Final Report

รายงานวิจัยฉบับสมบูรณ์

Basic Research for Supporting Peanut Production Project – Phase II

โครงการวิจัยพื้นฐานเพื่อสนับสนุนการผลิตถั่วลิสง – ระยะที่ 2

By

Professor Dr. Aran Patanothai

Supported by the Thailand Research Fund

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สัญญาเลขที่ **RTA/47/80001**

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Project Leader

Professor Dr. Aran Patanothai

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Supported by the Thailand Research Fund

(The opinions expressed in this report are of the researchers and are not necessary agreed by the Thailand Research Fund)

Acknowledgment

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Contents

Project Code: RTA/47/8001

Project Title : Basic Research for Supporting Peanut Production – Phase II

ชื่อโครงการ : การวิจัยพื้นฐานเพื่อสนับสนุนการผลิตถั่วลิสง – ระยะที่ 2

Executive Summary

Project leader:

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Type of funding support: Senior Research Scholar

Research area: Agriculture

Duration: 1 April 2004 – 30 September 2007

Research team:

Researcher – 10
Research assistants - 3
Ph.D. students – 11
M.S. students – 8

Overall objectives:

1. To generate basic knowledge for the development of technologies that will improve production efficiency and quality of peanut and peanut products.
2. To generate published papers in accredited international journals.
3. To improve the capability of researchers and train new researchers to produce high quality research.
4. To strengthen collaboration in peanut research between KKU and other institutes both within the country and overseas.

Expected outputs:

The project aimed to produce the following outputs:

1. Published 15 papers in accredited journals.
2. Capacity building of 11 researchers.
3. Produce 19 M.S. and Ph.D. graduates.
4. Organize annual technical meeting once a year.
5. Linkage with 5 oversea institutes.

Highlights of research:

Peanut is an important food legume and oil crop of Thailand. It is an important source of supplementary income to small farmers in all parts of the country and a source of protein for Thai people. The crop also plays an important role in soil improvement through its nitrogen fixing ability. Current demand for peanut is high, particularly for processed products for both internal and export markets. However, planted area of peanut is declining due to low productivity and high labor demand. In the future, Thai peanut and peanut products country will face a strong market competition. However, it is an opportunity to increase the export of peanut products, particularly with the large-seeded type, if their quality is improved to the international standard and production cost is reduced to a competitive level. Improvement of product quality and production efficiency is, thus, essential for peanut production in Thailand. These require a strong support in research.

Phase I of this project has undertaken basic research in three selected topics, i.e., peanut bud necrosis which is a new peanut disease in Thailand, the utilization of peanut residues for soil improvement, and the use of a crop simulation model, CROPGRO-Peanut, in assisting peanut variety evaluation. In this phase (Phase II), research on the utilization of crop residues was expanded to cover the entire cropping systems. The use of crop simulation model was also expanded to include studies on genotype x environment interactions and identification of desirable physiological traits for peanut genotypes. The project has also embarked upon a new area of research on drought resistance in a holistic approach both to support breeding for drought resistance/tolerance and to provide a means for reducing the problem of aflatoxin contamination in which direct breeding for its resistance has not yet been successful.

Research in Phase II was organized into four sub-projects:

Sub-project 1. Basic research to support breeding for resistance to peanut bud necrosis and thrips.

Sub-project 2. Basic research to support breeding for drought and aflatoxin resistance.

Sub-project 3. Utilization of peanut stover and other crop residues to improve crop productivity.

Sub-project 4. Application of crop simulation model in crop breeding and production.

Highlights of results for the individual subprojects are as follows:

Sub-project 1: Basic research to support breeding for resistance to peanut bud necrosis and thrips

1.1 Low temperature or relative humidity did not affect the transmissibility of *Peanut bud necrosis virus* (PBNV) by mechanical inoculation. The difference in disease incidences in the rainy and the dry seasons in Thailand could not be explained by the difference in climatic conditions but could possibly be accounted for by the difference in vector infestation.

1.2 Additive gene effects accounted for a major proportion of genetic control for PBNV resistance, and the three resistant parents (IC 10, IC 34 and ICGV 86388) could be used as sources of PBNV resistance.

1.3 Broad-sense heritability for peanut bud necrosis incidence and severity varied in different crosses, being high in the resistant x susceptible crosses. The two parameters were well associated, and both could be used to evaluate PBNV resistance in peanut.

1.4 Generation means analysis in three peanut crosses indicated additive gene effects in all the crosses. However, only additive gene effect was detected for the resistant x resistant cross, but non-additive gene effects were also observed for the resistant x susceptible crosses. Thus, select for PBNV resistance in these crosses would be possible.

1.5 Percentage of damaged plants and leaves by thrips showed higher heritability than those for thrips number parameters. Correlations between agronomic traits and thrips resistance parameters (thrips number and thrips damage) were rather low. Plant damage parameters would be the traits to select for the improvement of peanut for thrips resistance.

1.6 Investigation on the type of gene action for thrips number and for percentage of damaged plants and leaves in three peanut crosses revealed additive gene effect only for total thrips number in the cross IC 10 x Khon Kaen 60-1. Thus, improvement for thrips resistance would be possible only in the cross.

Sub-project 2: Basic research to support breeding for drought and aflatoxin resistance

2.1 The CSM-CROPGRO-Peanut model performed reasonably well in simulating pod yield and total biomass at harvest maturity and the relative yield reduction from drought stress of individual peanut cultivars. The model, thus, could be used to simulate the relative responses to different levels of moisture regime of peanut genotypes. The model also could provide information on the severity, duration, and growth stages at which drought stress occurred in different years for a particular location for which characterization of the drought stress pattern of the location could be derived.

2.2.1 The ability of genotypes to have higher N_2 fixed under mild drought stress was due largely to their high N_2 fixation under well-watered conditions and partly due to their ability to maintain high N_2 fixation under mild water stress, whereas the ability of genotypes to have higher N_2 fixation under severe drought stress was dependent primarily on their ability to maintain high N_2 fixation. There was a high correlation between N_2 fixed and biomass production under drought stress condition indicating that peanut genotypes with higher nitrogen fixation under water stress had higher biomass production than the genotypes with lower nitrogen fixation.

2.2.2 Drought stress increased % root length density by 10% and 19% at 2/3 AW and 1/3 AW, respectively. Growing roots deeper into the soil in response to drought stress occurred in a few peanut genotypes under mild drought stress, but was observed in more genotypes under severe drought stress. Deeper roots, however, did not contribute to biomass production or the ability to maintain high biomass

production under drought stress, but did contribute to pod yield and harvest index under drought stress conditions.

2.2.3 Chlorophyll density and chlorophyll content were found to be stable across environments. Strong positive correlations were shown between total dry matter and chlorophyll content, and between chlorophyll density and chlorophyll meter readings (SCMR). Chlorophyll density and SCMR were significantly correlated with transpiration efficiency (TE), suggesting that they could be used for indirect selection for drought resistance in peanut.

2.3 Under drought stress conditions, specific leaf area (SLA), SCMR, reduction in pod yield, reduction in total dry weight and N_2 fixed showed relatively high heritability estimates, but nodule dry weight, reduction in N_2 fixed and *A.flavus* infection had low to moderate heritability. Thus, improvement of these traits is possible in the studied peanut populations. The weak relationships among these traits suggested that their improvement could be done simulteneously.

2.4 An investigation on the inheritance of SLA and harvest index (HI) in three peanut crosses showed that gene effects governing the inheritance of both SLA and HI were largely additive, indicating that selection for high SLA and HI values in these crosses would be effective even in early generations.

2.5 At least six homologous proteins that could be putative proteins regulated by water deficit in peanut leaves were identified. The five proteins; 133, 190, 260, 277 and 33, were protein homologs in *Arabidopsis thaliana* (*At*) and only one protein, 357, was protein homolog in *Zinnia elegans* (*Ze*). The homologous protein 190 was identified as serine/threonin-protein phosphatase PP 1 isozyme. The remaining homologous proteins were identified as chaperone protein DnaJ (133), peroxidase 43 precusor (260), SNF1-related protein kinase regulatory subunit beta-2 (277), auxin-responsive protein IAA29 (331) and caffeoyl-CoA O-methyltransferase (357).

2.6 Evaluation of four peanut genotypes for SLW, RWC and DNA polymorphism identified 12 primers that showed polymorphism: Dimer001, Dimer013, Dimer017, Dimer018, SSR017, Trimer050, Trimer046, Trimer053, Trimer030, SSR022, SSR024 and PPSSR03. These are being used in identifying DNA markers associated with SLW and RWC under drought stress in peanut.

Sub-project 3: Utilization of peanut stover and other crop residues to improve crop productivity

3.1 For growing peanut and other legumes in rotation with sugarcane under the dry period planting system of sugarcane:

3.1.1 Hairy indigo, jack bean and peanut were the crops that gave the higher amount of N in the residues than other legumes. However, the residues of all the legumes decomposted fast, but being slowest for the pigeonpea residues. After 358 days, 24 % of pigeonpea residue still remained, but the remaining residues of other legumes were only 7-10 %. Incorporation of legume residues into the soil gave sugarcane yield as high as the application of a full rate of chemical fertilizers.

3.1.2 Peanut residues had better quality with high N and low lignin and polyphenol, while pigeon pea residues had poorer quality with low N and high lignin, and hairy indigo residue quality were intermediate of N and lignin but high in poly

phenol. As a consequent, peanut residues decomposed fastest and showed the largest N release, followed by hairy indigo residues and pigeonpea residues.

3.1.3 Application of peanut residues at the rate of 12.50 Mg ha^{-1} gave significantly higher sugarcane yield than those of other treatments including the treatment with chemical N fertilizer. The highest levels of N, K and Mg in the sugarcane plant were also obtained with added peanut residues. However, CO_2 emission was significantly higher with the application of legume residues than with mineral N fertilizer.

3.2 For sugarcane stover management in the legumes-sugarcane cropping system:

3.2.1 Incorporation of sugarcane stover to the soil increased soil microbial biomass N. However, upon ploughing at 96 days after planting, the different sugarcane stover managements had no significant effect on net mineral N content and microbial biomass N during the subsequent legume period.

3.2.2 Although a change from burning to sugarcane stover retention led to alterations in N cycling and improved soil organic matter, it did not significantly affect N_2 fixation of the legumes due to the uniforming action of ploughing and the extended time gap between sugarcane stover incorporation and legume planting.

3.2.3 N from legume residue was available and enough to get good sugarcane growth until 6 months after planting, but thereafter it was not enough for the need of sugarcane until final harvest.

3.3 For peanut residues and rice straw management in the peanut-rice cropping system:

3.3.1 It is possible to regulate N dynamics by mixing rice straw with peanut residues leading to a delayed mineral N release and potentially reduced leaching and N_2O losses during the pre-rice phase, but with a trade-off of increased CH_4 emissions.

3.3.2 Mixing peanut residues and rice straw could delay N release during the pre-rice lag period leading to an improved synchrony in N demand/supply, and consequently increasing growth and yield of the succeeding rice.

3.4 For the soybean-rice cropping system, application of soybean stover gave higher growth and yield of KDML 105 rice than the control treatment. The recommended rate is 1,875 kg ha^{-1} of soybean stover along with NPK fertilizers at 25, 25 and 12.5 kg ha^{-1} of N, P_2O_5 and K_2O, respectively. Groundnut stover decomposed faster than soybean stover; however, the patterns of NPK and Ca released from the two stovers were similar.

3.5 For peanut stover management in the peanut-maize rotation system:

3.5.1 Although initial stover removal of peanut at harvest and reapplication before the following maize crop gave the highest maize yield, it is difficult for farmers to implement. Early incorporation of peanut residue, though, resulted in a more efficient recycling of N, only small increases in economic yield over the surface application was obtained. Therefore, in practice the preferred method for smallholder farmers will remain surface application of peanut stover as there is no economic value attached to the reduced N losses when the stover is incorporated.

3.5.2 Weeds grown during the dry season and incorporated during seed bed preparations suppressed maize yields, but when weeds predominately consisted of native legumes and broadleaf species they significantly improved maize

performance. Therefore, manipulating weed composition during the dry season was crucial to optimize benefits of recycled groundnut stover and minimize N losses.

Sub-project 4: Application of Crop Simulation Model in Crop Breeding

4.1 The CSM-CROPGRO-Peanut model could predicted the relative performances and yield stability for pod yield of the test peanut lines for the 11 actual test sites reasonably well. Extending the range of the test environments to 11 additional sites did not provide additional advantage in performance evaluation of the test peanut lines. It can be concluded that the CSM-CROPGRO-Peanut model could be used in assisting yield performance and stability evaluation of peanut breeding lines.

4.2 GGE biplot analyses of simulated pod yield of 17 peanut lines at 130 locations covering all peanut production areas in Thailand for 30 years showed inconsistent results across years for location grouping as well as for the winning genotypes of the individual location-groups. The GGE biplot analysis of the mean data over 30 years also indicated a similarity in genotype discrimination for all locations. Thus, Thailand should be considered as one mega-environment for peanut breeding.

4.3 Analysis of simulated yields of peanut lines at 112 locations over 30 years showed different patterns of dynamic changes for the relative contributions of the genotype x location (G x L), genotype x year (G x Y) and G x L x Y interactions to total yield variation. The results of this study raise a question on the effectiveness of the strategy for using locations to replace years in varietal testing normally employed by breeders.

4.4 Peanut ideotypes were designed for Khon Kaen province growing environments using the CSM-CROPGRO-Peanut model. The characteristics of the designed peanut ideotypes are early flowering, moderate to high leaf area and SLA, high leaf photosynthesis rate, determinate growth habit and high partitioning of assimilates to pods and seeds, and short pod adding and moderate seed filling durations. Over 70 % improvement in yield performance over the current peanut cultivar KK 5 was shown for the designed ideotype genotype. Among all these traits, adjusting PODUR and SFDUR appeared to give the highest impact on yield improvement.

4.5 Results of the determination of cultivar coefficients (GCs) of peanut lines from serial planting date data revealed two groups of the derived GCs: those derived from planting dates 3 (February), 4 (March) and 5 (early-April) and those derived from planting dates 1 (December), 2 (January), 6 (May), 7 (June) and 8 (July). The GCs derived from a planting date could predict crop characters for the same planting-date group quite well, but could poorly predict crop characters for the different planting-date group. However, planting dates 3, 4 and 5 (February to early-April) are not part of normal growing season of peanut in Thailand. If this period is excluded, the genetic coefficient determination experiment for peanut lines could be planted at any time of the year.

4.6 It is possible to reduce the data collection for cultivar coefficients determination. The minimum data suggested is to determine two developmental stages, i.e., first flowering (R1) and harvest maturity (R8), and three plant samplings for growth analysis, i.e., around the stages of full seed (R6), physiological maturity (R7) and harvest maturity (R8).

4.7 Determination of yield gap in a peanut production area in Udon Thanee province in Northeast Thailand revealed considerably large yield gaps in all sub-zones, varying from 1,310 to 2,594 kg ha^{-1} or 40.7-69.6%. From field observations, the main factor reducing peanut yield in the dry season was water deficit, while poor soil preparation and low soil fertility were the major limiting factors in the rainy season. Drawing from the results of model simulation, in the dry season, a yield reduction of about 11.0% was from delayed planting and about 5.0% was from low plant population. In rainy season, however, inappropriate crop cultivar is the main cause of yield reduction (12.9%), while late planting and low plant population accounted for only 1.6% and 7.1% of yield reduction, respectively. The study has demonstrated that the CSM-CROPGRO-Peanut model could effectively be used in estimating yield gaps and identifying associate causes.

Project outputs

1) Capacity building of researchers

Research team:

Number of researchers: 10
Number of Ph.D. students: 11
Number of M.S. students: 8
Number of research assistants: 3

Improved research capacity of researchers

Researchers in the team have gained their experiences in conducting quality research and in supervising thesis research of graduate students both at the M.S. and Ph.D. levels.

All of the researchers in the team have the capability of seeking their own research funds, and have their own projects in which they are the project leaders.

Training of graduate students

Eleven Ph.D. and 8 M.S. students are trained under the project. Two of the Ph.D. students have finished their program, and 9 are expected to complete their degree program within the year 2008. All of the M.S. students have graduated.

2) Published papers in accredited journals (as of 22 October 2007):

Number of published or accepted papers: 19.
Number of submitted papers with revision: 4.
Number of first-submitted papers: 6.

3) Annual technical seminars

Three annual seminar had been held during the period of the project. All of these had been organized together with the Senior Research Scholar projects of Prof. Dr. Peerasak Srinives of Kasetsart University and Prof. Dr. Benjawan Rerkasem of Chiang Mai University.

4) Linkages with foreign institutes

Linkages have been established and collaborative research on peanut has been undertaken with the following foreign institutes:

4.1 USDA-ARS, Coastal Plain Experiment Station
Tifton, Georgia, USA

4.2 Queensland Department of Primary Industies
Kingaroy, Australia

4.3 Department of Biological and Agricultural Engineering,
University of Georgia,
Griffin, Georgia, USA.

4.4 Department of Agronomy, University of Florida,
Gainesville, Florida, USA

4.5 International Crop Research Insitute for the Semi-arid Tropic (ICRISAT)
Patancheru, Andar Pradesh, India.

4.6 Institute of Plant Production and Agroecology, University of Hohenheim
Stuttgard, Germany

Project Code: RTA47/80001

Project Title: Basic Research for Supporting Peanut Production – Phase II

ชื่อโครงการ : การวิจัยพื้นฐานเพื่อสนับสนุนการผลิตถั่วลิสง – ระยะที่ 2

Project leader:

Prof. Dr. Aran Patanothai
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Faculty of Agriculture, Khon Kaen University, Khon Kaen 40002
Tel: (043) 342 949 Fax: (043) 364 636
E-mail aran@kku.ac.th

Type of funding support: Senior Research Scholar

Research area: Agriculture

Duration: 1 April 2004 – 30 September 2007

Research team:

Researchers:

1. Associate Prof. Dr. Sanun Jogloy
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2. Associate Prof. Dr. Nimitr Vorasoot
   Department of Agronomy, Faculty of Agriculture, Khon Kaen University
3. Dr. Banyong Toomsan
   Department of Agronomy, Faculty of Agriculture, Khon Kaen University
4. Assist. Prof. Dr. Chutipong Akkasaeng
   Department of Agronomy, Faculty of Agriculture, Khon Kaen University
5. Assist. Prof. Dr. Kirk Pannengpetch
   Department of Agronomy, Faculty of Agriculture, Khon Kaen University
6. Dr. Poramate Banterng
   Department of Agronomy, Faculty of Agriculture, Khon Kaen University
7. Dr. Napaporn Tantisuwichwong
   Department of Biology, Faculty of Science, Khon Kaen University
8. Dr. Viboon Pensuk
   Agricultural Technology Program, Faculty of Science and Technology,
   Udorn Thanee Rachpat Institute
9. Dr. Piengpen Sarawat
   Khon Kaen Field Crop Research Center, Department of Agriculture, MOAC
10. Ms. Taksina Sansayavichai
    Khon Kaen Field Crop Research Center, Department of Agriculture, MOAC

Research Assistant:

1. Miss Arisara Phupaden, M.S.
2. Miss Sophaphis Photisak, B.Sc.
3. Miss Thanawan Tungthong, B.Sc.

Ph.D. Student:

1. Mr. Bhalang Suriharn
2. Miss Nittaya Phakamas
3. Mr. Jakarat Anothai
4. Miss Walaya Phutto
5. Mr. Patcharin Songsri
6. Mr. Teerayuth Kerdthai
7. Mr. Samran Pimrach
8. Ms. Srisuda Thippayarags
9. Miss Sukanya Promsakha Na Sakonnakhon
10. Miss Saowakon Hemwong
11. Miss Wanwipa Kaewpradit

M.Sc. Student:

1. Miss Sukanya Sujariya
2. Mr. Preecha Kapetch
3. Miss Ratchanok Meekaew
4. Miss Daungsamorn Jeeracheewanan
5. Mr. Saengjan Aekwisate
6. Miss Kanokwan Niyomsil
7. Mr. Chatchai Somee
8. Miss Prakobkit Phuthaisong

Overall objectives:

1. To generate basic knowledge for the development of technologies that will improve production efficiency and quality of peanut and peanut products.
2. To generate published papers in accredited international journals.
3. To improve the capability of researchers and train new researchers to produce high quality research.
4. To strengthen collaboration in peanut research between KKU and other institutes both within the country and overseas.

Expected outputs:

The project aimed to produce the following outputs:

1. Published 15 papers in accredited journals.
2. Capacity building of 11 researchers.
3. Produce 19 M.S. and Ph.D. graduates.
4. Organize annual technical meeting once a year.
5. Linkage with 5 oversea institutes.

Background:

Peanut is an important food legume and oil crop of Thailand. In 2006/07, planted area of peanut in Thailand was 41,443 ha, with a total production of 68,045 tons and a value of 970 million baths, and involving 211,000 farm families (Office of Agricultural Economics, 2007). It is grown by small farmers in all parts of the country, providing a significant source of income to a large number of rural people. It is consumed in various forms – as boiled and roasted peanut, various types of confectionery, and food ingredients. Being rich in protein with protein content in seeds of 25 %, peanut is an important source of protein for Thai people. It is also a major source of edible oil and protein for animal feed. Furthermore, the peanut crop plays an important role in soil improvement through its nitrogen fixing ability, which was found to be more efficient than soybean and cowpea (McDonagh *et al*., 1993). Under the current condition in which agricultural land has greatly degraded, incorporation of legumes in cropping systems is strongly needed for sustainable production. Peanut is a suitable crop to be incorporated in several cropping systems, particularly in rotation with sugar cane and cassava in Northeast Thailand where poor soils predominate.

Almost all of the nuts produced in Thailand are used domestically. However, Thailand imports considerable amount of unrefined peanut oil and cake. Lately, there has been increasing uses of peanut in food processing, both at home and industry levels. Various types of confectionery products have been developed with a wide variety of packaging. The demand for these products is high in both internal and overseas markets. There is also a great export potential of peanut products if their quality meet the international standard, especially on the level aflatoxin contamination. Currently, production of peanut in the country is insufficient for the demand. It was estimated that the demand for direct consumption and processing industry was more than 200,000 tons per year, and continuously increasing (Chanasenee, 1997). Production, on the other hand, has been declining. Planted area decreased from 104,000 ha in 1994/95 to 83,000 ha in 2001/02 and to 41,443 ha in 2004/05, and stabilized around this number in the following two years. Yields in these years varied from 1,506 to 1,643 kg/ha, and production ranged from 65,000-150,000 tons per year, much below the demand within the country. As a consequence, importation of peanut has increased substantially in the recent years. In 1997, the amount of peanut imported was 4,309 tons for a value of 36 million baths. In 2001, it was increased to 34,135 tons for a value of 644 million baths (Office of Agricultural Economics, 2002, 2007). This amount did not include illegal smuggling from neighboring countries, which was also quite substantial.

