season (Sukharomana and Dobkuntod, 2003).

Earliness of maturity is important for peanut adaptation to a wide range of cropping systems in semi-arid tropics. An early maturing variety may escape damage from drought or flooding and it is advantageous in multiple cropping systems to permit early removal of crop so that the following crop may be planted (Sleper and Poehlman, 2006). For large-seeded peanut of Virginia type, its maturity (more than 125 days) is much longer than small-seeded peanut of Valencia and Spanish types (100-110 days). In Thailand, the market potential of this peanut type is great if farmer can reduce peanut crop duration in the field.

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Early maturity is also disadvantageous. Plant size and yield may be reduced greatly in extremely early cultivars because the plant had shorter growing period to develop, manufacture and store nutrient materials (Sleper and Poehlman, 2006). The reduced crop duration without yield penalty is the most challenge of peanut breeders for earliness in case that the earliness is not extreme.

Crops need duration of growth and good partitioning of assimilates to economic yield obtain high yield. In case of limited crop duration, yield depends largely on partitioning of assimilates, including partitioning between reproductive and vegetative structures, the period to pod filling and the rate of pod establishment (Duncan *et al.*, 1978). In the initial growth period, the Cop Growth Rate (CGR) was dependent on the leaf area index (LAI); in the late growth period the CGR was dependent on the Net Assimilation Rate (NAR) and the Pod Growth Rate (PGR) depended on the NAR (Aboagye *et al.*, 1994). Seed number was positively related ($p<0.01$) to CGR ($R^2 = 0.66$) and to PGR ($R^2 = 0.72$) during the R3-R6.5 phase (seed number determination window), while crop growth during the grain-filling phase (i.e., between R6.5 and final harvest) was positively associated with grain number ($R^2 = 0.80$, $p<0.001$) (Haro *et al.*, 2007). They also found that seed number is generally associated with seed yield rather than weight of individual seeds.

The previous results indicated that PGR and CGR are heritable and can be used as selection criteria for yield improvement. Furthermore, a better understanding on the genetic linkages among these characters can help peanut breeders to formulate appropriate breeding strategies to achieve breeding objectives. However, limited information is available on the heritability of these traits. Ntare and Williams, (1998) found in peanut that heritability for crop growth rate, partitioning and reproductive duration was not as high as for yield.

In this study, we report heritability in broad sense and genotypic correlation of the CGR, PGR, partitioning coefficient and reproductive duration which would be used as selection criteria for pod yield of peanut genotypes with reduced growth period.

MATERIALS AND METHODS

The parents were preliminarily tested for maturity in the field during November 2005 to April 2006 and the experiment was conducted at the Agronomy Farm, Khon Kaen University during June 2006 to September 2006 with full irrigation. Two hundred breeding lines in the F_6 generation of ten peanut crosses of five commercial cultivars in Thailand and three introduced lines were arranged in a randomized complete block designed with two replications. Each cross had 20 progenies and they were selected randomly. Both Taiwan 1 and Tainan 9 varieties were developed in Taiwan, while, KKU 1, KK 4, KK 5 and KK 60-1 are locally developed varieties in Thailand and the list of parental lines is presented in Table 1.

Ethephon at the concentration of 0.02% was applied to the seeds to break possible seed dormancy to ascertain the uniform germination of the seeds. This practice was done because some of parental lines are Virginia type peanut that has seed dormancy. A fungicide chemical (captan) was also applied to the seeds at the rate of 5 g kg^{-1} seeds to prevent seedlings from *Aspergillus niger* damage. Seeds were sowed on two-row plots with 5 m in length and a spacing of 20 and 50 cm between plants and rows, respectively. Then, seedlings were thinned to one plant per hill after 17 days from sowing. A pre-emergence herbicide (alachlor) at the rate of 3,125 mL ha^{-1} was applied after sowing and mechanical weeding was also practiced two times at 15-20 days and 30 days after sowing. Chemical fertilizers of 12-24-12 of N P_2O_5 K_2O at the rate of 150 kg ha^{-1} was applied after the first mechanical weeding and gypsum ($CaSO_4$) at the rate of 312.5 kg ha^{-1} was applied after the second mechanical weeding and cabofuran 3%G was also applied at the same time to prevent pod damage from subterranean ants (*Dorylus orientalis* Westwood). Leaf diseases and insect pests were adequately controlled during crop growth for optimum yield performance. Mini-sprinkler irrigation was applied weekly from sowing to harvest.

Days to flowering were recorded for all entries as number of days in which 50% of plants in the plots had blooming flowers. At harvest, days to harvest maturity pods were recorded and dry pods and whole plant were weighted. In addition to, Crop Growth Rate (CGR) was determined as a ratio between whole plant weight and days from sowing to harvest as follows: CGR (g/plant/day) = total dry weight/maturity. In the same manner, pod growth rate (PGR) was determined as follows: PGR (g/plant/day) = pod dry weight/days from flowering

Table 1: List of parental lines used in this study

Parental line	Characteristics	Origin
Luhua 11	Large-seeded type peanut with erect stature and medium maturity (215 days)	China
Luhua 9	Large-seeded type peanut with erect stature and medium maturity (125 days)	China
Taiwan 1	Spanish peanut with medium seed size and pink pericarp	Taiwan
KK 60-1	Spanish peanut with maturity of 95-105 days	Thailand
Tainan 9	Spanish peanut widely grown in Thailand with small seed size	Thailand
KK 4	Valencia peanut with maturity of 95-100 days	Thailand
KK 5	Spanish peanut with medium seed size	Thailand
KKU 1	Spanish peanut with medium seed size and maturity of 95-100 days	Thailand

to harvest. Partitioning Coefficient (PC) was determined as the ratio of PGR/CGR. The PCS exceeding 1.0 indicate that pod growth rates were higher than crop growth rates. Furthermore, Reproductive Duration (RD), which means days to pod filling, was calculated as the difference between days to flowering and days to harvest.

Analysis of Variance (ANOVA) was conducted for each cross to determine the effects of lines and heritability was calculated as a ratio of variances, by expressing the proportion of the phenotypic variance that can be attributed to variance of genotypic values using (Visscher *et al*., 2008) formula as follows:

$$H^2 = \sigma_G^2 / \sigma_P^2$$

where: H^2 is broad-sense heritability; σ_G^2 is genotypic variance and σ_P^2 is phenotypic variance.

Standard deviation for mean of each cross (n = 40) was also calculated to determine a range of variation in a cross.

Phenotypic and genotypic correlation coefficients between four traits were determined according to Kown and Torrie (1964) as follows:

$$r_g = Cov_{gij} / (\sigma^2_{gi} \times \sigma^2_{gj})^{½}, \; r_p = M_{ij}/(M_{ii} \times M_{jj})^{½}$$

where, rg and rp are genotypic and phenotypic correlation coefficients, Cov_{gij} and b^2_{gi} are the estimates of covariance and variance, respectively, for traits i and j. M_{ij} is the mean product for genotypes and M_{ii} and M_{jj} are genotypes means squares for trait i and j, respectively.

RESULTS

Means of the extremely high cross (Luhua 11×Tainan 9; 8.3 g/m^2/day) and extremely low cross (Taiwan 1×Tainan 9) (5.8 g m^2/day) were statistically different for crop growth rate (CGR) and the others were in a range of standard errors, indicating similar performance for this trait (Table 2). The crosses were similar for Pod Growth Rate (PGR) and ranged from 1.4 g m^2 day in the cross Taiwan 1×KKU 1 to 3.0 g m^2/day in the cross Luhua 11×Tainan 9, but they were significantly different for Partitioning Coefficient (PC) and ranged from 0.2 in the cross Taiwan 1×KKU 1to 0.4 in the crosses Luhua 11×Tainan 9 and Taiwan 1 x KK 60-1. Differences among crosses were also observed for Reproductive Duration (RD), especially, for the crosses with extreme values. Reproductive duration ranged between 88.9 days in the cross Luhua 11×KK 60-1 to 99.7 days in the cross Taiwan 1×Tainan 9. The crosses with KK 60-1 as male parent had low reproductive duration.