In the future, under the WTO agreement, subsidies and tariffs for agriculture products will have to be eliminated. Peanut produces in the country will face a strong competition with imported peanut, and Thai peanut products also have to compete with products from other countries both in internal and international markets. However, it is an opportunity to increase the export of peanut products, particularly with the large-seeded type, if their quality is improved to the international standard and production cost is reduced to a competitive level. Improvement of product quality and production efficiency is, thus, essential for peanut production in Thailand. These require a strong support in research.

At present, peanut yield in Thailand is low compared to those of developed countries, even when grown under irrigation. Major constraints in production are

erratic rainfall (for rainfed crop), low soil fertility, improper management, insects, diseases, and weeds. Aflatoxin is an important problem which restricts the use of peanut, both for human consumption and for animal feed, and also poses a serious problem for marketing. Most of farmers are poor and can not afford high inputs. Research is needed to remove these constraints, particularly by technologies appropriate to the capital-scare small farmers.

On 30 May 1997, the Field Crops Program of the TRF organized a meeting of key resource persons at the Golden Valley Resort Hotel, Khao Yai, Nakhon Ratchasima to determine key issues for peanut research. Apart from the problem of aflatoxin contamination and the establishment of production system of large-seeded peanut which had on-going projects at that time, the meeting gave high priority to varietal improvement, on-farm research, and basic research to support the improvement of production efficiency and quality of peanut and peanut products. Phase I of this project has undertaken selected topics of such basic research, based on the expertise of researchers in the team. The main research topics in Phase I included peanut bud necrosis which is a new peanut disease in Thailand, the utilization of peanut residues for soil improvement, and the use of a crop simulation model, CROPGRO-Peanut, in assisting peanut variety evaluation.

In the TRF Senior Research Scholars Meeting in Chiang Mai during 13-15 December 2002, the working group on agriculture has identified in-depth understanding of the differential responses of genotypes to various stresses, both biotic and abiotic, and their control mechanisms as a priority area of basic research. This project in Phase II has addressed some of these, particularly drought stress and better understanding of the genotype x environment interactions. Work on peanut bud necrosis was continued in some aspects. Research on the utilization of crop residues was expanded to cover the entire cropping systems. The use of crop simulation model was also expanded to include studies on genotype x environment interactions and identification of desirable physiological traits for peanut genotypes. The project has embarked upon a new area of research on drought resistance in a holistic approach. The aim was not only to support breeding for drought resistance/tolerance but also to provide a means for reducing the problem of aflatoxin contamination in which direct breeding for its resistance has not yet been successful.

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Scope of research:

The project consisted of 4 sub-projects:

Sub-project 1. Basic research to support breeding for resistance to peanut bud necrosis and thrips.

Sub-project 2. Basic research to support breeding for drought and aflatoxin resistance.

Sub-project 3. Utilization of peanut stover and other crop residues to improve crop productivity.

Sub-project 4. Application of crop simulation model in crop breeding and production.

Results

Sub-Project 1.

Basic Research to Support Breeding for Resistance to Peanut Bud Necrosis and Thrips

Assoc. Prof. Dr. Sanun Jogloy

Sub-project Leader

Peanut bud necrosis disease (PBND) is by far the most important of all currently known virus disease of peanuts (*Arachis hypogaea* L.) in South Asia (Satyanarayana *et al*., 1996). It can cause yield losses of over 50% in peanut (Dwivedi *et al*., 1995) and many other crops including chilli, potato, tomato, tobacco, and early-maturing legumes such as mungbean and urd bean. In India, yearly losses caused by this virus were estimated at more than 89 million US dollars (Reddy *et al.*, 1995). PBND, however, is a relatively new disease in Thailand, first reported in 1985 (Wongkaew, 1987). The disease is most prevalent in the Northeastern and Eastern

regions. The incidence in some locations has been as high as 90% and these infected crops had a total yield loss (Wongkaew and Chuapong, 1996).

PBND is caused by peanut bud necrosis virus (PBNV), a distinct member of the genus *Tospovirus* of the family *Bunyaviridae,* which is transmitted by *Thrips palmi* Karny (Reddy *et al.*, 1992). Initial symptoms of PBND appear on young leaves as a mild chlorotic mottle or spots, which develop into necrotic and chlorotic rings and streaks. The leaflets become flaccid and droop, typically resulting in necrosis of the shoot tip. The virus spreads systemically and normally induces necrosis in all buds. Secondary symptoms are stunting, axillary shoot proliferation, and malformation of leaflets. If plants are infected early, they are stunted and bushy. If plants older than 1 month are infected, the symptoms may be restricted to a few branches or to the apical parts of the plant (Reddy *et al*.,1995; Buiel, 1996). Plants infected early in development may not produce any pods, while plants infected in later stages produce some pods (Singh and Srivastava, 1995).

Currently, there is no practical control measure for PBNV on peanut. However, the disease incidence can be reduced by some cultural practices such as adjusting sowing date to the period with low levels of vector activity, intercropping with fast growing cereals (Reddy *et al*., 2000) and close spacing (Basu, 1995; Buiel, 1996). A resistant genotype, therefore, appears to be the only viable alternative for disease management.

An effective screening method is a prime prerequisite for any disease resistant breeding program. Although field and greenhouse inoculation procedures to evaluate peanut genotypes for their reactions to PBNV have been reported (Dwivedi *et al*., 1995; Buiel, 1996; Buiel and Parlevliet, 1996), these procedures still have some drawbacks for breeding application. A more effective screening method for PBNV resistance, therefore, needs to be further explored. Also in field screening for PBNV resistance, only disease incidence has been used as a means to assess the peanut accessions (Buiel, 1996; Buiel and Parlevliet, 1996). The potential of other parameters to evaluate PBNV resistance has not been well documented.

Significant efforts have been invested in screening peanut accessions for resistance. Peanut genotypes have been intensively studied for resistance to PBNV at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Asia Center, Patancheru, India, and genotypic differences in field resistance to PBND have been reported among 8,000 peanut germplasm lines from a world collection (Dwivedi *et al*., 1995). In most cases, field resistance is associated with nonpreference to the vector. However, in a few genotypes, a lower field disease incidence was attributed to a slower multiplication of the virus in the plant. However, complete resistance (immunity) has not been found within *A. hypogaea* (Buiel, 1996).

The development of resistant cultivars is facilitated by knowing the types of gene action governing the inheritance of disease resistance. Currently, the genetic basis of resistance to PBNV is not well understood. Buiel (1996) reported a study on the inheritance of PBNV resistance in crosses of five resistant and two susceptible genotypes. He found that resistance to PBNV could be explained by at least three resistance factors which are additively inherited. Dominance and epistasis gene effects were absent. The resistance was also observed to be stable across environments.

Lower incidence of PBND can be achieved through cultivar resistance to the thrips vector. Several peanut lines have been identified as having low thrips damage in

the field (Amin *et al.*, 1985; Keerati-Kasikorn *et al.*, 1990; Dwivedi *et al.*, 1995). However, high level of thrips resistance is mostly found in wild *Arachis* species (Lynch and Stalker, 1997).

In Phase I of the projects, studies were conducted on biology of PBNV in relation to its epidemic, disease parameters to evaluate PBNV resistance, time for assessing PBNV resistance in field evaluation, effectiveness of grafting inoculation compared to the standard method of sap inoculation with hand rubbing and a high-pressure spray method, combining ability of field resistance to PBND, and type of gene action governing the inheritance of field resistance to PBND. Area under disease progress curve was found to be an alternative parameter to evaluate PBNV resistance, and the suitable time of assessment was 50-60 days after planting (Pensuk *et al.*, 2002a). Grafting inoculation was ineffective in the study as most of the scions were desiccated by 3-5 DAG resulting in no graft union being formed. However, improvement could be made by covering grafted plants with polyethylene bags for a period to maintain high humidity and to facilitate graft formation (Pensuk et al, 20002b). Gene effects governing the field resistance to PBND were found to be mainly additive, but non-additive gene effects were also present (Pensuk *et al.*, 2002c).

Research in Phase II consisted of 5 studies: (1) factors affecting the effectiveness of PBNV inoculation, (2) combining ability for PBNV resistance, (3) heritability, phenotypic and genotypic correlations of PBNV reaction parameters, (4) gene effects for parameters of PBNV resistance, and (5) heritability and phenotypic correlation of thrips resistance and agronomic traits in peanut.

Study 1-1. Factors affecting the effectiveness of PBNV inoculation for resistance evaluation

V. Pensuk, S. Jogloy and A. Patanothai

Peanut bud necrosis disease (PBND), caused by *Peanut bud necrosis virus* (PBNV) and transmitted by *Thrips palmi* Karny, is a serious virus disease of peanut in many countries in South Asia (Satyanarayana et al., 1996) and in parts of China, Nepal, Sri Lanka and Thailand (Reddy et al., 1995). The disease can cause substantial yield losses in peanut (Dwivedi et al., 1995) and in many other crops (Reddy et al., 1995). Currently, there is no practical control measure for PBNV on peanut, and cultivar resistance appears to be the most effective long-term strategy for management of the disease.

Successful inoculation of PBNV is necessary to evaluate the levels of resistance of peanut genotypes. Greenhouse screening using sap inoculation, the standard method, has been reported to yield different results for the same genotype. To improve the efficiency and consistency of mechanical transmission of the virus, a better understanding of the factors causing the variation of the results is needed. The differences in PBND incidence in the rainy and dry seasons in Thailand have led to a hypothesis that temperature and relative humidity might be the causal factors. This study aimed to investigate the effects of temperature and relative humidity on the effectiveness of PBNV inoculation on peanut.

Materials and methods

Two experiments were conducted, using the susceptible peanut genotype Tainan 9. For Experiment I, the treatments included maintaining the inoculated plants in an environmental growth chamber that was set at 25°C, 90 % relative humidity (RH) during a 12 h light period (a light intensity of 1,000 lk) and 20°C, 90 % RH during a 12 h dark period and outside the growth chamber at room temperature. The test plants were kept in the growth chamber after inoculation, i.e. 24, 48, 72 h and all the period after inoculation until the test was terminated. The plants were visually scored for PBNV symptoms at 14 and 28 days after inoculation. The experiment was repeated 5 times.

In Experiment II, the inoculated plants were kept in two environmental growth chambers that were set to the conditions representing the average climatic conditions in the dry season (32°C, 44 % RH, during an 11 h 30 min light period, and 22°C, 65 % RH, during a 12 h 30 min dark period) and the rainy seasons in Thailand (36°C, 46 % RH, during a 12 h 30 min light period, and 25°C, 70 % RH, during an 11 h 30 min dark period). The inoculated plants were kept in the two growth chambers for four weeks then were visually checked for PBNV symptoms. The experiment was repeated 3 times.

Results

The results showed that exposing the PBNV-inoculated plants to low temperature (25°C, 90 % relative humidity (RH) during a 12 h light period and 20°C, 90 % RH during a 12 h dark period) for a period of 24, 48, or 72 h or all the time during the experimental period did not increase the percentage of infected plants (Table 1.1). Two climate conditions representing the dry season (daytime, 32 °C, 44 % RH, night-time, 22 °C, 65% RH) and the rainy season (daytime, 36 °C, 46 % RH, night-time, 25 °C, 70% RH) in Thailand also showed no difference in the percentage of infected plants. These results indicated that low temperature or relative humidity did not affect the transmissibility of PBNV by mechanical inoculation. The difference in disease incidences in the rainy and the dry seasons in Thailand could not be explained by the difference in climatic conditions but could possibly be accounted for by the difference in vector infestation.

Publication

Pensuk, V., S. Jogloy and A. Patanothai. 2007. Effect of temperature and relative humidity on the effectiveness of *Peanut bud necrosis virus* inoculation on peanut. (submitted to Plant Disease).

Table 1.1 Incidences of PBNV infected plants obtained from mechanical inoculation under different environmental conditions.

Environmental condition	Mean percentage of symptomatic plants				
	Trial I	Trial II	Trial III	Trial IV	Trial V
Room condition[w]	67.31	100.00	93.75	73.96	71.88
In growth chamber for 24 h after inoculation[x]	57.14	100.00	96.88	77.23	65.63
In growth chamber for 48 h after inoculation[x]	55.80	100.00	100.00	75.00	93.75
In growth chamber for 72 h after inoculation[x]	58.78	100.00	100.00	71.88	62.50
In growth chamber all the time after inoculation[x]	61.88	100.00	87.50	93.75	41.17
F-test[y]	NS	NS	NS	NS	NS
C.V. (%)	39.05	-	8.1	23.78	34.11
Planting date	Sep. 8, 2004	Sep. 28, 2004	Feb. 25, 2005	Mar.10, 2005	Oct. 1, 2005
Inoculation date	Sep. 15,2004	Oct. 4,2004	Mar. 3, 2005	Mar. 16,2005	Oct. 7, 2005
[w] Room condition:					
Maximum temperature, range (^{o}C)[z]	27.5-34.3	30.6-33.2	23.1-41.6	24.0-42.5	27.5-34.5
Minimum temperature, range (^{o}C)[z]	20.7-25.0	18.5-23.6	11.4-25.1	18.5-26.7	19.4-25.7
Maximum Relative humidity, range (%)[z]	84.0-96.0	84.0-94.0	54.0-88.0	71.0-95.0	82.0-94.0
Minimum Relative humidity, range (%)[z]	40.0-67.0	34.0-51.0	22.0-44.0	20.0-70.0	43.0-69.0

[x] Growth chamber condition: 25 ^{o}C, 90 % RH during a 12 h light period and 20 ^{o}C, 90 % RH during a 12 h dark period.

[y] Data in trial I, IV, and V were transformed using the arcsine transformation before analysis; NS = Not significant.

[z] Data were recorded during the experimental period, i.e. 28 days after inoculation.

Study 1-2. Combining ability for *Peanut bud necrosis virus* (PBNV) resistance in peanut

N. Daenpuang and Sanun Jogloy

Combining ability is an ability of a parental genotype to give good progenies when it is crosses with other parent genotypes. Combining ability can be of two types: general and specific. General combining ability (GCA) is defined as the average performance of a parental line to give good progenies, whereas specific combining ability (SCA) is defined as the performance of a specific cross. GCA implies that additive gene effects are importance and thus can be fixed in progenies through selection, while SCA is associated with non-additive gene effects which can only be exploited in hybrid combinations (Fehr, 1987).

Combining ability is unique to the population under study, because populations in other studies may be different in genetic backgrounds. It is important for breeder to obtain this information for further determination of appropriate breeding strategies. For peanut bud necrosis virus (PBNV) resistance, genetic studies are rather limited (Pensuk et al., 2002b; Buiel, 1996) and further investigations are needed. The objective of this study was to evaluate GCA and SCA for the incidence and severity of peanut bud necrosis disease (PBND).

Materials and methods

Thirty crosses of peanut in the F_2 generation generated from a diallel mating of three PBNV resistant lines (IC 10, IC 34 and ICGV 86388) and three susceptible lines (JL 24, KK 4 and KK 60-1) were used in this study. They were tested in the dry season in a randomized complete block design with six replications at two PBND hot spots in Kalasin province under natural occurrence of the disease. Data were recorded on percentage of infected plants and disease severity, with rating scales of 1-5 at multiple evaluation times starting from 30 days after sowing (DAS) to 70 DAS with ten-day intervals. Combining ability analysis was performed on combined data of the two environments following Model 1 Method 3 of Giffing (1956).

Results

Significant GCA and SCA effects were found for both PBND incidence and severity at 60 and 70 DAS (Table 1.2). However, the mean squares for GCA were much greater than those for SCA for both characters, with the ratios ranging from 6:1 to 11:1. These results indicated that additive gene effects accounted for most of the genetic variations for PBND incidence and severity. Reciprocal effects were not significant statistically, indicating that reciprocal cross is not necessary to develop segregating population for further selection.

All resistant parents had negative GCA effects for both PBND incidence and severity (Table 1.3). For both characters, the highest negative effect was most favorable. The highest and negative GCA effects were shown for IC 10, whereas ICGV 86388 and IC 34 showed slightly different GCA effects depending on times of evaluation. These results suggested that additive gene effects accounted for a major proportion of genetic control for PBNV resistance, and that resistant parents were clearly differentiated from susceptible parents and could be used as sources of PBNV resistance.

Table 1.2 General combining ability (GCA), specific combining ability (SCA) and reciprocal mean squares for peanut bud necrosis disease (PBND) incidence and severity at two locations in Kalasin province evaluated at 60 and 70 days after sowing (DAS).

Sources of variation	df	PBND incidence		PBND severity	
		60 DAS	70 DAS	60 DAS	70 DAS
GCA	5	608.52**	620.16**	0.0173**	0.0260**
SCA	9	56.51**	63.67**	0.0025**	0.0042**
Reciprocal	15	3.23	3.99	0.0000	0.0000
Error	145	9.72	9.87	0.0003	0.0003
GCA/SGA		11:1	10:1	7:1	6:1

** significant at 0.01 probability level.

Table 1.3 General combining ability effects for peanut bud necrosis disease (PBND) incidence and severity at two locations in Kalasin province evaluated at 60 and 70 days after sowing (DAS)

Parental lines	PBND incidence		PBND severity	
	60 DAS	70 DAS	60 DAS	70 DAS
ICGV 86388	-7.037	-6.159	-0.0389	-0.0429
IC 10	-9.752	-10.214	-0.1498	-0.0637
IC 34	-6.791	-8.020	-0.0380	-0.0484
JL 24	7.660	7.635	0.0430	0.0513
KK 4	9.063	8.123	0.0480	0.0522
KK 60-1	6.920	8.080	0.0357	0.0515
r	0.986**	0.995**	0.991**	0.994**
SE (Gi)	1.001	1.001	0.005	0.005
SE (Gi-Gj)	1.657	1.559	0.008	0.008

** significant at 0.01 probability level

r = correlation coefficient between means of parental lines and their GCA effects

Publication

Daengpuang, N., S. Jogloy, S. Wongkaew, B. Toomsan, T. Kesmala and A Patanothai. 2007. Combining ability for *Peanut bud necrosis virus* (PBNV) resistance in peanut. Thai J. of Agric. Sci. (in press).

Study 1-3. Heritability, phenotypic and genotypic correlations of *Peanut bud necrosis virus* (PBNV) reaction parameters in peanut

Y. Tonsomros and Sanun Jogloy

Peanut bud necrosis disease caused *by Peanut bud necrosis virus* (PBNV) is a newly-emerging virus disease of peanut in Thailand. Currently, there is no effective control measure for the disease. Therefore, breeding of peanut for PBNV resistance is a goal of peanut breeding program at Khon Kaen University. Information on the heritability of PBNV resistance traits and their correlations would be useful for determining appropriate breeding strategy. Unfortunately, very limited information on these is available in the literature (Kesmala et al., 2004). The objective of this study was to assess the heritability and correlations among PBNV resistance traits in segregating peanut populations derived from crosses of PBNV resistant and susceptible genotypes.

Materials and methods

A total number of 300 families of peanut in F_4 generation were derived from 10 crosses (30 families each) involving three PBNV susceptible (JL 24, KK 4 and KK 60-1) and three PBNV resistant genotypes (IC 10, IC 34 and ICGV 86388). These families were evaluated for heritability and correlations of traits related to PBNV resistance under field conditions in two hot spots in Kalasin province. A randomized complete block design with four replications was used for both locations which located about 10 km apart. A susceptible check (Tainan 9) and two resistant checks (IC 10 and IC 34) were also included. The data were recorded for disease severity, using a 1-5 rating scale, and on percentage of infected plants at 30, 40, 50, 60, 70 and 90 day after sowing. The data were then subjected to analysis of variance, and heritability and phenotypic and genotypic correlations were derived following the methods described by Srinives (1982).

Results

Broad-sense heritability estimates ranged from 0.29 to 0.91 for disease incidence and 0.27 to 0.90 for disease score (Table 1.4). On the average, the susceptible x susceptible crosses had lower heritability estimates than the resistant x susceptible crosses. When crosses in resistant x resistant group were compared, the cross ICGV 86388 x IC 34 had higher heritability estimates for PBNV incidence and PBNV score than the cross ICGV 86388 x IC 10. Low to moderate heritability estimates were also found in the crosses between susceptible parents.

Phenotypic and genotypic correlations between disease incidence and disease score showed that both PBNV resistance parameters were well associated (Table 1.5). Genotypic correlations were clearly higher than phenotypic correlations. These results suggested that any of these two parameters could be used to evaluate PBNV resistance in peanut and the decision should be based on the comparative merit of the trait.

Table 1.4 Heritability estimates for peanut bud necrosis disease (PBND) incidence and PBND score in the F_4 generation of 10 crosses of peanut.

Cross	PBND incidence		PBND score	
	50 DAS	60 DAS	50 DAS	60 DAS
Resistant x resistant				
ICGV 86388 x IC 34	0.91	0.91	0.89	0.87
ICGV 86388 x IC 10	0.46	0.51	0.27	0.64
Resistant x susceptible				
ICGV 68388 x KK 4	0.90	0.91	0.84	0.90
ICGV 86388 x KK 60-1	0.76	0.76	0.45	0.79
IC 10 x KK 4	0.66	0.63	0.77	0.71
IC 10 x KK 60-1	0.77	0.77	0.79	0.79
IC 34 x KK 4	0.72	0.80	0.70	0.79
IC 34 x KK 60-1	0.77	0.78	0.84	0.83
Susceptible x susceptible				
JL 24 x KK 60-1	0.29	0.48	0.50	0.53
KK 4 x KK 60-1	0.57	0.50	0.50	0.40

Note: DAS=days after sowing

Table 1.5 Phenotypic (r_P) and genotypic (r_G) correlation between disease incidence and disease score of peanut bud necrosis disease (PBND) in the F_4 generation of 10 crosses of peanut.

Cross	50 DAS		60 DAS	
	r_P	r_G	r_P	r_G
Resistant x resistant				
ICGV 86388 x IC 34	0.88	0.85	0.98	1.00
ICGV 86388 x IC 10	0.97	0.99	0.99	1.00
Resistant x susceptible				
ICGV 68388 x KK 4	0.98	1.00	0.99	1.00
ICGV 86388 x KK 60-1	0.92	1.00	0.98	1.00
IC 10 x KK 4	0.92	1.00	0.93	1.00
IC 10 x KK 60-1	0.90	0.92	0.97	0.99
IC 34 x KK 4	0.94	1.00	0.97	1.00
IC 34 x KK 60-1	0.95	1.00	0.97	1.00
Susceptible x susceptible				
JL 24 x KK 60-1	0.90	1.00	0.95	1.00
KK 4 x KK 60-1	0.94	0.94	0.93	0.90

Note: DAS=days after sowing

Publication

Tonsomros, Y., S. Jogloy, S. Wongkaew, C. Akkasaeng T. Kesmala and A. Patanothai. 2006. Heritability, phenotypic and genotypic correlations of *Peanut bud necrosis virus* (PBNV) reaction parameters in peanut. *Songklanakarin J. Sci. Technol*., 28(3): 469-477.