Table 2: Means and standard errors for Crop Growth Rate (CGR), Pod Growth Rate (PGR), Partitioning Coefficient (PC) and Reproductive Duration (RD) of 10 peanut crosses in the F_6 generation

Cross	CGR (g/m^2/day)	PGR	PC (g/m^2/day)	RD (days)
Luhua 11×Tainan 9	8.3±1.2	3.0±1.0	0.4±0.1	94.7±5.24
Luhua 9×Tainan 9	7.0±1.3	2.0±0.9	0.3±0.1	95.9±6.15
Taiwan 1×KKU 1	6.4±0.8	1.4±0.6	0.2±0.1	92.8±5.64
Luhua 9×KK 4	7.1±1.5	2.5±1.0	0.3±0.1	96.6±4.63
Luhua 11×KK 60-1	7.6±1.0	2.6±0.5	0.3±0.1	88.9±1.71
Luhua 9×KKU 1	7.3±1.3	2.5±0.9	0.3±0.1	97.2±4.42
Luhua 9×KK 5	8.2±1.7	2.7±0.9	0.3±0.1	92.7±4.91
Taiwan 1×Tainan 9	5.8±0.8	1.5±0.6	0.2±0.1	99.7±3.80
Taiwan 1×KK 4	7.9±1.3	2.5±1.1	0.3±0.1	91.7±6.17
Taiwan 1×KK 60-1	7.4±2.0	2.7±1.3	0.4±0.1	89.5±1.96

The cross Luhua 11×Tainan 9 has the highest CGR, PGR and PC. Other crosses having Luhua 11 and Luhua 9 as female parent also performed well for one or more of these traits. For example, Luhua 9×KK 4 had intermediate CGR, PGR and PC and Luhua 9×KK 5 had high CGR and intermediate PGR and PC.

Similarly, the crosses with Taiwan 1 as female parent also performed well for studied traits. For example, Taiwan 1×KK 4 had high CGR, but it had intermediate PGR and PC. Taiwan 1×KK 60-1 had intermediate CGR, but it had high PGR and PC.

Heritability estimates in broad sense for CGR were not high and ranged from 0.00 to 0.60 (Table 3). The highest heritability estimates for CGR was obtained from Luhua 9×KK 4 (0.60), whereas the crosses having intermediate heritability estimates for CGR were Luhua 9×Tainan 9 and Taiwan 1×KK 60-1 (0.45), Luhua 11×KK 60-1 (0.46), Taiwan 1×KK 4 (0.47) and Luhua 9×KK 5 (0.48).

Heritability estimates for PGR were low to high and ranged from 0.04 to 0.72. The high heritability estimates were found in the crosses Luhua 11×tainan 9 (0.68), Luhua 9×KK 4 (0.71), Taiwan 1×KK 4 (0.72) and Taiwan 1×KK 60-1 (0.63).

Heritability estimates for PC were low to high, ranging from 0.00 to 0.82. So, the crosses with high heritability estimates for PC were Luhua 11×Tainan 9 (0.81), Luhua 9×KK 4 (0.82), Luhua 9×KKU 1 (0.73) and Taiwan 1×KK 60-1 (0.68).

Heritability estimates for reproductive duration were generally moderate to high except for low heritability estimates in the crosses Luhua 11×KK 60-1 (0.34) and Taiwan 1×KK 60-1 (0.17).

The highest correlation coefficients were observed for PGR and PC (0.84** for phenotypic and 1.00** for genotypic) (** indicates significant at 0.01 probability level) (Table 4). The relationship between PGR and CGR was positive and high (0.69** for phenotypic and 1.00** for genotypic). However, the relationship between PC and CGR though significant was positive but rather low (0.23** for phenotypic and 0.26** for genotypic).

Table 3: Heritability estimates in broad sense for Crop Growth Rate (CGR), Pod Growth Rate (PGR), Partitioning Coefficient (PC) and reproductive duration (RD) of 10 peanut crosses in the F_6 generation

Cross	CGR	PGR	PC	RD
Luhua 11×Tainan 9	0.00	0.68	0.81	0.83
Luhua 9×Tainan 9	0.45	0.17	0.00	0.82
Taiwan 1×KKU 1	0.00	0.41	0.60	0.59
Luhua 9×KK 4	0.60	0.71	0.82	0.69
Luhua 11×KK 60-1	0.46	0.30	0.60	0.34
Luhua 9×KKU 1	0.31	0.52	0.73	0.80
Luhua 9×KK 5	0.48	0.20	0.47	0.77
Taiwan 1×Tainan 9	0.28	0.04	0.14	0.73
Taiwan 1×KK 4	0.47	0.72	0.62	0.90
Taiwan 1×KK 60-1	0.45	0.63	0.68	0.17