Study 1-4 Gene effects for parameters of *Peanut bud necrosis virus* (PBNV) resistance in peanut

A. Poledate and Suwit Laohasiriwong

Breeding for PBNV resistance requires information on genetic control of the trait, but such information is very limited in the literature. The objective of this study was to investigate the relative importance of several types of gene effects controlling PBNV resistance in peanut using generation means analysis.

Materials and methods

Eight generations (P_1, P_2, F_1, F_2, BC_{11}, BC_{12}, $BC_{11}S_1$ and $BC_{12}S_2$) of three crosses involving three parents were used in this study. The parental lines were KK 60-1 (a high yielding PBNV susceptible variety), IC 10 and ICGV 86388 (both are PBNV resistant lines). The entries were planted in the dry season under natural occurrence of PBND in Kalasin province which is the hot spot for PBND. A randomized complete block design with six replications was used. Data were recorded on disease severity score of 1-5 and on percentage of infected plants. Generation means analysis was performed for each parameter at each sampling date to obtain unbias estimates of different types of gene effects. The notations of gamble (1962) were used to describe the genetic parameters and the calculations were performed using Hayman's (1958) model.

Results

Disease incidence was found to be the most important parameter for assessing PBNV resistance in peanut, while disease severity was rather difficult to evaluate. Therefore, only disease incidence is reported.

The expression of gene effects for PBND incidence varied in the different times of evaluation (Table 1.6). The types of gene effect detected for the different crosses also differred. Only additive gene effect was detected for the cross ICGV 86388 x IC 10, both of which are resistant lines. For the resistant x susceptible crosses, additive, dominant and additive x additive gene effects were significant for the cross ICGV 86388 x KK 60-1, while significant additive and additive x dominance gene effects were shown for the cross IC 10 x KK 60-1.

As additive gene effect is fixable through selection, these results indicated that it would be possible to select for PBNV resistance in these crosses. The presence of significant additive gene effect for PBND incidence in the resistant x resistant cross (ICGV 86388 x IC 10) suggested that further improvement in PBNV resistance could be obtained through selection of progenies of this cross.

Table 1.6 Gene effects for peanut bud necrosis disease incidence in three peanut crosses under natural infection of *Peanut bud necrosis virus* (PBNV) in the dry season of 2001.

Parameter	Disease incidence			
	30 DAP	40 DAP	50 DAP	60 DAP
ICGV 86388 x IC 10				
m	6.28±0.82**	11.80±1.87**	25.32±1.24**	15.47±4.93**
a	6.95±1.30**	8.18±2.09**	9.51±2.26**	13.26±6.46ns
d	-3.59±2.72ns	3.11±5.13ns	0.86±4.04ns	4.97±21.27ns
aa				22.85±21.54ns
ad				-5.03±10.08ns
dd				-42.33±38.76ns
χ^2	3.32ns	6.05ns	3.91ns	15.42**
ICGV 86388 x KK 60-1				
m	11.18±2.03**	21.73±3.75*	40.08±2.05**	39.56±1.86**
a		5.15±12.90ns	-7.09±3.17ns	-9.20±2.74*
d	-24.32±11.73ns	1.18±27.24ns	19.57±4.83*	22.69±4.35**
aa	-22.62±12.24ns	2.39±26.88ns	17.25±6.73ns	22.29±5.91*
ad		15.50±15.18ns		
dd	56.02±26.99ns	22.25±59.36ns		
χ^2	6.80ns	12.16**	8.75ns	5.68ns
IC 10 x KK 60-1				
m	4.27±1.18*	28.76±2.41**	41.50±7.81**	14.02±8.55ns
a	-3.75±1.54ns			-26.96±3.36**
d	-3.45±0.47ns	18.69±7.62ns	53.32±53.75ns	-73.05±55.85ns
aa			22.31±29.52ns	78.85±35.43ns
ad		17.23±2.87**	21.06±9.47ns	
dd				-388.1±209.7ns
χ^2	3.31ns	8.71ns	5.43ns	5.39ns

ns, *, ** not significant and significant at 0.05 and 0.01 probability levels, respectively.

Publications

Poledate, A., S. Laohasiriwong, P. Jaisil, N. Vorasoot, S. Jogloy, T. Kesmala and A. Patanothai. 2007. Gene effects for parameters of *Peanut bud necrosis virus* (PBNV) resistance in peanut. *Pakistan Journal of Biological Sciences*, 10(9): 1501-1506.

Study 1-5. Heritability and phenotypic correlation of thrips resistance and agronomic traits in peanut

S. Ekvised and Sanun Jogloy

Thrips (Thysanoptera: *Thripidae*) are important insect pests of a number of crops worldwide. In peanut, thrips not only causes direct damage on plant growth and yield but also are a vector of several viral diseases (Mound, 1996) especially peanut bud necrosis virus (PBNV) (Reddy et. al., 1992). Chemical application to control thrips under field condition is not effective. Therefore, breeding of peanut for thrips resistance remains a viable control measure. To achieve this goal, the information on the inheritance of thrips resistance is essentially required. The objectives of this research were to estimate heritability for thrips resistance traits and to evaluate the relationship between thrips resistance traits and agronomic traits.

Materials and methods

Four thrips resistant peanut lines (ICGV 86031, ICGV 86388, IC 10 and IC 34) were crossed to four high yielding, thrips susceptible cultivars (KK 60-3, KKU 72-1, KKU 72-2 and Luhua 11). The resulting 16 crosses were grown for generation-advance and a total of 182 F_2-derived families (12 families for each cross) were obtained. These families were tested under natural occurrence of thrips infestation in the dry season. Data were recorded on total number of thrips, number of juvenile thrips, number of adult thrips, number of damaged plants and leaves (percentage). Important agronomic characters namely number of pod/plant, shelling percentage, seed size and pod yield were also evaluated. Data were analyzed statistically and genetically.

Results

Heritability estimates of the 16 crosses were calculated for three thrips number parameters and three thrips damage parameters (Table 1.7). The heritability estimates varied among crosses and among characters, ranging from zero to 0.88. The heritability estimates for thrips number parameters were generally lower and lesser consistent than those for plant damage parameters. However, more consistent and moderate estimates for adult thrips number, juvenile thrips number and total thrips number were observed in the crosses KKU 72-1 x ICGV 86031, KKU 72-2 x IC 10 and KKU 72-1 x ICGV 86388, with the values ranging from 0.14 to 0.80. Heritability estimates of these crosses were less consistent than those for plant damage parameters.

Correlations between agronomic traits and thrips resistance parameters (thrips number and thrips damage) were observed both in positive and negative directions, but the values were low or even not correlated (Table 1.8). These results suggested that the inheritance of these traits are independent. Considering high heritability and simplicity to evaluate, plant damage parameters would be the traits to select for the improvement of peanut for thrips resistance.

Table 1.7 Estimates of broad sense heritability for thrips number parameters and plant damage parameters of 16 crosses of peanut evaluated across three environments under natural infestation of thrips population.

Cross	Adult thrips number		Larval thrips number		Total thrips number		Percentage of damaged plants		Percentage of damaged leaves		Thrips damage rating	
	50DAS	60DAS	60DAS	70DAS	60DAS	70DAS	50DAS	60DAS	50DAS	60DAS	60DAS	70DAS
KK 60-3 x IC 10	0.54	0.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
KK 60-3 x IC 34	0.00	0.09	0.28	0.57	0.46	0.50	0.00	0.54	0.48	0.41	0.61	0.33
KK 60-3 x ICGV 86031	0.32	0.41	0.43	0.01	0.00	0.51	0.54	0.11	0.56	0.62	0.47	0.68
KK 60-3 x ICGV 86388	0.60	0.78	0.00	0.00	0.32	0.05	0.00	0.08	0.67	0.51	0.67	0.57
KKU 72-1 x IC 10	0.72	0.49	0.00	0.00	0.00	0.00	0.22	0.38	0.40	0.25	0.56	0.19
KKU 72-1 x IC 34	0.24	0.00	0.00	0.00	0.00	0.47	0.77	0.52	0.81	0.78	0.64	0.73
KKU 72-1 x ICGV 86031	0.49	0.78	0.48	0.60	0.59	0.69	0.64	0.10	0.35	0.68	0.06	0.58
KKU 72-1 x ICGV 86388	0.29	0.80	0.14	0.53	0.63	0.50	0.00	0.09	0.00	0.00	0.06	0.37
KKU 72-2 x IC 10	0.61	0.64	0.56	0.37	0.80	0.40	0.52	0.00	0.49	0.82	0.28	0.74
KKU 72-2 x IC 34	0.00	0.00	0.00	0.00	0.00	0.00	0.58	0.47	0.62	0.59	0.65	0.51
KKU 72-2 x ICGV 86031	0.12	0.53	0.00	0.51	0.00	0.58	0.41	0.49	0.57	0.60	0.39	0.61
KKU 72-2 x ICGV 86388	0.00	0.08	0.00	0.06	0.00	0.42	0.80	0.68	0.50	0.74	0.00	0.80
Luhua 11 x IC 10	0.00	0.00	0.13	0.23	0.26	0.00	0.57	0.53	0.78	0.66	0.66	0.50
Luhua 11 x IC 34	0.00	0.11	0.64	0.19	0.60	0.29	0.29	0.51	0.76	0.88	0.65	0.83
Luhua 11 x ICGV 86031	0.12	0.14	0.22	0.40	0.07	0.00	0.00	0.00	0.38	0.68	0.53	0.50
Luhua 11 x ICGV 86388	0.65	0.00	0.54	0.00	0.71	0.00	0.28	0.23	0.38	0.30	0.53	0.49

Table 1.8 Simple linear correlation coefficients between thrips resistance parameters and agronomic traits of 16 crosses of peanut evaluated in one environment in Kalasin in 2005 under natural infestation of thrips population

Trait	Pod number/plant	Pod weight/plant	Seed weight/plant	Plant dry weight/plant	Shelling percentage	100 seed weight
Adult thrips number 60 DAP	-0.022	0.017	0.017	0.018	0.011	0.062
Adult thrips number 70 DAP	-0.199**	-0.182**	-0.217**	-0.210**	-0.247**	-0.034
Juvenile thrips number 60 DAP	0.164**	0.162**	0.162**	0.103**	0.128**	0.026
Juvenile thrips number 70 DAP	0.189**	0.208**	0.254**	0.278**	0.306**	0.049
Total thrips number 60 DAP	0.115**	0.134**	0.131**	0.080	0.098*	0.059
Total thrips number 70 DAP	0.018	0.043	0.057	0.077	0.079	0.021
Percentage of damaged plants 50 DAP	-0.036	-0.020	-0.067	-0.071	-0.110*	0.040
Percentage of damaged plants 60 DAP	0.050	0.051	0.000	-0.019	-0.059	0.003
Percentage of damaged plants 50 DAP	-0.009	0.014	-0.020	-0.012	-0.038	0.119*
Percentage of damaged plants 60 DAP	0.034	0.017	-0.027	-0.027	-0.065	0.032
Thrips damage rating 60 DAP	0.070	0.060	0.028	0.018	-0.005	0.035
Thrips damage rating 70 DAP	0.005	-0.034	-0.075	-0.108	-0.115*	-0.018

*,** Significantly different from zero at 0.05 and 0.01 probability levels, respectively

Publications

Ekvised, S., S. Jogloy, C. Akkasaeng, M. Keerati-kasikorn, T. Kesmala, I. Buddhasimma and A. Patanothai. 2006. Field evaluation of screening procedures for thrips resistance in peanut. *Asian Journal of Plant Sciences*, 5(5): 838-846.

Ekvised, S., S. Jogloy, C. Akkasaeng, M. Keerati-kasikorn, T. Kesmala, I. Buddhasimma and A. Patanothai. 2006. Heritability and correlation of thrips resistance and agronomic traits in peanut. *Asian Journal of Plant Sciences*, 5(6): 923-931.

Study 1-6. Generation means analysis for thrips resistance in peanut

K. Niyomsil and Sanun Jogloy

Thirps are insect pests of peanut that are difficult to control using chemicals and other cultural practices. Although several chemicals are effective against thrips, the problem still exist from their continued migration from weeds (Ananthakrishnan, 1993). Therefore, host plant resistance is the aim for its control measure, and information on the inheritance of thrips resistance is required for an effective breeding program. The objective of this study was to investigate the relative importance of gene actions controlling the inheritance of thrips resistance in peanut using generation means analysis.

Materials and methods

Seven generations (P_1, P_2, F_1, F_2, F_3, $BC_{11}S_1$ and $BC_{12}S_1$) of three peanut crosses (ICGV 86388 x KK 60-1, IC 10 x KK 60-1 and IC 10 x ICGV 86388) were evaluated under field conditions for total number of thrips, number of juvenile thrips and number of adult thrips. Number of plants and leaves which showed thrips damage were also recorded. Generation means analysis was performed for each parameter at each sampling date to obtain unbias estimates of different types of gene effects. The notations of gamble (1962) were used to describe genetic parameters and the calculations were performed using Hayman's (1958) model.

Results

The results showed that, for total thrips number, additive gene effect was important in cross ICGV86388 x IC 10, while additive and additive x dominant gene effects were important in the cross IC 10 x Khon Kaen 60-1, but no gene effect was significant in the cross ICGV 86388 x Khon Kaen 60-1 (Table 1.9). However, for adult thrips number, dominance gene effect was important in the cross ICGV86388 x IC 10, but dominant and dominant x dominant effects were important in the cross ICGV 86388 x Khon Kaen 60-1, while additive x dominant gene effect was significant in the cross IC 10 x Khon Kaen 60-1. For juvenile thrips number, genetic effect was detected only additive x dominant in the cross IC 10 x Khon Kaen 60-1. Thus, improvement for thrips resistance would be possible only in the cross IC 10 x Khon Kaen 60-1 because of the presence of additive gene effect.

Table 1.9 Estimates of gene effects with their associated standard errors for total thrips number, adult thrips number and larval thrips number in the three crosses of peanut

Cross	Gene effect	Thrips number		
		Total	Adult	Juvenile
ICGV86388 x IC 10	m	2.91±0.17	2.91±0.17	2.22±0.30
	a	NS	NS	NS
	d	1.56*±0.41	1.56*±0.41	NS
	aa	NS	NS	NS
	ad	NS	NS	NS
	dd	NS	NS	NS
ICGV 86388 x Khon Kaen 60-1	m	2.85±0.10	3.08±0.09	2.24±0.16
	a	NS	NS	NS
	d	NS	0.01±0.25	NS
	aa	NS	NS	NS
	ad	NS	NS	NS
	dd	NS	-2.98*±0.21	NS
IC 10 x Khon Kaen 60-1	m	2.93±0.04	1.91±0.20	2.04±0.10
	a	-0.31*±0.07	NS	NS
	d	NS	NS	NS
	aa	NS	NS	NS
	ad	0.64*±0.06	-2.71*±1.26	0.48*±0.18
	dd	NS	-0.48±1.26	NS

Note: m = mean, a = sum of additive effects, d = sum of dominance effects, aa = sum of additive x additive epistatic effects, ad = sum of additive x dominance epistatic effects, dd = sum of dominance x dominance epistatic effects.
NS, * not significant and significant at 0.05 probability level.

Publication

Niyomsil, K., S. Jogloy, C. Akkasaeng, M. Keerati-kasikorn, T. Kesmala and A. Patanothai. 2007. Generation means analysis for thrips (Thysanoptera: Thipidae) number and leaf damage by thrips feeding in peanut. *Asian Journal of Plant Sciences*, 6(2): 269-275.

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Sub-Project 2:

Basic Research to Support Breeding for Drought Resistance

Assoc. Prof. Dr. Sanun Jogloy

Sub-project Leader

Peanut is grown on 23.8 million ha worldwide with a total production of 34.5 million tons. More than 80% of world's peanut production comes from rainfed agriculture in which drought is a major abiotic stress affecting yield and quality of peanut. In Thailand, more than 60 % of peanut production area is under rainfed, and certainly drought is one of the major constraints to production (Patanothai *et al.*, 1987).

Drought effects on peanut are manifested in several ways both on quantity and quality. Water deficits, depending on the timing of occurrence, can cause significant reduction in yield by affecting physiological processes i.e. nitrogen fixation (Ludwing and Matthew, 1993; Ramos *et al.*, 1999; Serraj *et al.*, 1999), photosynthesis (Williams and Boote, 1995), and calcium uptake by developing pods (Rajendrudu and Williams, 1987). Crop responses to drought can be morphological and physiological, including reduction in leaf area and size of new leaves, leaf senescence, changing leaf angle, increasing stomata resistance, reducing leaf water potential, and increasing root length and density (Wright and Nageswara Rao, 1994). Ramos *et al.* (1999) found that increasing level of drought stress resulted in greater reduction in stover dry weight, total biomass, root dry weight, nodule dry weight, nodule number and nitrogenase activity. Effect of drought in reducing nitrogen fixing ability of peanut by reducing nitrogenase activity was also reported by Nambiar and Dart (1983) and Venkateswarlu *et al.* (1990).

Drought also affect peanut quality, particularly the contamination of aflatoxin produced by *Aspergillus flavus* and *A. parasiticus*. It is well documented that end-of season drought can predispose the crop to aflatoxin contamination which can severely impact the economic value of the crop (Davidson *et al.* 1983; Mehan, 1989). The level of aflatoxin contamination was found to increase with the length of the drought predisposal period (Sander *et al.*, 1985). Thus, the problem of drought contributes significantly to the problem of aflatoxin contamination.

Plants have evolved complex, integrated adaptive mechanisms against drought stresses. Plant utilize more photo-assimilates to promote root growth at the expense of shoot growth in order to explore more volumes of soil as drought becomes progressively severe. Changes in leaf size, leaf thickness, stomatal density, and cuticle thickness are morphological adaptation of plant leaves under water stress. These adaptive mechanisms allow plants to maximize water uptake while minimize water loss during drought stress (Kramer, 1980; Wright and Nageswara Rao, 1994; Xiong and Zhu, 2002). Under drought conditions, plant cells loose water resulting in a decrease in turgor pressure. This would trigger signaling cascades leading to expression of two groups of water-stress-inducible genes. The first group includes functional proteins that are indirectly responsible for regulating osmotic adjustment and involved in protecting cellular processes under drought conditions (Bray, 1997). Those in the second group are regular proteins or transcription factors involved in further regulation of signal transduction and gene expression (Shinozaki and Yamaguchi-Shinozaki, 1997).

Although morphological and physiological responses of peanut cultivars to drought stresses have been reported (Collino *et al.*, 2001; Nautiyal *et al.*, 2002; Wright and Nageswara Rao, 1994), cellular mechanisms responsible for drought tolerance are largely unknown and warrant further investigation.

The peanut breeding program at Khon Kaen University has embarked upon breeding for drought resistance (or for improving water-use efficiency) as a major objective. Although the problem of aflatoxin contamination is of prime importance, breeding for aflatoxin resistance in peanut has not been successful anywhere including Thailand (Patanothai *et al.*, 1993). The aim of breeding for drought resistance is not only to alleviate the problem of yield reduction from drought alone but also to reduce the problem of aflatoxin contamination. Experiences in breeding for drought resistance at ICRIAT were considered as a lesson learned. At ICRISAT, an empirical approach was first followed for selection among segregating populations and evaluation of advanced breeding lines for their sensitivity to mid-season and end-season droughts, based on pod and seed yields. While the empirical approach was partly successful, it was concluded that a more efficient breeding approach requires the selection of traits associated with drought resistance. There has been significant improvement in physiological understanding of the genotypic response to drought in peanut, suggesting scope for selecting genotypes with traits contributing to superior performance under water limited conditions (Nageswara Rao and Nigam, 2001). Selection for physiological traits associated with drought resistance is the approach taken by the KKU peanut breeding program.

This sub-project has undertaken basic research to generate information that would be useful to breeding for drought resistance. A comprehensive approach was adopted, i.e. examining from the field level down to the crop, cell and molecular levels. The lengths and frequency of drought stress occurring in major peanut production areas were determined to establish the conditions of drought stress for subsequent studies. Responses to drought stress were examined in terms of yield and yield components, morphological and physiological characters, and biochemical processes. Techniques to evaluate peanut genotypes for their resistance to drought were investigated, including molecular markers. Studies were also conducted on the inheritance of drought resistance and of the associated trait (SLA), and on the relationship of drought resistance to aflatoxin contamination and N-fixing efficiency.

Six studies were conducted under this sub-project:

2-1. Characterization of drought stress in different peanut production areas.

2-2. Morphological and physiological responses of peanut genotypes to different levels of drought stress.

2-3. Heritability, phenotypic and genotypic correlation of drought resistance and yield, aflatoxin contamination and efficiency of N-fixation.

2-4. Generation mean analysis for specific leaf area and harvest index in peanut.

2-5. Isolation and Identification of Peanut Leaf Proteins Regulated by Water Stress.

2-6. Developing DNA markers for drought tolerance selection in peanut.

Study 2-1. Characterization of drought stress in different peanut production areas

P. Dangthaisong, P. Banterng, S. Jogloy, N. Vorasoot,
A. Patanothai and G. Hoogenboom

Drought stress is common under rainfed growing conditions, but even under irrigation water deficit also often occurs during the growing season, resulting in some to substantial reduction in crop yield. As the time of occurrence and severity of drought stress varies in different locations, characterization of drought stress patterns of major production areas and information on crop responses to various levels of drought stresses are needed for the development of appropriate management strategies for individual locations. Such information is either lacking or incomplete, and will require extensive data collection and experimentation to be able to obtain.

The Cropping System Model (CSM) CROPGRO-Peanut has been developed to simulate vegetative and reproductive development, growth and yield as a function of crop characteristics, climatic factors, soil characteristics and crop management scenarios (Hoogenboom et al., 1994). The ability of the CSM-CROPGRO-Peanut model to simulate growth and yield as influenced by growing environments, agronomic practices and cultivar traits offers an opportunity for utilizing the model in characterizing drought stress patterns in different locations. However, the applicability of the model for such an application depends very much on the ability of the model to correctly predict growth and development of peanut under different water regimes. The objectives of this study were to evaluate the ability of the CSM-CROPGRO-Peanut model in predicting drought stress conditions and to characterize drought stress patterns in major peanut production areas in Thailand.

Materials and methods

This study consisted of two parts. The first part was the evaluation of the CSM-CROPGRO-Peanut model in predicting drought stress condition, and the second part was the characterization of drought stress patterns in major peanut production areas of Thailand.

For the first part, seven peanut cultivars (KK60-3, Tainan 9, ICGV86308, ICGV98324, ICGV98348 Tifton 8 and a non-nodulating line) were tested under three levels of soil moisture (field capacity (FC), 2/3 available water (AW) and 1/3 available water) in a split-plot in a randomized complete block design with 4 replications. The experiments were conducted under field conditions in the dry seasons of 2004 and 2005. Growth and development data of the peanut cultivars under the three soil moisture regimes were compared with the corresponding simulated data from model simulation using the CSM-CROPGRO-Peanut model.

For the second part, surveys of major peanut production areas were conducted to obtain information on soil characteristics, cultivar grown, planting date, fertilization and other management practices, harvesting date and yield at each location. The surveys covered major production areas in the early-rainy season (rainfed), late-rainy season (rainfed) and dry season (irrigated). Long-term weather data were obtained from near-by weather station, and genetic coefficients of the peanut cultivars for KK 60-3 and Tainan 9 cultivars were obtained from a previous study (Banterng, 2004). The CROPGRO-Peanut model was used to determine time when drought stress occurred, lengths of periods of water deficit, and frequency of occurrence over the past 30 years.

The results were used to characterize drought stress conditions at each production location.

Results

The differences between observed and simulated means for pod yield and total biomass were not considerably large, being within 40 % of observed value for pod yield and 18 % for total biomass (Table 2.1).

In order to evaluate how well the model can simulates the relative responses of the seven peanut cultivars to the three soil moisture regimes, biomass of each cultivar at 2/3 AW and at 1/3 AW were calculated as the percentage of their respective biomass obtained from the F.C. moisture treatment. This analysis was done for both the observed and simulated values and the results are shown graphically in Fig. 2.1. Visual inspections of the graphs indicated that the model could simulate the relative responses to different soil moisture regimes of the seven peanut cultivars quite well. In addition, average relative yield reduction percentages of the seven peanut cultivars obtained from simulated data were close to those obtained from observed data for both years (data not shown).

The results indicated that the CSM-CROPGRO-Peanut model performed reasonably well in simulating pod yield (data not shown) and total biomass at harvest maturity date. The model also simulated relative yield reduction from drought stress of individual peanut cultivars quite well. It was concluded that the CSM-CROPGRO-Peanut model could be used to simulate the relative responses to different levels of moisture regime of peanut genotypes.

Table 2.1 Means for observed (Obs.) and simulated (Sim.) pod yield and total biomass and corresponding yield differences

Treatment	Pod yield (kg ha^{-1})			Total biomass (kg ha^{-1})		
	Sim.	Obs.	(Sim.Obs.) x 100/Obs.	Sim.	Obs.	(Sim.Obs.) x 100/Obs.
Water regime						
1. F.C.	2202.2	2236.2	-1.3	9211.4	8048.1	14.5
2. 2/3 A.W.	1572.1	1745.1	-9.9	6538.5	6380.2	2.5
3. 1/3 A.W.	1068.6	1195.0	-10.6	4381.4	4561.6	-4.0
Cultivar						
Tifton 8	2075.8	1556.3	33.4	6951.0	7563.5	-8.1
Tainan 9	1818.0	1627.3	11.7	6089.7	6045.0	0.7
KK 60-3	1895.3	1653.7	14.6	8459.5	7392.2	14.4
ICGV98308	1056.4	1759.2	-40.0	6949.3	6404.8	8.5
ICGV98324	1183.0	1577.6	-25.0	7082.8	6195.2	14.3
ICGV98348	1452.9	1600.1	-9.2	6350.8	6398.2	-0.7
Non-nod	860.8	1257.0	-31.5	5089.8	4311.2	18.1

FC = Field capacity AW = Available soil water

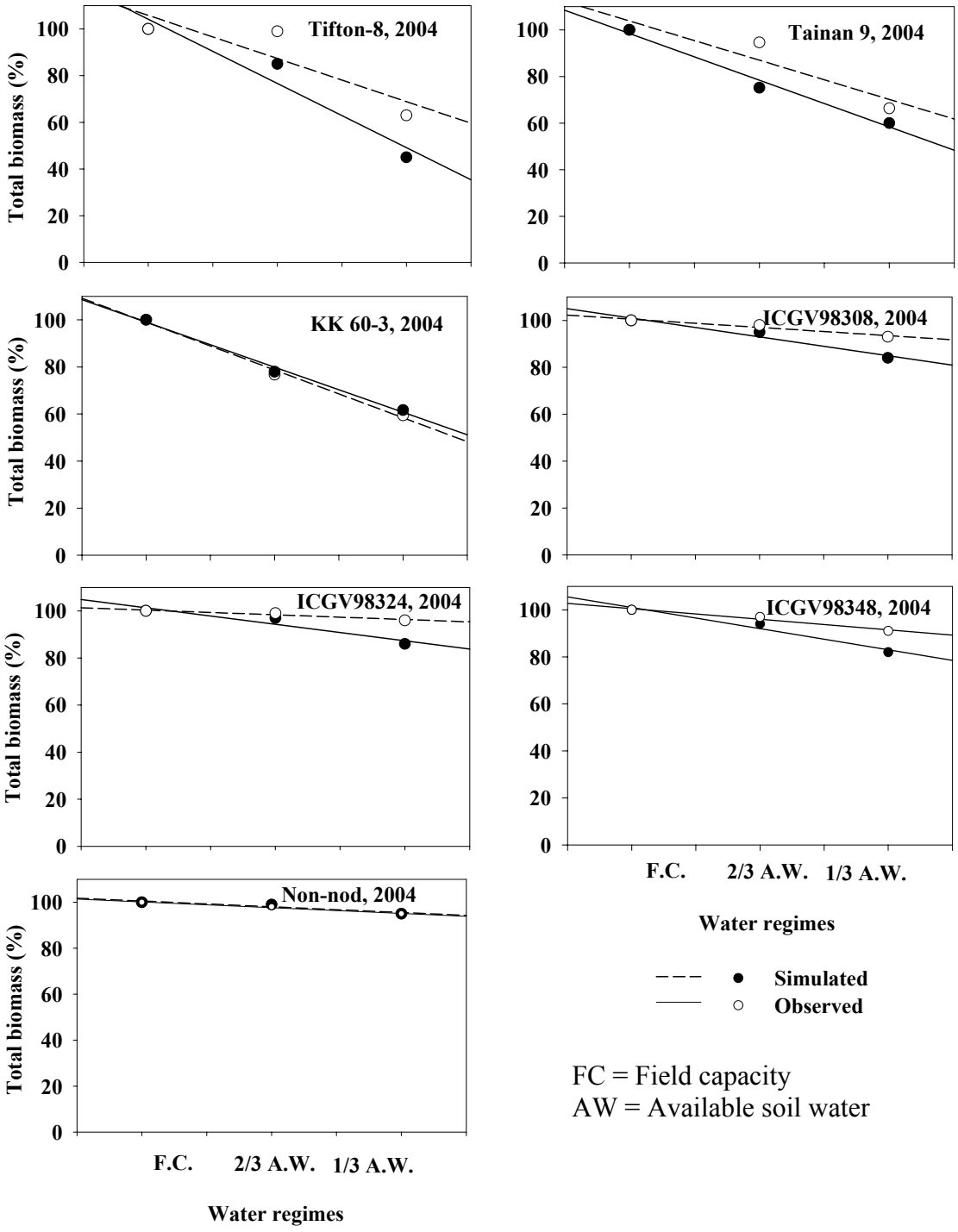

Fig. 2.1 Observed and simulated total biomass of seven peanut cultivars grown under three soil moisture regimes in 2004, expressed as percentage of their corresponding biomass at F.C.

Good characterization of patterns of drought stress in the different peanut growing areas were obtained by the model simulation. The model could provide information on the severity, duration, and growth stages at which drought stress occurred in different years for a particular location.

Publication

Dangthaisong, P., P. Banterng, S. Jogloy, N. Vorasoot, A. Patanothai and G. Hoogenboom. 2006. Evaluation of the CSM-CROPGRO-Peanut Model in Simulating Responses of Two Peanut Cultivars to Different Moisture Regimes. Asian Journal of Plant Sciences, 5 (6): 913-922.

Study 2-2. Morphological and physiological responses of peanut genotypes to different levels of drought stress

This study consists of three parts:

2-2-1. Relationship between biomass production and nitrogen fixation under drought stress conditions in peanut genotypes with different levels of drought resistance

S. Pimratch, S. Jogloy, N. Vorasoot, B. Toomsan,
A. Patanothai and C.C. Holbrook

Drought is a major factor limiting yield of peanut under rainfed conditions in many countries. As access to irrigation in these areas is limited, utilization of drought resistant genotypes is a viable alternative to alleviate the problem. Direct selection for high yield under drought stress has been the main strategy for breeding for drought resistance in peanut. Drought resistant peanut lines identified through this process are those that performed well and gave high yield under drought stress conditions (Nageswara Rao *et al*. 1994). The physiological basis for achieving these higher yields under drought stress is normally not known. Information on physiological traits contributing to high yield under drought stress might reveal the underlying mechanism from which improved strategies could be developed to enhance the effectiveness and progress in breeding for drought resistance in peanut.

In assessing drought resistance of peanut genotypes, total biomass can be used to indicate their potential productivities under drought stress. As a leguminous crop, peanut can fix nitrogen which is an essential element for crop growth. Several studies have shown that drought stress reduced nitrogen fixation in leguminous species (Hassan and Hall 1987, Serraj *et al*. 1997). High N_2 fixation under drought stress could be a means for a legume genotype to achieve high yield under water-limited conditions.

The objective of this study was to determine the effect of drought on biomass production and N_2 fixation by evaluating the relative values of these two traits under well watered and water-stress conditions of peanut genotypes with different degrees of drought resistance.

Materials and methods

Twelve peanut genotypes were tested in a split-plot in a randomized complete block experiment with four replications for two years under field conditions. Main-plot treatments were three soil moisture levels [field capacity (FC), 2/3 available soil water (2/3 AW) and 1/3 available soil water (1/3 AW)], and sub-plot treatments were 12 peanut lines.

Traits were measured to determine biomass production and nitrogen fixation under non stress and stress condition. The reduction in biomass and nitrogen fixation were calculated. Simple correlation was used to determine the relationship between biomass production and fixed nitrogen under drought stress conditions.

Results

The results clearly showed that drought stress reduced biomass production of the peanut crop. Averaging over all genotypes, drought stress at 2/3 AW and 1/3 AW reduced biomass production by 13.0% and 32.7%, respectively (Table 2.2). Significant differences among peanut genotypes were observed for biomass production at all water regimes. Biomass production under FC and the reduction in biomass production at 2/3 AW contributed 78.8% and 15.5%, respectively to biomass production at 2/3 AW (Table 2.3). The contributions of biomass production under FC and the reduction in biomass at 1/3 AW were 60.0% and 31.8%, respectively.

There were differences among the tested genotypes in N_2 fixed at all water regimes. On the average, drought stress at 2/3 AW and 1/3 AW water regimes reduced N_2 fixed by 27.5% and 54.1%, respectively (Table 2.4). There were also significant differences among tested genotypes in reductions in N_2 fixation for both stress levels

Regression analysis showed that the contributions of N_2 fixed under FC and the reduction in N_2 fixed at 2/3 AW were 60.0% and 36.7%, respectively (Table 2.3). The relative contributions of these factors was reversed at 1/3 AW where the contributions of N_2 fixed under FC and the reduction in N_2 fixed at 1/3 AW were 28.6% and 67.2%, respectively. The ability of genotypes to have higher N_2 fixed under mild drought stress was due largely to their high N_2 fixation under well-watered conditions and partly due to their ability to maintain high N_2 fixation under mild water stress, whereas the ability of genotypes to have higher N_2 fixation under severe drought stress was dependent primarily on their ability to maintain high N_2 fixation.

Correlation coefficient between N_2 fixed and biomass production under well-watered conditions were positive ($r=0.50$), though not significant, and became higher and significant at 2/3 AW ($r=0.77$, $P < 0.01$) (data not shown) and 1/3 AW ($r=0.86$, $P < 0.01$) (Fig. 2.2). The results might imply that N_2 fixation is very important for plant growth especially under severe water stress. This may be due to the inability of a plant to use soil nitrogen effectively, arising from the difficulty of roots to mine soil nitrogen in drying soil.

Our results also supported the assumption that peanut genotypes with higher nitrogen under water stress had higher biomass production than the genotypes with lower nitrogen.

Table 2.2 Biomass production and the reductions in biomass production of 11 peanut genotypes under different water regimes.

Genotypes	Biomass production				
	(kg ha^{-1})			Reduction (%)	
	FC	2/3 AW	1/3 AW	2/3 AW	1/3 AW
Tifton-8	8820ab	7425a	5349ab	10.7	34.4
KK 60-3	8875a	7384a	5919a	14.7	32.1
ICGV 98300	8267abc	7010ab	5291b	14.2	35.7
ICGV 98348	7504abc	6734ab	4733bc	9.3	35.9
ICGV 98353	8063abc	6666ab	4912bc	17.0	38.8
ICGV 98324	7719abc	6450ab	4936bc	14.7	34.8
ICGV 98330	6766c	6311ab	4995bc	6.7	20.1
ICGV 98308	7164c	6241b	4456c	10.9	36.3
ICGV 98305	7334bc	6234b	4827bc	15.1	34.2
ICGV 98303	7449abc	5948b	5141bc	18.2	27.9
Tainan 9	7169c	5896b	4791bc	12.2	30.1
Mean	7739	6573	5032	13.0	32.7

Figures in each column follow by different letters are significantly different at $P < 0.01$ by Duncan's multiple range test.
FC = field capacity, AW = available soil water.

Table 2.3 Contribution of potential of biomass production at field capacity and reduction of biomass production under drought conditions to biomass production and N-fixed under drought conditions.

Category	Explained by regression (%)	
	Biomass	N_2 Fixed
At 2/3 AW		
Regression	94.4**	96.7**
Potential of biomass production at FC	78.8**	60.0**
Reduction in biomass production at 2/3 AW	15.5**	36.7**
At 1/3 AW		
Regression	91.8**	95.8**
Potential of biomass production at FC	60.0**	28.6**
Reduction in biomass production at 1/3 AW	31.8**	67.2**

** = Significant at the 0.01 probability level.
FC = field capacity, AW = available soil water.

Table 2.4 Nitrogen fixation and the reductions in N_2 fixation of 11 peanut genotypes under different water regimes.

Genotypes	Nitrogen fixation				
	(kg N ha^{-1})			Reduction (%)	
	FC	2/3 AW	1/3 AW	2/3 AW	1/3 AW
Tifton-8	146a-d	118a-d	78ab	18.1b	46.0de
KK 60-3	179ab	135a	97a	23.2ab	44.2e
ICGV 98300	158a-d	118a-d	76ab	24.3ab	51.8b-e
ICGV 98348	167abc	135a	67b	18.8b	58.1bc
ICGV 98353	183a	123ab	56b	31.8ab	68.9a
ICGV 98324	140bcd	97c-f	58b	28.5ab	56.7bc
ICGV 98330	139d	82f	62b	35.1ab	55.0bcd
ICGV 98308	148a-d	109a-d	58b	24.9ab	60.1ab
ICGV 98305	146a-d	102b-f	74ab	28.6ab	50.0cde
ICGV 98303	144a-d	87f	71b	29.7ab	45.9de
Tainan 9	155a-d	91ef	63b	39.8a	58.3bc
Mean	155	109	69	27.5	54.1

Figures in each column follow by different letters are significantly different at $P < 0.01$ by Duncan's multiple range test.
FC = field capacity, AW = available soil water.

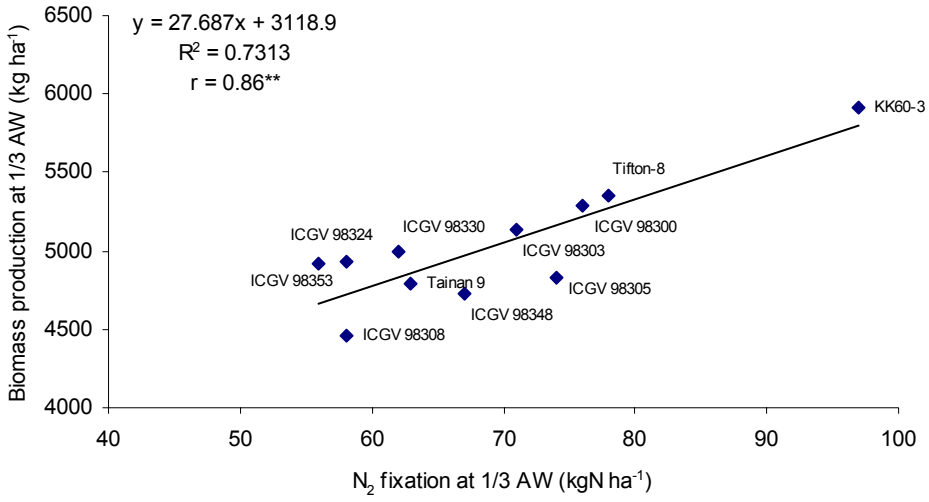

Fig. 2.2 Relationship between biomass production and N_2 fixation of peanut genotypes at 1/3 AW

2-2-2. Root distribution of drought resistant peanut genotypes in response to drought stress

P. Songsri, S. Jogloy, N. Vorasoot, C. Akkasaeng,
A. Patanothai and C.C. Holbrook

Breeding for drought resistance has been an important strategy in alleviating the problem. However, progress has been slow because of the complexity of the trait. A better understanding of the underlying mechanisms of drought resistance should accelerate the progress in breeding for this trait.

Drought resistance may be enhanced by improving the ability of the crop to extract water from the soil. Deep rooting, root length density (RLD) and root distribution have been identified as drought adaptive traits (Ludlow and Muchow 1990) that can be used as selection criteria for drought resistance. In peanut, Pandey *et al*. (1984) reported that drought increased RLD in the lower soil profile of a peanut genotype. Rucker *et al.* (1995) found that some peanut genotypes with large root systems under non-stress conditions gave high yield under drought stress conditions, and they suggested that these genotypes possessed drought avoidance traits. However, the direct assessment of deep rooting, RLD and root distribution of peanut genotypes under different water regimes to see how peanut genotypes respond to drought stress in term of these traits has not been clearly demonstrated.

The objective of this study was to evaluate genetic variations in RLD and distribution among peanut genotypes in response to different available soil water levels, and the relevance of root traits for yield in peanut under limited soil moisture.

Materials and methods

Eleven peanut genotypes with different level of drought resistance were tested in a split-plot in a randomized complete block experiment with four replications for two years under field condition. Main-plot treatments were three soil moisture levels [field capacity (FC), 2/3 available soil water (2/3 AW) and 1/3 available soil water (1/3 AW)], and sub-plot treatment were 11 peanut lines.

Samples were taken for root measurements. The tube of root sampler was centered over the tap root and a sample was taken to a 1.0 m depth from each plot at 97 day after sowing. The core was sectioned into 0.2 m lengths. The roots were washed from the soil cores and were measured for root length. Root length densities (RLD) were calculated as the ratio between root lengths (cm) to soil volume (cm^3). RLD from the first (0-20 cm) and second (20-40 cm) sections were added together and defined as a single upper soil section (RLD_{USS}), while RLD at the deeper sections (third to fifth) were combined to form a single lower soil section (RLD_{LSS}). The percentage of RLD in the lower soil section (%RLD_{LSS}) was calculated.

Drought tolerance index (DTI), as suggested by (Neutiyal et al. 2002), was calculated for % RLD_{LSS} (DTI- RLD_{LSS}). Shoot dry matter, pod yield and harvest index were determined at final harvest. DTI for biomass (DTI-BIO), pod yield (DTI-PY) and harvest index (DTI-HI) were calculated as the ratio of each parameter under stress treatments (2/3 AW or 1/3 AW) to that under well watered (FC) condition.

Results:

Drought stress increased % RLD_{LSS} by 10% and 19% (DTI = 1.10 and 1.19) at 2/3 AW and 1/3 AW, respectively (Table 1). The changes in root distribution in response to drought stress by growing roots deeper into the soil occurred in a few peanut genotypes even under mild drought stress conditions and in more genotypes under severe drought stress.

ICGV 98300 and ICGV 98303 was found to increase there % RLD_{LSS} at 2/3 AW. At 1/3 AW, the increases in % RLD_{LSS} of ICGV 98300, ICGV 98303, ICGV 98305, ICGV 98308, ICGV 98353 and KK 60-3 were 45, 84, 47, 31, 13 and 29%, respectively (Table 2.5). Other genotypes were not adaptive, showing % RLD_{LSS} similar to those under FC.

Drought stress reduced biomass production, pod yield and harvest index. The correlation between the ability to increased % RLD_{LSS} and biomass production was not significant at 2/3 AW and 1/3 AW (Fig. 2.3). The results clearly indicated that deeper roots did not contribute to biomass production or the ability to maintain high biomass production under drought stress.

However, DTI-%RLD_{LSS} was found to significantly correlate with pod yield ($r = 0.61$, $p \leq 0.05$) and drought tolerance index of pod yield (DTI- correlate with pod PY) (0.71 $p \leq 0.05$) (Fig 1). DTI-HI was also found to significantly correlate with DTI-%RLD_{LSS} ($r=0.72$, $p \leq 0.05$). This means that RLD in deeper soil did contribute to pod yield and harvest index under drought stress conditions.

Table 2.5 Percentage of root length density (RLD) distribution in lower soil section (40-100 cm) (%RLD_{LSS}) and drought tolerance index (DTI) for 11 peanut genotypes grown under different water regimes at 97 DAS in the dry seasons 2003/04 and 2004/05.