Table 4: Phenotypic and genotypic correlations (r_P and r_G) among Crop Growth Rate (CGR), Pod Growth Rate (PGR), Partitioning Coefficient (PC) and Days to Pod Filling (DPF) of 10 peanut crosses in the F_6 generation

	CGR		PGR		PC	
	r_P	r_G	r_P	r_G	r_P	r_G
PGR	0.69**	1.00**				
PC	0.23**	0.26**	0.84**	1.00**		
RD	-0.34**	-0.45**	-0.37**	-0.44**	-0.26**	0.30**

** Significant at 0.01 probability level

Significant and converse relationships between reproductive duration with crop growth rate, pod growth rate and partitioning coefficient, but the relationships were rather weak with low correlation coefficients ranging from -0.26** to -0.37** for phenotypic correlations and -0.30** to -0.45** for genotypic correlations.

DISCUSSION

Longer growth period generally results in higher productivity of peanut when other factors are optimum for plant growth and yield (Canavar and Kaynak, 2010; Naab *et al.,* 2005). However, under intensified cropping systems, the crops have less time to grow to maturity and the early mature varieties are required. In rice-based cropping systems in Thailand, for example, there is a follow period during January to April. This includes the required time for soil preparation and peanut to grow. The suitable peanut varieties under this condition should be mature earlier than 120 days to avoid flooding by early season rain or the shortage of irrigated water in the late growing season. The early mature varieties should provide an earlier harvest date without significant yield loss. Reduction of yield penalty associated with early maturity is a challenge to peanut breeders.

Obtaining high yield in early mature varieties is possible if the earliness is not extreme. In peanut, earliness and general adaptation of the varieties did not impair the expression of significant genetic variation for some traits relative to flowering, productivity and physiology (Clavel *et al.,* 2004). In cotton, earliness strategies (combinations of factors associated with earliness including early varieties) had higher yields and earlier maturity than standard practice at cooler locations, but at warmer locations, earliness strategies gained little earliness and had lower yields than standard practice (Roberts and Constable, 2001).

Three physiological processes including partitioning of the assimilate between the reproductive and vegetative structures, the length of the pod filling period and the rate of the pod establishment best explain the variation in peanut yield (Duncan *et al.,* 1978; Williams, 2000). The heritability estimates for Crop Growth Rate (CGR), Pod Growth Rate (PGR), Partitioning Coefficient (PC) and Reproductive Duration (RD) were therefore investigated in a segregating population of peanut to understand if there is useful genetic variation for these traits and these traits could be used as selection criteria for yield in early mature peanut genotypes.

The crosses were rather similar for pod growth rate and selection for high pod growth rate in these peanut crosses would not be effective. However, selection among cross would be possible for high crop growth rate, high partitioning coefficient and low reproductive duration because there were significant differences among crosses. Exploitation of variances among crosses and selection of superior genotypes using variances within crosses would be a possible strategy in this peanut population.

Genetic variances within crosses as indicated by heritability estimates were rather low for crop growth rate in the crosses with high means, indicating uniformity within crosses. Ntare (1999) found low regression coefficients for CGR in the $F_{2:F3}$ (0.10±0.08) and $F_{3:F4}$ (0.12±0:23) generations. Therefore, progress in selection would be limited for this trait.

The cross Luhua 11×Tainan 9 was interesting as it had the highest mean for CGR and high heritability estimates for PGR, PC and RD. In addition to Luhua 11×Tainan 9, Luhua 11×KK 60-1 was an interesting cross as it had the lowest mean for RD and rather high heritability estimates for PGR, PC. Luhua 9×KKU 1 was another interesting cross because of rather high mean for CGR and intermediate to high heritability estimates for PGR, PC and RD.