	RLD distribution (%) in lower soil section (%RLD_{LSS})					
Genotype	FC	2/3 AW	1/3 AW	DTI-2/3AW	DTI-1/3AW	
ICGV 98300	30.49 ab	42.57 a	44.06 a	1.40 ab	1.45 ab	
ICGV 98303	14.62 c	23.32 bc	26.93 bcd	1.60 a	1.84 a	
ICGV 98305	23.86 abc	25.03 bc	35.02 ab	1.05 b	1.47 ab	
ICGV 98308	25.69 ab	24.17 bc	33.56 bc	0.94 b	1.31 abc	
ICGV 98324	25.75 ab	27.50 bc	22.90 d	1.07 b	0.89 bc	
ICGV 98330	33.37 a	31.51 b	26.40 bcd	0.94 b	0.79 c	
ICGV 98348	27.13 ab	28.93 bc	26.68 bcd	1.07 b	0.98 bc	
ICGV 98353	29.72 ab	29.82 bc	33.48 bc	1.00 b	1.13 bc	
Tainan 9	21.86 bc	20.86 c	22.69 d	0.95 b	1.04 bc	
KK 60-3	26.86 ab	27.31 bc	34.55 abc	1.02 b	1.29 abc	
Tifton -8	27.23 ab	27.72 bc	24.61 cd	1.02 b	0.90 bc	
Mean	*26.05*	*28.07*	*30.08*	*1.10*	*1.19*	

Mean in the same column with the same letters are not significantly different by Duncan's multiple range test (DMRT) (at $p<0.05$).
DTI for a genotype were calculated by the ratio of stress (2/3 available water (AW) or 1/3 AW)/non stress (field capacity; FC) conditions.

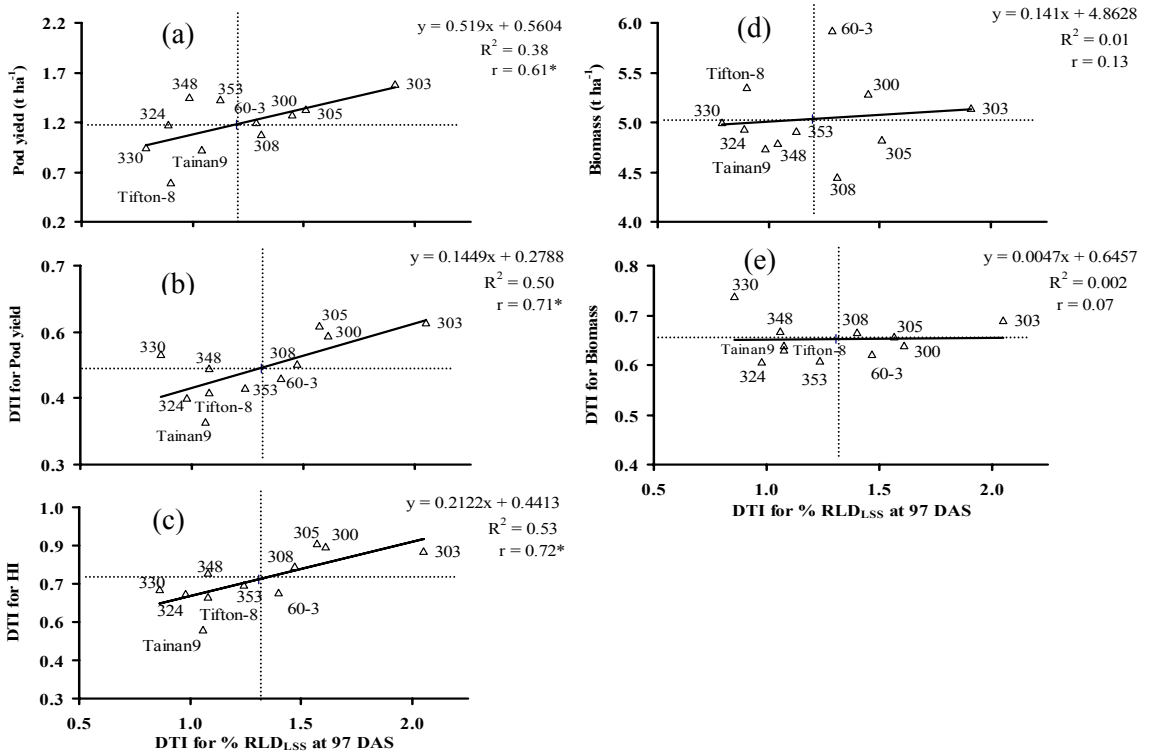

Fig.2.3 DTI for %RLD_{LSS} (40-100 cm) at 97 DAS related to pod yield (a), DTI for pod yield (b), DTI for HI (c), biomass (d) and DTI for biomass (e) under 1/3 AW condition of 11 peanut genotypes in 2003/04 and 2004/05.

2-2-3. Chlorophyll stability is an indicator of drought tolerance in peanut

A. Arunyanark, S. Jogloy, C. Akkasaeng, N. Vorasoot,
N.R. Rachaputi, G.C. Wright and A. Patanothai

The conventional approach of breeding for drought resistance has been based primarily on pod yield, a complex trait which integrates a number of local adaptation factors. Although such an approach has generally been successful for a given location, it has not been successful across locations due to large genotype x environment interactions for yield (Jackson *et al.,* 1996; Araus *et al.,* 2002). An alternative approach is to identify and use such surrogate traits in breeding programs, which are positively associated with yield under drought conditions and less affected by environmental variations. There is therefore a need to explore alternative selection criteria in order to breed for drought resistance.

Transpiration efficiency (TE) has been widely perceived as a useful trait for drought resistance (Richards, 1997). TE is strongly correlated with the carbon isotope discrimination (Δ) in peanut. However, further research has shown that Δ and TE are strongly correlated with the easily measurable trait i.e., specific leaf area (SLA) (Wright *et al.,* 1994).

Chlorophyll content in leaves has been shown to be closely linked with photosynthetic capacity in many crop plants. Drought is known to affect chlorophyll content in many crops. The ability to maintain chlorophyll density under water deficit conditions has been suggested as a drought resistance mechanism in barley (This *et al*., 1999) and potato (van der Mescht *et al*., 1999). However, there is little information on the relationship between leaf chlorophyll status and drought tolerance in peanut.

Recent research has shown that the leaf chlorophyll content can be rapidly assessed using the SPAD chlorophyll meter (Samdur *et al*., 2000; Akkasaeng *et al.,* 2003). Furthermore, close relationships between SPAD chlorophyll meter readings (SCMR), SLA, in peanut suggest that SCMR could be used as a rapid and *in situ* tool for assessing leaf chlorophyll in peanut.

The aim of the current study were to (1) understand genotype x drought interactions for chlorophyll status in peanut leaves, (2) assess if chlorophyll stability under drought can be used as a potential selection criterion for drought tolerance in peanut, and (3) assess the potential of using SCMR as a selection tool for assessing chlorophyll status in peanut genotypes.

Materials and methods

Two experiments were carried out under field conditions for two seasons. The treatments consisting of three water regimes [field capacity; F.C., 2/3 available water (A.W.) and 1/3 A.W.] and twelve peanut cultivars with different level of drought resistance were laid out in a split plot design with four replications. Water regimes were assigned in main plots and peanut cultivars in subplots.

Data were recorded for SCMR, chlorophyll density and chlorophyll content at 30, 60 and 90 days after emergence (DAE) to monitor the chlorophyll status from five random plants of each plot. Ten plants in each plot were randomly sampled at 30, 60 and 90 DAE, and the aerial parts without root of the plants were oven-dried at 80 ^{o}C for 48 hours before recording dry weights (TDM). The TE was calculated as TDM/T, where T = water transpired.

Results:

Combined analysis of variance based on the two-season data showed significant effects of g x s as well as g x w interactions for total dry matter ($P<0.05$), transpiration ($P<0.01$) and transpiration efficiency but not for chlorophyll density or chlorophyll content per plant, suggesting the stability of the latter two traits across environments (data not shown). At 90 DAE, there was a trend for an increase in chlorophyll density (CHlD) under drought conditions (Fig. 4). On the other hand, total chlorophyll content (ChlT) per plant was significantly reduced from 8.4 mg/plant at FC to 5.0 mg/plant at 1/3 AW.

There was a strong positive correlation ($P<0.01$) between TDM and ChlT when data was pooled across irrigation treatments in both years (Table 2.6), suggesting a critical role of total chlorophyll content in varietals growth performance under drought stress. The correlation coefficients between chlorophyll density and SCMR (Fig. 2.5) were positive and significant across sampling dates and irrigation treatments ($r = 0.67$-0.93 $P \leq 0.01$), indicating a close and consistent relationship between chlorophyll density and SCMR in both years. Significant correlations between transpiration efficiency and chlorophyll density, transpiration efficiency and SCMR were found at

all dates of sampling in both years (Table 2.7). The similarity of TE-chlorophyll density relationship and TE-SCMR relationships indicated that chlorophyll density and SCMR could be used as a surrogate measure of TE. The results also indicated that SCMR might be a good tool for indirect assessment of chlorophyll density.

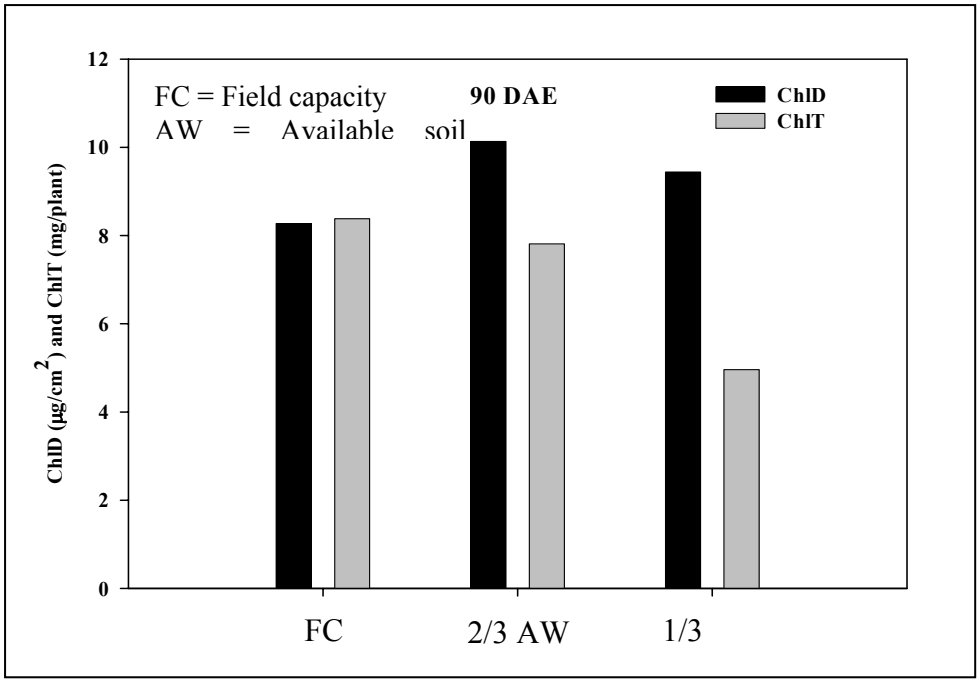

Fig. 2.4 Effect of drought treatment on chlorophyll density (ChlD) and total chlorophyll content (ChlT) per plant at 90 day after emergence (pooled over genotypes and seasons).

Table 2.6 Correlation coefficients (r) (n = 36) between total dry matter (g/plant) and chlorophyll content (mg/plant) in 2003-04 (Year1) and 2004-05 (Year2).

Chlorophyll content (mg/plant)	Total dry matter (g/plant)							
	Year 1				Year 2			
	30 DAE	60 DAE	90 DAE	harvest	30 DAE	60 DAE	90 DAE	harvest
30 DAE	0.88**			0.51**	0.79**			0.63**
60 DAE		0.91**		0.70**		0.76**		0.74**
90 DAE			0.85**	0.78**			0.83**	0.84**

** Significant at the 0.01 probability levels.

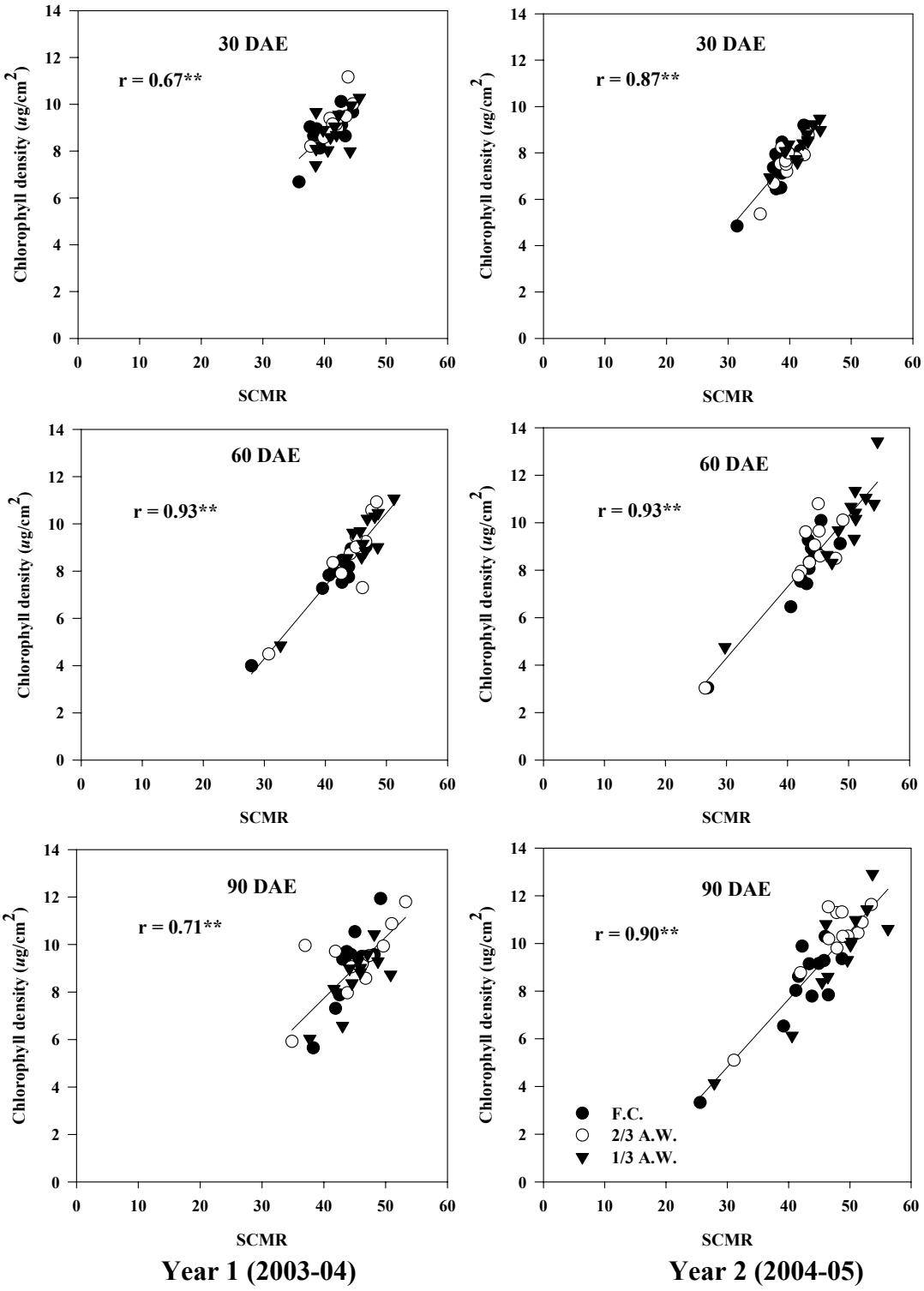

Fig. 2.5 Relationship between chlorophyll density and SCMR in Year 1 and Year2; r = correlation coefficients (n=36), *, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table 2.7 Relationship between TE and chlorophyll density (ChlD), and between TE and SCMR in Year 1 (2003-04) and Year 2 (2004-05).

	Year 1	Year 2
	r (n=36)	r (n=36)
TE & ChlD		
30 DAE	0.65 **	0.71 **
60 DAE	0.77 **	0.70 **
90 DAE	0.46 **	0.61 **
TE & SCMR		
30 DAE	0.58 **	0.74 **
60 DAE	0.80 **	0.79 **
90 DAE	0.41 *	0.76 **

*' ** Significant at the 0.05 and 0.01 probability levels, respectively.

Publications

Arunyanak A., S. Jogloy, C. Akkasaeng, N. Vorasoot, G.C. Wright, N.R. Rachaputi and A. Patanothai. Chlorophyll contents as an indicator of drought tolerance in peanut. Submitted to *Annals of Applied Biology*.

Pimratch, S., S. Jogloy, N. Vorasoot, C. Akkasaeng, A. Patanothai and C.C. Holbrook. Relationships between biomass production and nitrogen fixation under drought stress conditions in peanut genotypes with different levels of drought resistance. Submitted to *Agronomy and Crop Science*. (recommended for publication after minor revision).

Songsri, P., S. Jogloy, N. Vorasoot, C. Akkasaeng, A. Patanothai and C.C. Holbrook. Root distribution of drought resistant peanut genotypes in responses to drought stress. Submitted to *Agronomy and Crop Science*. (recommended for publication after minor revision).

Study 2-3 Heritability, phenotypic and genotypic correlations of drought resistance and yield, aflatoxin contamination and efficiency of N_2-fixation

A. Arunyanak, S. Pimratch, P. Songsri, S. Jogloy,
N. Vorasoot and A. Patanothai

The success in breeding of peanut for drought resistance requires not only the knowledge of mechanisms underlying drought resistance but also the knowledge of the inheritance the traits. The objectives of this study were to estimate heritability in broad sense and genotypic and phenotypic correlations for the three groups of agronomic characters namely traits related to drought resistance, aflatoxin contamination parameters and nitrogen fixation parameters, and also to relate these characters with yield and yield components.

Materials and methods

Four crosses between two drought resistant parents (ICGV 98308 and ICGV 98324) and two high yielding cultivars (KK 60-3 and Tainan 9) were generated, and the F_1 hybrids were planted for generation advance. Thirty five lines of each cross were selected randomly in the F_4 generation, and the lines were further grown for seed multiplication in the F_5 and F_6 generations to obtain apple F_7 seeds.

The F_4-derived lines in the F_7 generation were tested in a field experiment during dry seasons of 2005/2006 and 2006/2007. Data were recorded on SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) at 60 after emergence (DAE). At harvest, the data were recorded for nodule number, nodule dry weight, shoot dry weight, total nitrogen, fixed nitrogen, yield and yield components, and traits related to aflatoxin contamination.

Results:

Under drought stress conditions, relatively high heritability estimates were obtained for specific leaf area (SLA) (0.81-0.95), SCMR (0.89-0.96), reduction in pod yield (0.86-0.96), reduction in total dry weight (0.81-0.93) and N_2 fixed (0.87-0.92) (Table 2.8). However, low to moderate heritability estimates were observed for nodule dry weight (0.50-0.75), reduction in N_2 fixed (0.26-0.58) and *A.flavus* infection (0.49-0.57). These results suggested that improvement of individual traits is possible in these peanut populations. Although the heritability estimates were based on total genetic variation, they should indicate the effectiveness of selection as the populations under study were in advance generation in which genetic variations should be largely additive.

Phenotypic and genotypic correlations among traits were in similar pattern, with the values of genotypic correlation coefficients being slightly higher than those of phenotypic correlation coefficients (Table 2.9). Specific leaf area was found to be positively but weakly correlated with pod yield, total dry weight, N_2 fixed and *A. flavus* infection, with the phenotypic correlation coefficients ranging from 0.09* to 0.23** and the genotypic correlations ranging from 0.10* to 0.33**. Similarly, SCMR was positively correlated with pod yield, total dry weight and N_2 fixed, but negatively correlated with *A. flavus* infection. However, these relationshipss, though significant statistically, were also weak.

Reduction in total dry weight was negatively correlated with all other traits, with the phenotypic correlation coefficients ranging from -0.14** to -0.57** and the genotypic correlation coefficients ranging -0.17** to -0.55. However, no relationship was found between total dry weight reduction and *A. flavus* infection.

Reduction in pod yield was found to be negatively correlated with pod yield itself, with total dry weight, and with nodule dry weight, with the phenotypic correlation coefficients ranging from -0.17** to -0.58** and the genotypic correlation coefficients ranging from -0.19** to -0.58**. These relationships were similar to those of the reduction in total dry weight, except that the relationship with *A. flavus* infection was positive rather than negative.

The above relationships suggested that it would not be appropriate to use specific leaf area and SCMR as surrogate traits for pod yield, nitrogen fixation and aflatoxin contamination. Total dry weight reduction and pod yield reduction might be more useful for indirect selection for pod yield, total dry weight and N_2 fixed, but this is still not conclusive because the correlations were not high enough. Rather good

association between the reduction in pod yield and *A. flavus* infection indicates that drought resistant genotypes are favorable under drought stress conditions.

Table 2.8 Broad sense heritability estimates for drought resistant traits, traits related to N_2 fixation and *A. flavus* infection under drought stress of four crosses of peanut combined for two years in dry season 2005/2006 and dry season 2006/2007.

Peanut crosses	SLA	SCMR	Reduction in pod yield	Reduction in total dry weight
ICGV 98308 x KK 60-3	0.93	0.89	0.86	0.93
ICGV 98308 x Tainan 9	0.81	0.96	0.92	0.81
ICGV 98324 x KK 60-3	0.91	0.92	0.87	0.85
ICGV 98324 x Tainan 9	0.95	0.96	0.96	0.86
Peanut crosses	Nodule dry weight	N_2 fixed	Reduction in N_2 fixed	*A. flavus* infection
ICGV 98308 x KK 60-3	0.50	0.92[1/]	0.58[1/]	0.49[1/]
ICGV 98308 x Tainan 9	0.75	0.92	0.26	0.57
ICGV 98324 x KK 60-3	0.50	0.87	0.48	0.52
ICGV 98324 x Tainan 9	0.50	0.90	0.53	0.57

[1/] = Data from the 2005/2006 dry season only.

Table 2.9 Phenotypic and genotypic correlation of drought resistant traits with pod yield, with traits related to nitrogen fixation and with *A. flavus* infection in four crosses (140 families) of peanut in the F_7 generation under well-watered conditions (FC) in dry season of 2005/2006.

Character	Specific leaf area (SLA)	(SCMR)[1/]	Reduction in total dry weight	Reduction in pod dry weight
Phenotypic correlation (r_P)				
Pod yield	0.17**	0.22**	-0.33**	-0.58**
Total dry weight	0.20**	0.13**	-0.57**	-0.52**
Fixed N	0.09*	0.13**	-0.39**	-0.36**
Nodule dry weight	0.05	0.01	-0.14**	-0.17**
A. flavus infection	0.23**	-0.20**	-0.01	0.22**
Genotypic correlation (r_G)				
Pod yield	0.19**	0.22**	-0.38**	-0.58**
Total dry weight	0.23**	0.14**	-0.55**	-0.55**
Fixed N	0.10*	0.14**	-0.38**	-0.40**
Nodule dry weight	0.05	0.01	-0.17**	-0.19**
A. flavus infection	0.33**	-0.28**	0.00	0.32**

[1/] SPAD chlorophyll meter reading

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

Study 2-4. Gene effects for specific leaf area and harvest index in peanut

B. Suriharn, A. Patanothai and S. Jogloy

Specific leaf area (SLA) and harvest index (HI) are traits that might be used for indirect selection for improving yield, particularly under water limited conditions. SLA is related to photosynthetic efficiency and drought tolerance. It is simple and inexpensive to measure, thus, has been suggested to be used as a surrogate for selecting for water use efficiency (WUE) in peanut.

Harvest index (HI) is directly related to yield as it represents the proportion of total biomass partitioned into grain. Increased HI has been a major factor in the improvement of grain yield in many crops. In peanut, high WUE and HI can lead to improvement in yield.

To formulate an appropriate breeding strategy for a particular trait, a good understanding of its inheritance is required. The objective of the present study was to determine gene effects for SLA and HI in three peanut crosses.

Materials and methods

Three peanut genotypes varying in SLA (ICGV 86388, IC 10 and KK 60-1) were selected for used as parents to generate seven populations in different generations (P1, P2, F1, F2, F3, BC11S and BC12S) for this study. These populations were grown in a field experiment using a group balance block design with six replications was. The three crosses formed three treatment-groups and the seven populations of each cross were treatments within each group. Measurement of SLA was done on every plant in each plot at 70 days after planting. At maturity, shoot and pod weight were recorded and then harvest index was calculated.

For each character, a generation means analysis was separately conducted for each cross to determine additive, dominant and epistatic gene effects following Mather and Jinks (1971) using their coefficients for different generations based on F-infinity metric. The relative importance of different gene effects was estimated by partitioning the regression sum of squares of the best-fit model into individual parameters, each with one degree of freedom. Percentages of the total regression sum of squares attributable to individual gene effects were calculated to indicate their relative contribution to the variations in SLA and HI among different generations of the crosses.

Results

For SLA, additive gene effects were predominant in all three crosses, accounting for 80-95% of total genetic variability (Table 2.10). The dominance and epistatic gene effects contributed to very small portion of total genetic variability. For HI, additive gene effect also accounted for the largest proportion of total genetic variation in all three crosses, ranging from 63-76% (Table 2.11). The additive x additive gene effect accounted for 21% in the cross ICGV 86388 x KK 60-1 and 11% in the cross ICGV 86388 x IC 10. Both additive and additive x additive gene effects are fixable. These two types of gene effects accounted for almost all of total genetic variance in these crosses, leaving a small portion to the additive x dominance gene

effect that is non-fixable. No dominance or dominance x dominance gene effect was detected in any of the crosses.

It was concluded that gene effects governing the inheritance of both SLA and HI were largely additive, and that selection for high SLA and HI values in these crosses would be effective even in early generations.

Table 2.10 Variability (%) accounted for by different gene effects for SLA in three crosses of peanut.

Gene effect [a]	ICGV 86388 x KK 60-1 [b]	ICGV 86388 x IC 10 [b]	IC 10 x KK 60-1 [b]
a	94.90	79.84	94.29
d	0.06	NS	NS
aa	NS	7.53	NS
ad	4.20	10.02	3.18
dd	0.70	NS	NS

[a] a = Sum of additive effects, d = Sum of dominance effects, aa = Sum of additive x additive epistatic effects, ad = Sum of additive x dominance epistatic effects, dd = Sum of dominance x dominance epistatic effects.
[b] NS = Non significant.

Table 2.11 Variability (%) accounted for by different gene effects for harvest index (HI) in three crosses of peanut.

Gene effect [a]	ICGV 86388 x KK 60-1 [b]	ICGV 86388 x IC 10 [b]	IC 10 x KK 60-1 [b]
a	76.41	67.80	62.83
d	NS	NS	NS
aa	21.04	11.12	NS
ad	1.56	17.38	NS
dd	NS	NS	NS

[a] a = Sum of additive effects, d = Sum of dominance effects, aa = Sum of additive x additive epistatic effects, ad = Sum of additive x dominance epistatic effects, dd = Sum of dominance x dominance epistatic effects.
[b] NS = Non significant.

Publication

Suriharn, B., A. Patanothai and S. Jogloy. 2005. Gene Effects for Specific Leaf Area and Harvest Index in Peanut (*Arachis hypogaea* L.). Asian Journal of Plant Sciences. 4(6): 667-672.

Study 2-5. Isolation and identification of peanut leaf proteins regulated by water stress

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S. Jogloy and A. Pathanothai

Drought stress brings about physiological and morphological changes in peanut crop allowing the plant to maximize water uptake while minimizing water lost (Wright and Nageawara Rao, 1994). However, the cellular mechanism of responses in peanut plants to water stress is not well documented. Under water stress conditions, signaling cascades are initiated leading to the activation or suppression of gene expression (Bray, 2004; Yamaguchi-Shinozaki and Shinozaki, 2006). Some of the gene products are regulatory and functional proteins working in concert to cope with oxidative stress and cellular abnormalities (Bray et al., 2000. The objective of this study was to isolate and identify peanut leaf proteins regulated by water stress conditions.

Materials and methods

A drought-susceptible peanut variety, Khon Kaen 4, was grown in a phytotron climate simulator. On day 30 after seedling emergence, plants were subjected to water stress treatment and compared to control plants. Leaf samples were harvested, and leaf water potential and relative water content were measured for both water stress and control treatments. The first fully expanded leaf for protein separation. The second fully expanded leaf was used for determining relative water content The third up to fifth fully expanded leaves on the main stem were used for leaf water potential determination.

Total proteins in leaves were extracted using lysis buffer. The protein extracts were cleaned using a Clean Up Kit (Amersham Biosciences). Individual 13-cm IPG strips were rehydrated overnight with 250 µl rehydration buffer containing 30 µg proteins in a reswelling tray at 20ºC. Isoelectric focusing was carried out at 20ºC using Amersham Biosciences Multiphor II system equipped with cooling system and Amersham Biosciences 3500XL power supply. Proteins in each leaflet sample were separated in duplicated gels.

Proteins in gels were visualized by silver nitrate staining The gels were scanned with ImageScanner equipped with Labscan version 5.0 (Amersham Biosciences). Image analysis of gels was performed using ImageMaster 2D Platinum 5.0 (Amersham Biosciences). Differential expression of proteins in peanut leaves under adequate water supply and water stress was determined. Water-stress regulated proteins with M_r and pI were recorded. M_r and pI were used for searching protein identities using TagIdent of the ExPasy tools.

Results

Relative water contents of non-stressed plants were between 94% and 96%. Withholding watering for 4 to 6 days caused a large reduction in relative water contents from 97% to 69% (Figure 2.6A). Leaf water potential of plants receiving adequate water supply were between -0.06 and -0.09 MPa. Under stress conditions, leaf water potential declined from -0.06 MPa to -0.27 MPa (Figure 2.6B).

Annotation for proteins using M_r and pI online resulted in at least six homologous proteins that could be putative proteins regulated by water deficit in peanut leaves (Table 2.12). The five proteins; 133, 190, 260, 277 and 33, were protein homologs in *Arabidopsis thaliana* (*At*) and only one protein, 357, was protein homolog in *Zinnia elegans* (*Ze*). M_r, pI and protein accessions were indicated. The homologous protein 190 was identified as serine/threonin-protein phosphatase PP 1 isozyme. The remaining homologous proteins were identified as chaperone protein DnaJ (133), peroxidase 43 precusor (260), SNF1-related protein kinase regulatory subunit beta-2 (277), auxin-responsive protein IAA29 (331) and caffeoyl-CoA O-methyltransferase (357) (Table 2.12).

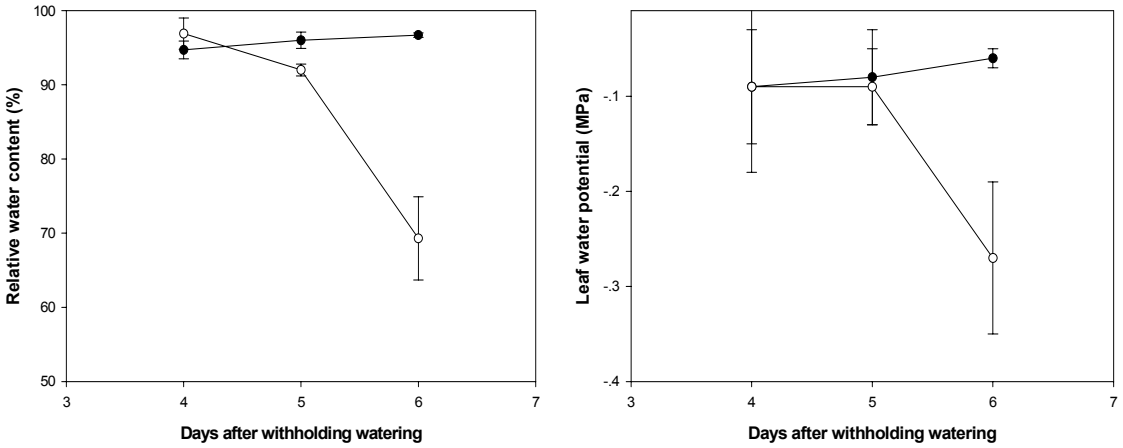


Fig. 2.6 Changes in relative water content (A) and leaf water potential (B) of peanut leaves variety Khon Kaen 4 during a period of water stress. Soil moisture contents in pots were maintained at field capacity (—●—) or under water deprivation (—○—). Vertical bars represent standard deviations.

Table 2.12 Properties of proteins regulated by water stress and their protein homologs.

Protein no.	pI/ M_r (kD)	Protein homologs		
		Identity	Species/Protein Accession	pI/ M_r
133	5.14/45	Chaperone protein DnaJ	*At*/Q8GYX8	5.17/44.7
190	5.14/36	Serine/threonine-protein phosphatase PP 1 isozyme	*At*/P48482	5.16/35.5
260	5.34/32	Peroxidase 43 precursor	*At*/Q9SZH2	5.36/32.7
277	5.18/31	SNF1-related protein kinase regulatory subunit beta-2	*At*/Q9SCY5	5.17/31.9
331	5.8/28	Auxin-responsive protein IAA29	*At*/Q93WC4	5.88/28.6
357	5.88/27	Caffeoyl-CoA O-methyltransferase	*Ze*/Q41720	5.88/27.6

Publication

Akkasaeng, Chutipong, Napaporn Tantisuwichwong, Issariya Chairam, Narumon Pakrongrak, Sanun Jogloy and Aran Patanothai. 2007. Isolation and identification of peanut leaf proteins regulated by water stress. Pakistan J. of Biological Science 10(10): 1611-1617.

Study 2-6. Developing DNA markers for drought tolerance selection in peanut

N. Tantisuwichwong, S. Boontang, C. Rattanamalee, C. Akkasaeng,
S. Jogloy and A. Pathanothai

Peanut is grown largely in the semi-arid tropics where rainfall is erratic (Wright and Nageswara Rao, 1994). It is often affected by drought stress during crop growth, resulting in the severe reduction in pod yield (Roy *et al*., 1988). The use of drought resistant cultivars is the most promising strategy to cope with this problem (Holbrook and Stalker, 2003). Nuatiyal *et al* (2002) demonstrated that peanut genotypes with low specific leaf area (SLA) under drought stress could maintain higher relative water content (RWC) and more steady growth than those with high SLA. Peanut genotypes with low SLA also had higher Riburose – 1,5-bisphosphate carboxylase - oxygenase (Rubisco). This enzymes is well known to involve in photosynthesis pathway. SLA is closely correlated with water use efficiency (WUE) and has positive correlation with carbon isotope discrimination (CID) (Craufurd *et al*., 1999; Asalatha *et al.*, 1999). Upadhyaya (2005) suggested the use of SLA as a selection criterion for drought resistance. Although it is important, this character is highly variable in term of evaluation times and leaf ages. Furthermore, both additive and non-additive gene effects are involved in the inheritance of the traits depending on materials used (Nigam *et al*., 2001).

DNA markers provide a useful tool for gene mapping and selection for important characters. This can speed up selection program than conventional methods because it can be conducted in early generation of segregating population with more accuracy (Stalker and Mozingo, 2001). Thus, in this study, the markers associated with specific leaf weight (SLW) and RWC will be identified. This information will be useful for peanut breeding programs aiming to develop peanut cultivars with resistance to drought.

The objectives of this study were (1) to evaluate genetic variability among peanut lines different in SLW and RWC using DNA markers, and (2) to identify DNA markers associated with SLW and RWC under drought stress in peanut**.**

Materials and methods

1. Evaluation of four peanut genotypes for SLW, RWC and DNA polymorphism

Pot experiment was conducted under field conditions for two seasons. Two water regimes (field capacity and 1/3 available soil water) were imposed to the crop. Four peanut genotypes (ICGV98324, ICGV98353, ICGV98305 and KK4) were laid out in a 2 x 4 factorial in RCBD with 6 replications. Plants were grown in cylindrical pots with 0.75 m in length and 0.25 m in diameter. Soil was separated in three columns,

and water was supplied to each soil column through plastic tubes. Data were recorded for SLW and RWC at 40, 50 and 60 day after emergence (DAE).

Leaf samples were harvested, and DNA was extracted from leaf tissue of 9 – day old plants. DNA was quantified either by visual comparison with lambda DNA on ethidium bromide stained agarose gel. Simple sequence repeat (SSR) and Random Amplified Polymorphic DNA (RAPD) were used to characterize polymorphism between the peanut lines. PCR products were separated in 8% polyacrylamide gel and visualized with silver staining. The dendrogram was used to determine the cluster of genotypes using the Un-weighted Pair Group Method with Arithmetic Averages (UPGMA) running in PHYLIP V6.3 program.

2. Identification of DNA markers linked to specific leaf weight and relative water content under drought stress in peanut

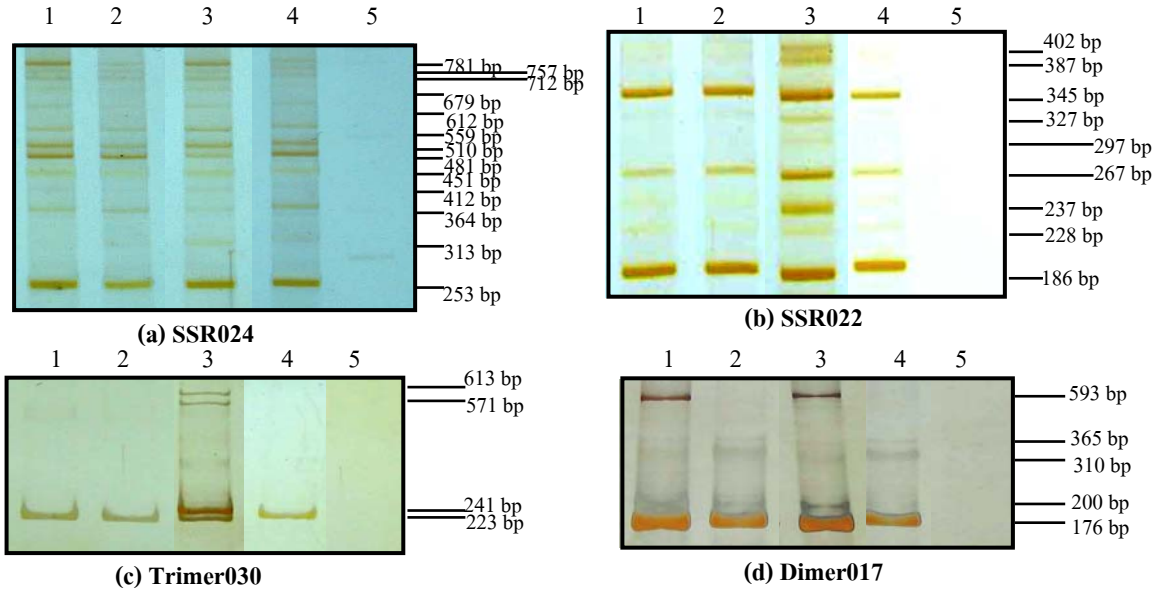
Peanut genotypes with high (KK 4) and low (ICGV 98324) SLW and RWC were crossed to produce F_1 hybrid. The resulting F_1 hybrid was further self-pollinated to produce an F_2 population from which the 150 F_2 plants that were used as mapping population were derived.

Two pot-experiments were conducted. In experiment 1, two parental lines, F_1 hybrid and 129 F_2 plants were planted. Water stress (1/3 AW) was imposed between 20-60 DAE. In experiment 2, two parental lines, an F_1 cross and 150 $F_{2:3}$ plants were planted. Pots were arranged in RCBD with 4 replications. Water deficit was withhold between 20-60 DAE with 1/3 AW. Fully expanded leaves were taken from the second node from the top of main stem during 9.00-11.00 h. SLW and RWC were evaluated at 60 DAE.

Leaves from F_2 individuals and parental lines were extracted for genomic DNA. SSR and RAPD markers were screened for polymorphisms between parental lines. BSA were produced by pooling equal quantities of DNA from 10 putatively tolerant plants (high SLW and RWC) and 10 putatively susceptible plants (low SLW and RWC). Polymorphic markers between the parents were selected to investigate in 1) the tolerant parent, 2) the susceptible parent, 3) pooled DNA of the most tolerant F2 plants and 4) pooled DNA of the most susceptible F_2 plants. Only bands present in tolerant parent and pooled of the most tolerant F_2 plants were linked to SLW and RWC. Markers from BSA were used to characterize all 150 F_2 progenies. Linkage group analysis and QTL mapping were performed using MAPMAKER software.

Results

A total of 160 alleles from 46 primers were obtained with an average of 3.48 allele numbers per locus. H value varied from 0 to 0.94, giving a mean number of 0.82. PIC value varied from 0 to 0.92, giving a mean number of 0.76. Among 46 primers, 12 were found to be polymorphic; Dimer001, Dimer013, Dimer017, Dimer018, SSR017, Trimer050, Trimer046, Trimer053, Trimer030, SSR022, SSR024 and PPSSR03. For example, four polymorphic primers are shown in Figure 2.7 and Table 2.13.



(a) primer SSR024, (b) primer SSR022, (c) Trimer030 , (d) primer Dimer017
Lane 1: ICGV 98353 2: ICGV 98305 3: Khon Kaen 4
4: ICGV 98324 5: sterile distilled water

Fig. 2.7 Detection of polymorphic eSSR in four peanut cultivars using four primer pair, SSR024, SSR022, Trimer030 and Dimer017, specific to an eSSR.

Table 2.13 Allele size, allele frequencies and PIC of some polymorphic eSSR markers

Primer name (locus)	Allele size and allele frequencies in parenthesis										H	PIC
	1	2	3	4	5	6	7	8	9	10		
SSR024	253 (0.09	313 (0.02)	364 (0.09)	412 (0.04)	451 (0.09)	481 (0.09)	510 (0.09)	559 (0.09)	612 (0.09)	679 (0.07)	0.94	0.92
SSR022	188 (0.17)	228 (0.17)	237 (0.17)	267 (0.17)	297 (0.04)	327 (0.04)	345 (0.17	387 (0.04)	402 (0.04)	-	0.89	0.85
Trimer030	223 (0.14)	241 (0.14)	571 (0.14)	613 (0.57)	-	-	-	-	-	-	0.71	0.61
Dimer017	176 (0.36)	200 (0.10)	310 (0.18)	365 (0.18)	593 (0.18)	-	-	-	-	-	0.84	0.76

- = null alleles

There were significant differences between parental lines under drought stress ($P < 0.01$). Transgressive segregation resulted in wide range of SLW value in progeny, ranging from 57.75 g m^2 ($F_{2:58}$) to 32 g m^2 ($F_{2:2}$), compared to 53.545 g m^2 for KK4 and 33.75 g m^2 for ICGV98324. The mean RWC of plants ranged from 90.25 (ICGV98324) to 60 ($F_{2:61}$), while in KK4 and F_1 were 65 and 68, respectively.

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Sub-Project 3.

Utilization of Peanut Stover and Other Crop Residues to Improve Crop Productivity

Dr. Banyong Toomsan

Sub-project Leader

Legumes are widely known through their ability to fix atmospheric nitrogen when they are symbiotically living with bacteria in gerera *Allorhizobium, Azorhizobium Rhizobium, Bradyrhizobium, Mesorhizobium and Sinorhizobium* (Giller, 2001). The fixed N can reduce the amount of N fertilizer requirement of the hosts and thus help conserve soil nitrogen (sparing effect). The sparing N and residue N (when ploughed under) can benefit the succeeding crops and lowering their N fertilizer requirements. Inclusion of legumes in cropping systems is, thus, desirable for long-term sustainability of land productivity.

The amount of N_2 fixed by legumes varied widely ranging from 34 to 897 kg N ha^{-1} $year^{-1}$ depending on types of legumes (FAO, 1984), cultivars of legumes (Giller *et al.*, 1987; McDonagh *et al.*, 1995; Kucey and Toomsan, 1988; Toomsan *et al.*, 1995), rhizobia strains (Kucey *et al.*, 1988) and environments (Giller, 2001; Sprent and Sprent, 1990). Not all legumes are soil fertility (nitrogen) builder. This depends on the amount of N removed in economic yield (% nitrogen harvest index, % NHI) and the amount of nitrogen fixed (% nitrogen derived from air, % Ndfa). A grain legume can be a soil fertility building crop only when its % NHI is lower than its % Ndfa, providing that its stover be returned to the soil. In this context, peanut is a soil fertility building crop because the amount of N removed in economic yield (%NHI) is less than the amount of fixed nitrogen (%Ndfa) (McDonagh *et al.*, 1993; McDonagh *et al.*, 1995; Toomsan *et al.*, 1995). Peanut stover yields of 3-6 tons ha^{-1} were reported to contain 60–160 kg N ha^{-1}, and when returned to the soil could increase growth and yield of succeeding crops such as maize (Suwanarit *et al.*, 1986; McDonagh *et al.*, 1993; Toomsan *et al.*, 1993; McDonagh *et al.*, 1995; Toomsan *et al.*, 1995) and cassava (Toomsan *et al.*, 2002).

Management of nutrient release from crop residues to meet crop demands is a major challenge for research. Most of the studies that showed benefit of peanut stover to succeeding crops were conducted either by growing succeeding crops immediately after peanut harvest or by storing peanut stover and applying them just before planting the succeeding crop. The practice of growing succeeding crops immediately after peanut harvest can be done only in areas where rainy season is long. However, in areas where the rainy season is short and only one crop can be grown, the peanut stover must be either left in the field or stored in the shade. Storing peanut stover requires extra labor and space due to its bulkiness. Management of stover during the period from peanut harvesting to planting the succeeding crop in the following year is, therefore, important. What happens to the nutrients in peanut stover when left in the field? Would it still be beneficial to succeeding crop when left in the field for 6-8 months? What is the role of weeds in nutrient conservation during the fallow period? What is the fate of N in peanut residue during the fallow period? How much is it absorbed by the succeeding crop? These are the questions that need to be answered in order to help us utilize peanut residue N effectively and thus help conserve the environment. Research

conducted under this sub-project has been aiming at finding answers to these questions. The cropping systems investigated include peanut in sugar cane system, peanut in paddy system and peanut in rotation with maize.