Regression coefficients for the partitioning were 0.45±0.17 in the $F_{2:F3}$ generation and 0:46±0.17 in the $F_{3:F4}$ generation (Ntare, 1999). The author also reported regression coefficients for reproductive duration of 0.10±0.03 in the $F_{2:F3}$ generation. Moderate to high heritability estimates for maturity were also reported in okra (*Abelmoschus esculentus* L.) and this trait is related to reproductive duration (Adeniji, 2007). In cowpea

(*Vigna unguiculata*), the estimates of broad sense heritability was 94% for duration of reproductive phase (Omoigui *et al.,* 2006), but it has not been reported in peanut.

Compared to previous studies in early segregating generation, the heritability estimates in this study, though they are in broad sense, are more useful for effective selection because they are estimated in nearly-inbred generation.

Both Luhua 9 and Luhua 11 are local peanut varieties in China with phenotypic similarity (Zhang *et al.,* 2009). Luhua 11 also had high general combining ability for pod yield, seed size, but its combining ability for maturity was negative (Kesmala *et al.,* 2003). However, it is susceptible to peanut bud necrosis virus (Kesmala *et al.*, 2003; Puttha *et al.,* 2008).

The cross Taiwan 1×KK 60-1 was, also, interesting as it had high mean for PC, low mean for RD, although, its heritability estimates for CGR (0.45), PGR (0.63), PC (0.68) and RD (0.17) were low to moderate (Table 3).

Pod growth rate was closely related to crop growth rate. However, partitioning coefficient was rather dependent on pod growth rate than crop growth rate, but, reproductive duration was negatively correlated with CGR, PGR and PC as shown in Table 4 Direct selection for long seed-filling periods may increase yield and, conversely, selection for higher yield in many crops resulted in longer seed-filling periods (Egli, 2004). In soybean, late maturity genotypes had higher yield than early ones (Liu *et al.,* 2005). In peanut that recovered from drought, Puangbut *et al.* (2009) found that high biomass production high leaf area and high leaf chlorophyll concentration were associated with high pod yield. Egli (1981) also found the variation in the length of the Effective Filling Period (EFP) among cultivars within a species of 13 grain crops. The negative correlations between reproductive duration and traits associated with pod yield (CGR, PGR and PC) in this study are contrasted to those found in grain crops. However, Chishti *et al.* (2000) reported very high heritability estimates for days to flowering and maturity in peanut. Additive genes could account for high heritability estimates (Adeniji, 2007).

The difference in the results might be due to the difference in phonology of the crops and the difference in germplasm used. Higher yield in early maturing genotypes in this study could be due to more synchronous pod formation in early maturing genotypes than in late genotypes. Selection of genotypes with synchronous pods and narrow pod distribution from the main stems is a strategy to obtain early maturity and high yield in peanut with indeterminate growth habit (Kotzamanidis *et al*., 2006). Synchrony in pod maturity is associated with early maturity in mungbean (Tah and Saxena, 2009).

Because of similarity in days to flowering, the rapid decrease in generative stages is an important character for early maturity in this peanut population. In soybean, the correlation between the yield with days to maturity was not important but with days to flowering it was significant (Machikowa and Laosuwan, 2009). The differences in characters determining maturity and yield in the two crop species could be due to difference in phonology of the crops.

CONCLUSION

Improvement of large-seeded Virginia type peanut for shorter maturity to fit into cropping systems in the tropics is necessary as its crop duration is much longer than Spanish and Valencia peanut types. It might be possible to maintain high yield potential under reduced crop duration if the crop duration is not extremely short. This might be achieved by selecting peanut genotypes with high crop growth rate, high pod growth rate, high partitioning efficiency and short reproductive duration as days to first flowering in peanut is very similar among peanut genotypes with differences in maturity.

By using variances among crosses, selection for individual characters would be possible with different degrees of expected success because the variations in CGR, PGR, PC and RD were different among crosses.

By using variances with in crosses, selection for individual characters would be possible in the crosses with high heritability estimates. High success would be expected for PC and RD because many crosses showed high heritability for these characters. However, limited success would be expected for CGR and PGR because the heritability estimates were rather low.

Simultaneous selection would be also possible for all characters as CGR, PGR and PC were positively associated, but they were negatively associated with RD. Selection for high CGR, PGR and PC would result in shorter RD and shorter crop duration. Therefore, improvement of large - seeded Virginia peanut type for early maturity will not be detrimental to yield potential.

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