Five studies were conducted under this sub-project:

3-1. Effect of peanut and other legumes for sugarcane production under dry season planting system.

3-2. Effect of sugarcane stover management on growth and yield of some grain legumes and their residual N effect on growth and yield of succeeding sugarcane.

3-3. Effect of peanut residues and rice straw management on growth and yield of succeeding rice.

3-4. Effect of soybean stover on growth and yield of rice.

3-5. Effect of peanut stover application and weed management on growth and yield of maize in the next rainy season.

Study 3-1. Effects of peanut and other legumes for sugarcane production under dry period planting system

Srisuda Thippayarugs and Banyong Toomsan

Sugarcane is an important economic crop of Northeast Thailand. In this area, sugar cane is generally grown in October and harvested 14 months later for the cane-planted crop. Generally, one more ratoon crop can be harvested, and harvesting time is in December to April of the following year. After harvesting the ratoon crop, there is a lag period of 4–8 months before planting the next sugar cane crop. During this period, the fields are generally left idle and are vulnerable to erosion. A logical approach is to grow legumes during this period to gain benefit not only from nitrogen fixed by the legumes but also the improvement of soil physical properties from legume residues.

Many studies have shown that the use of green manure legumes can increase the yield of a subsequent field crop and reduce the requirements for inorganic N fertilizer. There are many legumes that can be grown during fallow periods as green legumes. Peanut is one of the few grain legumes that grown successfully in this area as the sandy texture and long dry spell. After harvesting it leaves significant amount of green residues as well as economic yield. Other legumes that can be used for green manure are pigeonpea, sunnhemp, jackbean and leguminous weeds (indigo and hairy vetch) that grows vigorously in the farmer field.

The goal of this study was to investigate the benefit of introducing grain or green manures during the fallow period to improve soil fertility. The objectives were:

1. To study nodulation, N_2 fixation and yield of peanut, pigeon pea, sun hemp, sword bean, indigo and hairy vetch grown after sugar cane.
2. To study the residual N benefits of different legumes on growth and yield of sugar cane under field and glasshouse conditions.
3. To study decomposition and nitrogen release patterns of different legume residues under both field and laboratory conditions.

4. To quantify the amount of N in legume residues taken up by succeeding sugar cane.

Materials and methods

This study consists of three experiments:

Experiment 1. Utilization of residues of peanut and other legumes to partially supply nitrogen to the succeeding sugar cane

Six legumes namely peanut, pigeon pea, sun hemp, sword bean, indigo and hairy vetch were grown during June to September after sugar cane harvest. Growth, nodulation and nitrogen fixation (^{15}N isotope dilution) were measured. Sugar cane cultivar UT1 was grown after the legumes in October. Growth and yield of sugar cane were measured at 6 months after planting and at final harvest. Total N uptake and N recovery from legume residues were quantified using ^{15}N labeled residues. The experiment was conducted in 2000 in which the legumes were planted without chemical fertilizers except the peanut plots. The experiment was repeated in 2001 in which chemical fertilizers were applied to all the legumes at the rate of 56 kg P_2O_5 ha^{-1} and 37 kg K_2O ha^{-1}.

Experiment 2. Interactions in decomposition and N mineralization between tropical legume residue components

This experiment was conducted using 2 L pot. Legume residues at the rate equivalent to 6.25 Mg ha^{-1} were incubated with 200 g of soil, and soil moisture was adjusted to 60% of field capacity. The legume residues were stems, leaves, leaf litters, roots and the mixture of stems leaves and leaf litter using the ratio in actual field condition of three legumes, peanut, pigeonpea and hairy indigo. Decomposition and N mineralization were determined at 7, 14, 28, 42, 63, 84, 105 and 133 days after incubation. Decomposition was determine from residues remained at the date of determination and N mineralization determined from analyzing ammonium N and nitrate N in the soil. Interaction of different plant parts in the mixed components was determined from deviation of actual effect from predicted effect. Predicted effect was calculated from single component effect using weighted mean of actual ratio.

Experiment 3. Effects of tropical legume for N dynamic, C emission and sugarcane growth and nutrient content

The residue of leguminous crops including grain legume, peanut (*Arachis hypogaea* L.), common green manure legumes, pigeonpea (*Cajanus cajan* (L.) Millsp.), jackbean (*Canavalia ensiformis* (L.)), sunnhemp (*Crotalaria juncea* (L.)) and two local leguminous weeds, *Crotalaria striata* and hairy indigo (*Indigofera hirsuta*) (Harvey) were investigated for their contribution to mineral N dynamic and C emission. Nutrient contents and growth of sugarcane were also investigated in pots using the green manure residues and mineral N application as $(NH_4)_2SO_4$ equivalent to 49 kg ha^{-1}.

The experiment was conducted in 28 L pots with two rates of legume residues. All of the legume residues were added at the rate equivalent to 6.25 Mg ha^{-1} and only peanut, pigeonpea and hairy indigo residues were additionally added at the rate equivalent to 12.50 Mg ha^{-1}. Altogether, there were nine treatments of incorporating legume residues, one treatment with chemical fertilizer N, and a non-treated control.

All the treatments were replicated four times and received chemical P_2O_5 and K_2O fertilizers at the rate equivalent to 49 kg ha^{-1}.

Results

Effect of peanut and other legumes on soil fertility for sugarcane production under dry period planting system

In both years, sunnhemp produced the highest biomass, i.e., 12 Mg ha^{-1}. In the first year experiment hairy indigo and pigeonpea biomass was 11 and 9 Mg ha^{-1}, respectively, while the rest ranged from 5-7 Mg ha^{-1}. In the second year, with added fertilizers, the legumes produced higher biomass, ranging from 8-11 Mg ha^{-1} (Table 3.1).

In the first year, N content was highest in hairy indigo, 150 Mg ha^{-1}, followed by peanut, 142 Mg ha^{-1}, but was lowest in jackbean, 59 Mg ha^{-1}. In contrast, in the second year, N content was highest in jackbean residue, 220 Mg ha^{-1}, while N contents in other legumes were lower, ranging from 141 to 165 Mg ha^{-1} (Table 3.1).

The assessment of N fixation of the legumes by ^{15}N dilution method showed that N fixation was highest in hairy indigo and jackbean, being 81% of their total N, and was lowest in *C. striata*, being 61% of their total N.

Evaluation of decomposition using litterbag showed that most legume residues showed fast decomposed at early stage (49 days after burial) with non-nod peanut was the fastest, 0.016 day^{-1}, and pigeonpea was the slowest, 0.007 day^{-1}. After 134 days, the residues decomposed slowly. After 358 days, 24 % of pigeonpea residue still remained, but the remaining residues of other legumes were 7-10 %.

The assessment of N recovery by ^{15}N enriched method showed that N recovery from jackbean residues was highest, being 87 %, of which 62 % was still in the soil especially at 0-20 cm depth (43 %), 15 % was in sugarcane plant, and 9 % was in the undecomposed residues. Peanut residue showed lowest N recovery, i.e., 47%.

Sugarcane yield was significantly higher with adding either full rate of chemical fertilizer or half rate of chemical fertilizer in the plots that incorporated legume residues than without adding any fertilizer with and without incorporated weed residues. The highest yield (112 Mg ha^{-1}) was obtained from the treatment that received the full rate of N fertilizer and all plant residues were removed. However, this yield level was not significantly different from those obtained from the plots receiving peanut as well as pigeonpea and hairy indigo residues (Table 3.1).

Table 3.1 Legume residue biomass, N content, N fixation and sugarcane yield in the experiment conducted in 2000 and 2001.

Legumes	Biomass DW of residues (kg ha^{-1})		N (kg ha^{-1})		N fixed (%)	Millable cane FW (Mg ha^{-1})	
	2000	2001	2000	2001	2000	2000	2001
Non-nod peanut	1,636 e		21 c			107 ab	
Peanut	5,141 de	7,227 c	88 abc	147 b	80	105 ab	68
Peanut+PK	6,639 cd		142 a		74	100 abc	
Pigeonpea	9,382 abc	10,295 ab	115 ab	141 b	78	96 abcd	69
Jackbean	4,626 de	10,268 ab	59 bc	220 a	81	96 bcd	71
Sunnhemp	12,074 a	12,309 a	117 ab	149 b	79	94 bcd	66
C. striata	7,216 bcd	9,745 b	82 abc	165 b	61	94 bcd	71
Hairy indigo	10,917 ab	9,613 b	150 a	146 b	81	102 abc	59
Weed+N	3,452 de	6,407 c	26 c	81 c		106 ab	56
Weed	4,376 de	6,403 c	31 c	82 c		81 d	55
Bare soil+N						112 a	
Bare soil						87 cd	
F-test	**	**	**			*	ns
CV(%)	30	14	46			11	20

$^{ns, *, **}$ Non-significant and significant at $P < 0.05$ and $P < 0.01$, respectively.

Interactions in decomposition and N mineralization between tropical legume residue components

Chemical characteristics of the residues were different among plant species and plant components. Peanut residues had better quality with high N and low lignin and polyphenol, while pigeon pea residues had poorer quality with low N and high lignin, and hairy indigo residue quality were intermediate of N and lignin but high in poly phenol. Among the plant components, quality of leaves were considered the best as they were high in N and low in lignin even though they were high in poly phenol. Leaf litter had characteristic with lower N, C and polyphenol, and higher in acid-detergent fiber (ADF), lignin than green leaves. Stems and roots were lowest in N content.

Peanut residues decomposed fastest and showed the largest N release, being in agreement with their high N concentration and low ADF:N ratio. Hairy indigo residues that having higher in polyphenol than pigeonpea was decomposed faster because of the higher N and lower lignin content. Leaves showed initially the fastest dry weight loss even though pigeonpea leaves were strongly retarded in later stage. Stems of peanut decomposed relatively fast while pigeonpea and hairy indigo stems were retarded during the early stages of incubation. Leaf litters of peanut and pigeonpea was slowest among the plant parts tested, while leaf litter of hairy indigo did not followed this pattern. Decomposition of the mixture of plant parts followed the decomposition pattern of its main component (Fig. 3.1).

Net N mineralization in all peanut components was always positive, while most components of pigeonpea and hairy indigo except leaves showed negative net N mineralization, indicating immobilization of mineral N even though some showed positive in the later stage of incubation (Fig. 3.2).

The interactions were small in the mixtures of peanut and pigeonpea as high proportion of low quality of stems that was a major component. While mixture of hairy indigo showed positive interaction effect on dry weight loss and also N mineralization. Plant components of hairy indigo were of intermediate chemical quality compared to the other two legumes and appeared to provide the largest opportunities for interaction.

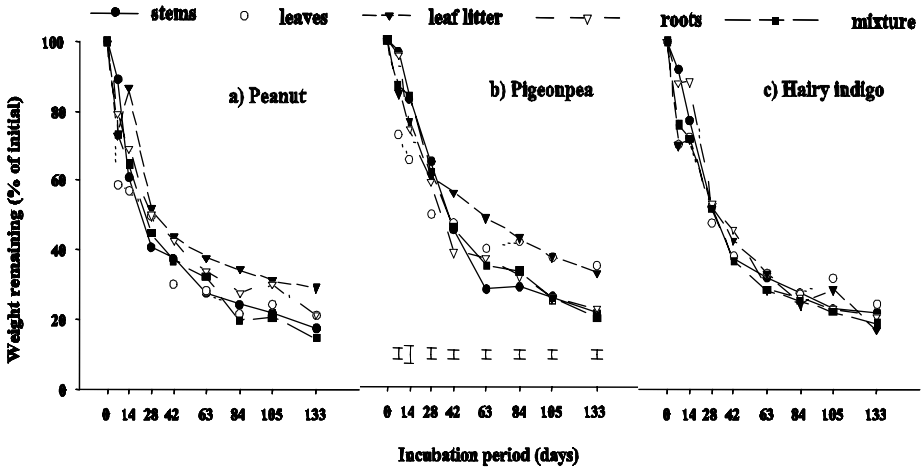

Fig. 3.1 Percent weight remaining of initial weight added of five legume components of a) peanut, b) pigeonpea and c) hairy indigo.

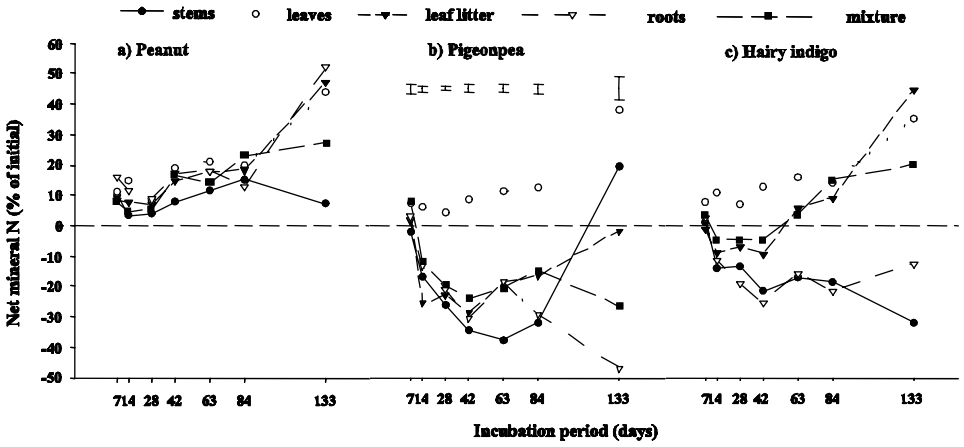

Fig. 3.2 Percent of net mineral N released of the initial added of five legume components of a) peanut, b) pigeonpea and c) hairy indigo

Effects of tropical legume for N dynamic, C emission and sugarcane growth and nutrient content

Peanut residues had good chemical quality for decomposition and N mineralization with high N concentration but low lignin and polyphenol concentration as well as C:N ratio. At 53 days after mixing the soil with legume residues and chemical fertilizers, mineral N was lower in the plot with peanut residues than those with sunnhemp and chemical N fertilizer. After this period, mineral N was the highest in the treatment with peanut residues equivalent to 12.50 Mg ha^{-1}.

Sugarcane biomass was highest in the plot receiving 12.50 Mg ha^{-1} of peanut residues, but the amount obtained was not significantly different from those plots that received peanut, sunnhemp, or *C. striata* residues at the rate of 6.25 Mg ha^{-1}. On the other hand, yield obtained from peanut residue application at the rate equivalent to 12.50 Mg ha^{-1} was significantly defferent from those of other treatments including the treatment with chemical N fertilizer (Table 3.2).

Application of peanut residues resulted in the highest levels of N, K and Mg in the sugarcane plant, while application of the hairy indigo gave the highest P content, and chemical N fertilizer application gave the highest in Ca content. CO_2 emission was significantly higher after adding legume residues than with mineral fertilizer N. The emissions increased with rate of residue incorporation. Pigeonpea residues at 12.50 Mg ha^{-1} showed the highest CO_2 emission.

Table 3.2 Effects of adding legume residues on biomass production and nutrient contents of sugarcane.

Legume residues	Added legume dry wt. (kg ha^{-1})	Sugarcane biomass DW (g pot^{-1})	N	P	K	Ca	Mg
			(mg pot^{-1})				
Peanut	6.25	296 abc	942 bc	334 abcd	2155 bc	334 bc	452 bc
Pigeonpea	6.25	259 bc	864bc	320 bcd	1787 cd	331 bc	413 bc
Hairy indigo	6.25	258 bc	848 bc	315 cd	1844 cd	310 bc	413 bc
sunnhemp	6.25	292 abc	955 bc	338 abc	1664 cde	362 abc	493 ab
jackbean	6.25	279 bc	899 bc	300 cd	1546 de	337 bc	441 bc
C. striata	6.25	280 abc	829 bc	313 cd	1923 cd	272 c	428 bc
Peanut	12.5	348 a	1340 a	389 ab	2784 a	401 ab	577 a
Pigeonpea	12.5	285 abc	977 bc	369 abc	2066 bcd	296 bc	449 bc
Hairy indigo	12.5	312 ab	1011 b	401 a	2561 ab	250 c	459 abc
Soil+N	0	252 bc	951 bc	275 d	963 f	475 a	432 bc
Soil	0	233 c	722 c	266 d	1172 ef	328 bc	367 c
F-test		**	**	**	**	*	**
CV%		12	15	11	15	23	14

ns, *, ** Non-significant and significant at $P < 0.05$ and $P < 0.01$, respectively.

Published paper

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Study 3-2. Effect of sugarcane stover management on growth and yield of some grain legumes and their residual N effect on growth and yield of succeeding sugarcane

Saowakon Hemwong and Banyong Toomsan

Burning of sugarcane residues either before or after sugarcane harvest is widely practiced in many tropical countries. However, residue burning may adversely affect soil fertility due to the fact that it causes losses of some nutrients and organic matter over time. Recently, sugarcane producers have been required to adopt alternative sugarcane stover management practices (e.g. stover retention).

Sugarcane is usually grown under rainfed conditions. In northeast of Thailand only one or two ratoon crops may be harvested due to poor fertility of the very sandy soils. Here, sugarcane is generally planted during October to December and harvested in December to April of the following year. Thus, there is a time gap of 6-8 months between the last ratoon crop harvest and the next sugarcane planting. Farmers are now being encouraged not to burn sugarcane residues and to grow green manure legumes instead during this fallow period. However, green manure legumes do not generate an economic return and are not generally accepted by small farmers who have limited resources. Grain legumes such as peanut and soybean are other alternatives because they can provide cash income as well as improve soil fertility.

This study hypothesizes that mulching and incorporation of high C:N ratio sugarcane residues instead of burning can play a significant role in improving soil fertility, growth and yield and N_2 fixation of peanut and soybean during the fallow phase between two sugarcane cycles. These, in turn could contribute to increases in yield and N use efficiency of a following sugarcane crop when peanut and soybean residues are subsequently recycled.

The objective of this study were:

1. To assess the effects of burning, mulching and incorporation of sugarcane stover on soil N dynamics and then upon soil preparation (ploughing), its residual effect on N_2 fixation, growth and yield of peanut and soybean grown between two sugarcane cycles.
2. To assess the effects of mulching or incorporation of sugarcane stover as alternative to burning on soil N dynamics after sugarcane planting and sugarcane yield.
3. To assess residual nitrogen effect of previous fallow period treatments, i.e. grain legumes vs natural weed fallow, on N dynamics, growth and yield of succeeding sugarcane crop.
4. To compare the effectiveness of legume residues to mineral N fertilizer on N use efficiency, N recovery (and losses) from the system (^{15}N balance), soil fertility and sugarcane yield.

Material and methods

The experiment consisted of three phases: the sugarcane stover management phase, the legume crop phase and the sugarcane crop phase.

The sugarcane stover management phase included burning, mulching and incorporating sugarcane stover. In this phase, the experiment was conducted using a randomized complete block design with 4 replicates. In the legume crop phase, the experiment was a split-plot in RCBD with 4 replications. The main-plot treatments were 3 sugarcane stover management and the sub-plot treatments included of 2 grain legumes, i.e., peanut and soybean, and a fallow (control) treatment (Table 3.3). The sugarcane crop phases consisted of two periods, i.e., from planting to 6 months and from 6 months to harvesting. For the first period, the experiment conducted was a split plot in RCBD, with the main-plot treatments being 3 sugarcane stover management methods and the sub-plot treatments being 2 grain legumes and a fallow plot. For the secondary period, the experiment was a aplit-split-split plot in RCBD. The main-plot treatments were 3 sugarcane stover management methods, the sub-plot treatments were 2 grain legumes and a fallow, and the sub-sub plot treatments were with and without N chemical fertilizer.

Table 3.3 Treatments in the experiment during the legume crop phase.

Treatment	Main-plot	Sub-plot
1	Burned	Soybean
2	Burned	Peanut
3	Burned	Fallow
4	Mulched	Soybean
5	Mulched	Peanut
6	Mulched	Fallow
7	Incorporated	Soybean
8	Incorporated	Peanut
9	Incorporated	Fallow

After sugarcane harvest, 9.38 t DW ha^{-1} of sugarcane stover was applied to the field during February 19-20, 2004. Weeds were allowed to grow during sugarcane stover management (dry season), according to the treatments. They were harvested, weighed and incorporated into the soil before maize, groundnut and soybean planting. Samples were taken to determine dry weight and nitrogen contents.

Following the sugarcane stover management phase, the field was ploughed and seedbed prepared for the subsequent legume phase. Peanut cultivar Khon Kaen 60-1 and soybean cultivar SJ. 5 were planted during July 12, 2004 to October 2004. Peanut and soybean were sampled to assess nodulation and growth at 45 and 60 DAP.

After legume harvest the field was ploughed and seedbed prepared for the subsequent sugarcane phase. The sugarcane variety UT 1 was planted in 8 rows, 6 m long, 1.2 m apart each of 9.6 x 6 m^2. For the experiment during the period from sugarcane planting to 6 months (early November 2004 to May 2005), the main-plot treatments were the three previous sugarcane stover management treatments (burned, mulched and incorporated), and the sub-plot treatments were the previous soybean,

peanut, and fallow plots. At the beginning of the sugarcane phase, the two fallow plots were divided into fallow without mineral N and fallow with mineral N fertilizer (47 kg N ha^{-1} as $NH_4(SO_4)_2$). Legume treatments did not receive mineral N in order to test if they can substitute the commonly used basal mineral N fertilizer application at sugarcane planting. At the time of planting, phosphorus (P) at 21 kg P ha^{-1} and potassium (K) at 39 kg K ha^{-1} were applied to all plots as recommended for sugarcane.

At 6 months after sugarcane planting (May 2005), groundnut and soybean treatment plots were divided in half (4 rows, 6 m long) and half of plots received a topdressing of 47 kg N ha^{-1} as $NH_4(SO_4)_2$. Phosphorus (P) at 21 kg P ha^{-1} and potassium (K) at 39 kg K ha^{-1} were again applied to all plots as recommended for sugarcane. Total stalk numbers and height of sugarcane in each plot were recorded at 6, 8, 10, 12 and final harvesting (14 months after planting). Also, percentage of N and SPAD reading (Minolta SPAD-502 meter) of fully expanded functional leaves of sugarcane (4^{th} from the apex) were collected at 9 and 10 months after planting. Leaves, stem and tiller dry weights were determined at 6 months after planting and taken 4 hill $plot^{-1}$. The plants were cut at the ground level; tops were taken to determine dry weight and N, P, K and Ca contents. The final harvest was done on January 9-11, 2006. Sugarcane plant was separated into cane stem, dead leaves, top leave and tiller to determined dry weight and N, P, K and Ca contents. Also, ten stalk samples were taken and mixed from the upper, mid and lower inter-nodes for determination of the commercial content of sugar (CCS) value. Soils were sampled during and after sugarcane stover application, legume crop and sugarcane crop phases to determine mineral N and microbial biomass N.

Results

Increased soil microbial biomass N was observed when sugarcane stover was incorporated compared to burning or surface application at 14 days after stover management initiation. Thereafter, high N mineralization associated with stover incorporation was accompanied by a reduction in microbial biomass N, indicating that mineralized N was derived from microbial N turnover. However, upon ploughing after 96 days the different previous sugarcane stover management strategies had no significant ($P>0.05$) effect on net mineral N content and microbial biomass N during the subsequent legume period.

Although ^{15}N enrichment in control reference plants and plant N uptake indicated significant N immobilization effects due to stover retention persisting into the legume crop phase, the proportion of N derived from N_2 fixation (% Ndfa) or amount of N_2 fixed were not significantly different between sugarcane stover management treatments (Table 3.4). Soybean fixed more N_2 (78 %Ndfa, 234 kg N fixed ha^{-1}) than peanut (67 % Ndfa, 170 kg N fixed ha^{-1}) probably due to its larger N demand and a poorer utilization of soil N (64 vs 85 kg N ha^{-1}). Peanut led to a positive soil N balance while that of soybean was negative due to its high nitrogen harvest index. Legume residues returned 61 and 146 kg N ha^{-1} to the soil for soybean and peanut respectively, compared to only 34–39 kg N ha^{-1} by fallow weeds. At the end of the legume phase, sugarcane stover retention improved soil organic matter and N content.

The results suggested that although a change from burning to sugarcane stover retention led to alterations in N cycling and improved soil organic matter, it did not significantly affect N_2 fixation due to the uniforming action of ploughing and the extended time gap between stover incorporation and legume planting.

Table 3.4 Percentage atom^{15}N excess, N derived from air (%Ndfa) and total N_2 fixed by soybean and groundnut as affected by sugarcane stover management at final harvest

Stover management /Legume	% ^{15}N excess	% Ndfa	Total N_2 fixed (kg N ha^{-1})
Burned	0.1128	69	178
Mulched	0.0902	78	223
Incorporated	0.1025	71	204
SED	0.0056*	5^{ns}	21^{ns}
C.V. (%)	13	14	20
Soybean	0.0432	78	234
Peanut	0.0659	67	170
Non-nod peanut	0.1964	na	na
SED	0.0145**	2**	13**
C.V. (%)	35	6	15

na = not applicable
SED = standard error of the differences between means.
$^{ns, *, **}$ non-significant and significant at $P<0.05$ and $P< 0.01$, respectively.

Higher dry matter yield and N uptake were observed under stover burning than other mulching and incorporation treatments at 6 months after planting. However, the millable cane and sugar yield were positively affected by sugarcane residue mulching and incorporation (Table 3.5) suggesting remobilization of previously immobilized N during the later stages of plant development. Legumes had a positive residual effect on sugarcane yield compared to the fallow-N treatment. However, the two legumes induced a different response patterns due to their inherent different quality characteristics and the different amounts of residue N recycled. Both legume residues treatments resulted in higher tiller number and dry matter yield than the fallow–N and even the fallow+N treatments. However, the soybean treatment also improved subsequently sugarcane performance due to the extended later decomposition. This delayed decomposition led to a better conservation of soybean N in the system as less N losses, presumably due to leaching, and this was confirmed by the larger proportional residue ^{15}N recovery in the system.

The lower response of soybean compared to peanut can be explained by the lower amount of N recycled by soybean. Sugarcane dry matter yields under legume residues treatments were not different from that in the N fertilizer application treatment during the 6 months after planting. However, sugarcane yields under N fertilizer application treatment were greater than the non-N fertilizer treatment at final harvest. This suggests that legume residue N was available and enough to get good sugarcane growth until 6 months after planting, but thereafter it was not enough for sugarcane need until final harvest. ^{15}N recovery data indicated that sugarcane could absorbed

more N from the N fertilizer application treatment than the residue retention treatments at both 6 months after planting and final harvest. This might be due to N in the fertilizer treatment was readily available to the plant after application while those in plant residues need to be decomposed before becoming available.

Table 3.5 Effect of sugarcane stover management, plant residue and N fertilizer during the previous fallow phase on yield of sugarcane at final harvest (14 months after sugarcane planting).

Treatment	Stalk number ha^{-1}	Tiller numbr ha^{-1}	Millable cane ($t\ ha^{-1}$)	Stalk DW ($t\ ha^{-1}$)	Total DW ($t\ ha^{-1}$)	Sugar yield ($t\ ha^{-1}$)
Sugarcane stover management method						
Burned	7726	967	112	34	42	16
Mulched	8888	1127	125	39	48	18
	8666	1463	118	35	44	18
Incorporated						
SED	355*	41**	3*	1**	1*	0.6*
C.V. (%)	15	12	10	10	13	12
Plant residue						
Soybean	8111	1326	116	36	44	17
Peanut	8914	1379	127	37	47	19
Fallow	8255	852	112	35	44	17
SED	235*	58**	3**	0.8^{ns}	1^{ns}	0.5**
C.V. (%)	10	17	9	9	11	10
N fertilizer						
+ N	8553	1259	123	37	46	18
- N	8300	1112	114	35	44	17
SED	244^{ns}	42**	2*	0.8*	1^{ns}	0.5**
C.V. (%)	12	15	10	10	15	12

SED = standard error of the differences between means.
$^{ns, *, **}$ non-significant and significant at $P<0.05$ and $P< 0.01$, respectively.

Published papers

Hemwong, S., G Cadisch, B. Toomsan, V. Limpinuntana, P. Vityakon and A. Patanothai. 2007. Dynamics of residue decomposition and N_2 fixation of grain legumes upon sugarcane stover retention instead of burning. Soil and Tillage Research. (Submitted).

Study 3-3. Effects of peanut residues and rice straw management on growth and yield of succeeding rice

Wanwipa Kaewpradit and Banyong Toomsan

Peanut as a pre-rice crop is usually harvested 1-2 months before rice transplanting. During this lag period, much of N in the residues could be lost due to rapid N mineralization of groundnut residues. Mixing of abundantly available rice straw with peanut residues may be a means for regulating N dynamics in soil and thus reducing N losses. The objectives of this experiment were:

1. To investigate the effect of mixing peanut residues and rice straw in different proportions during lag period on (i) regulating N dynamics, (ii) potential microbial interactions during decomposition, and iii) associated nitrous oxide (N_2O) and methane (CH_4) emissions at weekly intervals during the lag phase until rice transplanting.
2. To investigate the effect of the peanut residues and rice straw mixing treatments on a) growth and yield of succeeding rice, b) residue N use efficiency, and c) N losses (^{15}N balance) from the plant-soil system.

Materials and methods

The experiment consisted of 6 treatments: (i) control (no residues), (ii) NPK (at recommended rate), (iii) peanut residues at 5 t ha^{-1}, (iv) rice straw at 5 t ha^{-1} (v) mixed residues 1:0.5 (groundnut residues 5 t : rice straw 2.5 t ha^{-1}), and (vi) mixed 1:1 (penut residues 5 t : rice straw 5 t ha^{-1}). After incorporation period, a decomposition experiment was conducted using the litter bag technique. In this experiment, microbial biomass C, N, mineral N, methane (CH_4), nitrous oxide (N_2O) and litter bag were collected at weekly intervals during the lag phase until rice transplanting. After rice transplanting (KDML 105), rice samples were periodically collected to determined growth and nutrient uptake. Nitrous oxide and methane emissions were measured weekly until final harvest. At final harvest, dry weight, nutrient content and ^{15}N recovery of labeled groundnut residues were measured.

Result

Decomposition (dry weight and N loss) was fastest in peanut resides (i.e. 64 % N lost) with a positive interaction when mixed with a moderate amount of rice straw (1:0.5). Adding peanut residues significantly increased mineral N initially, while added rice straw led to an initial microbial N immobilization. Mineral N of mixed residue treatments remained significantly ($P < 0.01$) higher than that of the control and single residue treatments until the end of the experiment. Soil microbial biomass N and apparent microbial efficiency were highest, while absolute and relative microbial C were lowest, in peanut and mixing treatments at most sampling dates. Microbial C:N ratio increased with increasing proportion of added rice straw, suggesting a change in microbial community or microbial efficiency. N_2O losses were highest in the peanut treatment and reduced by adding rice straw, while CH_4 emissions were greatest in mixed residue treatments. Mixing residues resulted in a significant interaction in that observed gaseous losses were greater than predicted from a purely additive effect.

Results of the first part suggest that it is possible to regulate N dynamics by mixing rice straw with peanut residues leading to a delayed mineral N release and potentially reduced leaching and N_2O losses (Table 3.6) during the pre-rice phase, however, at a trade-off of increased CH_4 emissions (Table 3.7).

At rice transplanting, mineral N of mixed residue treatments was significantly ($P < 0.01$) higher than the control. Significant effects of residue management treatments on rice development were observed after 30 days of transplanting. At final harvest, the highest seed yield and N content of rice were obtained in the 1:1 mixed treatment followed by 1:0.5 > peanut residue > rice straw > NPK > control treatments (Table 3.8). There was a significant relationship between mineral N content in soil at transplanting and rice yield at harvest. N_2O and CH_4 in mixed residue treatments had a slightly ($P < 0.1$) higher ^{15}N recovery (13%) in rice than the groundnut alone (10%) treatment but was below recovery from NPK treatment (29%) (Table 3.9). The highest ^{15}N recoveries in all treatments were observed in the topsoil (0-15 cm) where over 80% of recovered ^{15}N was located. Systems N losses were similar from peanut residues (32%) as from NPK (30%) but lowest from the 1:1 mixed treatment (15%). The highest $\delta^{13}C$ value was obtained from residue treatment according to lowest agronomy efficiency N. Result from the second part showed that mixing peanut residues and rice straw management could delay N release during the pre-rice lag period leading to an improved synchrony in N demand/supply, and consequently increasing growth and yield of the succeeding rice.

Published paper

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Table 3.6 Nitrous oxide emission and relative nitrous oxide emission at 1 week, average 2-6 week after residue incorporation.

Residues management	N_2O emissions (mg N_2O-N m^{-2} hr^{-1})		Relative N_2O emission[1/] (mg N_2O-N hr^{-1} gN^{-1} added)	
	1 wk	av. 2-6 wk	1 wk	av. 2-6 wk
Control	5.96	4.79	na	na
GN	6.77	4.92	0.0680 a	0.0103
RS	5.51	4.82	-0.0377 c	0.0017
1:0.5 (GN:RS)	6.21	4.64	0.0203 ab	-0.0130
1:1 (GN:RS)	5.95	4.74	-0.0003 bc	-0.0043
SED	0.31*	0.16[ns]	0.02*	0.015ns

[1/] = net nitrous oxide emission / N added in each treatment.

Numbers in the same column followed by the same letters are not significantly different at P = 0.05; na = not applicable.

SED = Standard error of the differences between means.

[ns,] * Non-significant and significant at $P \leq 0.05$, respectively.

Table 3.7 Cumulative methane emission and relative methane emission residue incorporation.

Residue treatment	CH_4 emissions ($g\ CH_4\ m^{-2}$)	Relative CH_4 emissions[1/] ($g\ CH_4$ g C added)
Control	5.9 c	na
Peanut (GN)	27.4 bc	0.08 b
Rice straw (RS)	50.4 b	0.27 a
1:0.5 (GN:RS)	87.5 a	0.23 a
1:1 (GN:RS)	108.6 a	0.24 a
SED	7.1**	0.03**

[1/] = net methane emission / C added in each treatment.
Numbers in the same column followed by the same letters are not significantly different at P = 0.05; na = not applicable.
SED = Standard error of the differences between means.
** = significantly different at $P \leq 0.01$

Table 3.8 Yield, N uptake and nutrient efficiency.

Residue treatment	Yield ($t\ ha^{-1}$)	N uptake ($kg\ N\ ha^{-1}$)	IE_N ($kg\ kg^{-1}$)	RE_N (%)	AE_N ($kg\ kg^{-1}$)	PEP_N ($kg\ kg^{-1}$)
Control	2.8 d	39 c	71.0 a	na	na	na
NPK	2.9 cd	45 c	65.1 ab	19 ab	5.1 b	90 b
GN	3.1 b	51 bc	61.2 bc	10 b	2.9 b	26 c
RS	3.0 bc	46 c	65.4 ab	28 a	10.0 a	120 a
1:0.5 (GN:RS)	3.5 a	65 a	55.8 c	20 ab	5.8 b	27 c
1:1 (GN:RS)	3.7 a	60 ab	61.7 bc	15 b	6.5 ab	26 c
SED	0.1**	4**	3.5*	5**	1.7**	2**

SED = Standard error of the differences between means.
*,** Significantly different at $P \leq 0.05$ and $P \leq 0.01$, respectively.
Numbers in the same column followed by the same letter are not significantly different at P = 0.05.

Table 3.9 ^{15}N recovery of rice, weed, remaining residue, soil, total and loss

Residue treatment	Rice (%)	Weed (%)	Residues (%)	Total (%)		Loss (%)
				soil	recovery	
NPK	29.1 a	4.3	4.8 c	32.2 a	70.3 b	29.7 a
GN	10.0 b	4.0	22.4 b	31.2 a	67.7 b	32.3 a
1:0.5 (GN:RS)	12.3 b	5.6	27.3 ab	39.5 a	84.7 a	15.3 b
1:1 (GN:RS)	12.7 b	6.7	31.9 a	20.9 b	72.7 b	27.3 a
SED	2.5**	1.3^{ns}	2.2**	5.6*	5.8*	5.8*

SED = Standard error of the differences between means.
ns,*,** Non-significant and significantly different at $P \leq 0.05$ and $P \leq 0.01$, respectively.
Numbers in the same column followed by the same letter are not significantly different at P = 0.05.

Study 3-4. Effect of soybean stover management on growth and yield of KDML 105 rice

Chatchai Somee and Banyong Toomsan

In many parts of Thailand, soybean is grown after rice harvest during December to January and harvested during March to April. It is usually cut at the ground level, stocked, dried and then threshed using a modified rice threshing machine. Soybean residues after threshing are usually left in piles and burned. This practice does not add organic matter to the soil, and can result in some losses of plant nutrient, i.e., nitrogen and phosphorus. Toomsan et al. (1995) reported that the stover yield of soybean cultivar S.J.4 grown after rice was 2.5 tons ha^{-1} and had a N content of 2.5 kg N ha^{-1}. If the stover is returned to the field, it can certainly improve soil fertility and also increase the growth and yield of the succeeding rice crop.

The study hypothesizes that soybean stover which has a high C:N ratio, if returned to the field, would be beneficial to the succeeding rice, regardless of the application of a supplemental N fertilizer. The objectives were:

1. To study the effects of soybean stover application rates in combinations with chemical fertilizers on growth and yield of KDML 105 rice.
2. To study decomposition rate and nutrients release of soybean and groundnut stover by using the "litter bag technique".

Materials and methods

A randomized complete block design (RCBD) with 4 replications was employed in the study. There were 15 treatments, i.e., without soybean stover and chemical fertilizers (T1, control), soybean stover application at the rate of 1,875 kg/ha plus N_0PK (no N addition plus PK at the rates of 25 and 12.5 kg ha^{-1} of P_2O_5 and K_2O at 7 day after transplanting (DAT), respectively) (T2), N_1PK (NPK fertilizers at the rates of 25, 25 and 12.5 kg ha^{-1} of N, P_2O_5 and K_2O at 7 DAT, respectively) (T3), N_2PK (PK at the rates of 25 and 12.5 kg ha^{-1} of P_2O_5 and K_2O, respectively, at 7 DAT plus 14.4 kg ha^{-1} of N at panicle initiation period) (T4), soybean stover application at the rate 3,750 kg ha^{-1} plus N_0PK, N_1PK, and N_2PK (T5, T6 and T7, respectively), soybean stover application at the rate 5,625 kg ha^{-1} plus N_0PK, N_1PK, and N_2PK (T8, T9 and T10, respectively), no soybean stover application plus N_0PK, N_1PK, N_2PK and $(N_1+N_2)PK$ (recommended rate) (T11, T12, T13 and T14, respectively), and peanut stover application at the rate of 3,750 kg ha^{-1} plus N_2PK (T15).

The experiment was conducted in a rainfed paddy field at Ban Muoang, Muang district, Khon Kaen province from July to November 2004. The field was prepared on 7th July 2004 and stover was applied to the field on 14th July 2004. Rice was transplanted on 28th July and harvested on 26th November of the same year.

Results

The results revealed that application of soybean and peanut stover gave higher growth and yield of KDML 105 rice than the control treatment (T1)(Table 3.10). There was no significant difference among the soybean application treatments. However, there was a tendency of increasing growth and yield of rice with increasing rate of stover application. Among the soybean application treatments that receiving different

chemical fertilizers (N_0PK, N_1PK and N_2PK), the treatment that received N_1PK had higher growth and yield of rice than the other treatments. Maximum yield of rice was obtained in the treatment that the stover was applied at the rate of 5,625 kg ha^{-1} plus N_1PK (3106 kg ha^{-1}). However, it was not significantly different from that applied with recommended fertilizer rates ((N_1+N_2)PK) and those applied with soybean stover at the rates of 1,875 and 3,750 kg ha^{-1} plus N_1PK. N_2PK applied to treatments that received different soybean rates had a tendency to give lower growth and yield of rice than those receive N_1PK. The treatments that did not received soybean stover but only received N_0PK, N_1PK and N_2PK did not give higher growth and yield of rice than the control treatment (T1). Peanut stover application at the rate of 3,750 kg ha^{-1} plus N_2PK gave the growth and yield of rice that was not significantly different from the best treatment and the recommended fertilizer treatment. It is therefore recommended that when soybean stover is applied to the succeeding rice crop, it should be applied at the rate of 1875 kg ha^{-1} along with NPK fertilizers (25, 25 and 12.5 kg ha^{-1} of N, P_2O_5 and K_2O, respectively).

The study on decomposition and nutrients released from soybean and groundnut stover using "litter bag technique" indicated that N application had a tendency to hasten the decomposition rate of soybean stover.

Table 3.10 Dry matter yield and seed dry weight of KDML 105 rice as affected by different stover and fertilizer treatments

Treatment	Dry matter yield (kg ha^{-1})			HI
	Stubble and straw	Seed	Total	(%)
1. Control	2175 c	2031 bc	4206 e	48.28 a
2. Soybean residue 1,875 kg/ha + N_0PK	2675 abc	2319 abc	5000 a-e	46.44 abc
3. Soybean residue 1,875 kg/ha + N_1PK	3663 ab	1438 a	6731 ab	45.54 bc
4. . Soybean residue 1,875 kg/ha + N_2PK	3206 abc	2775 abc	5988 a-d	46.38 abc
5. Soybean residue 3,750 kg/ha + N_0PK	2675 abc	2463 abc	5144 a-e	47.94 abc
6. Soybean residue 3,750 kg/ha + N_1PK	3363 abc	3019 a	6388 abc	47.30 abc
7. Soybean residue 3,750 kg/ha + N_2PK	3344 abc	2875 abc	6219 a-d	46.24 abc
8. Soybean residue 5,625 kg/ha + N_0PK	3144 abc	3000 a	6144 a-d	49.10 a
9. Soybean residue 5,625 kg/ha + N_1PK	3663 ab	3106 a	6769 ab	45.89 abc
10. Soybean residue 5,625 kg/ha + N_2PK	3431 abc	2944 abc	6375 abc	46.17 abc
11. N_0PK	2219 c	1900 c	4119 e	46.09 abc
12. N_1PK	2619 abc	2006 bc	4631 cde	43.40 c
13. N_2PK	2531 abc	2388 abc	4919 b-e	48.53 a
14. (N_1+N_2)PK	3831 a	3088 a	6919 a	44.62 bc
15.Peanut residue 3,750 kg/ha + N_2PK	3713 ab	2806 abc	6519 abc	43.05 bc
F-test	**	*	*	*
C.V.(%)	19.31	22.07	21.54	5.83

*,** Significantly different at $P \leq 0.05$ and $P \leq 0.01$, respectively.
Numbers in the same column followed by the same letter are not significantly different at P = 0.05.

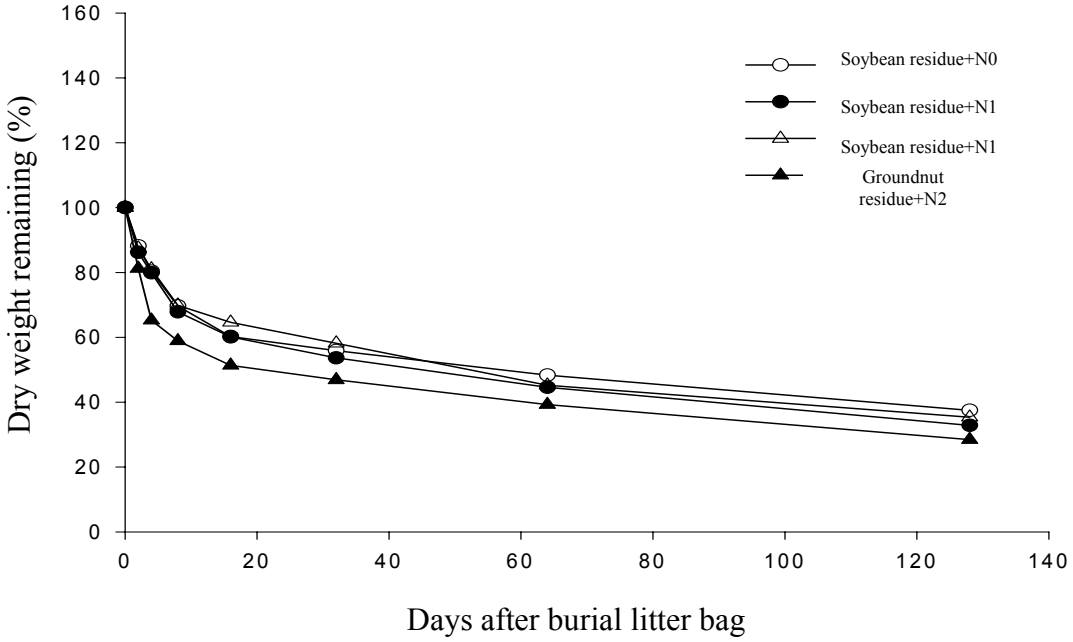

Fig. 3.3 Dry weight remaining of soybean and peanut residues in litterbag.

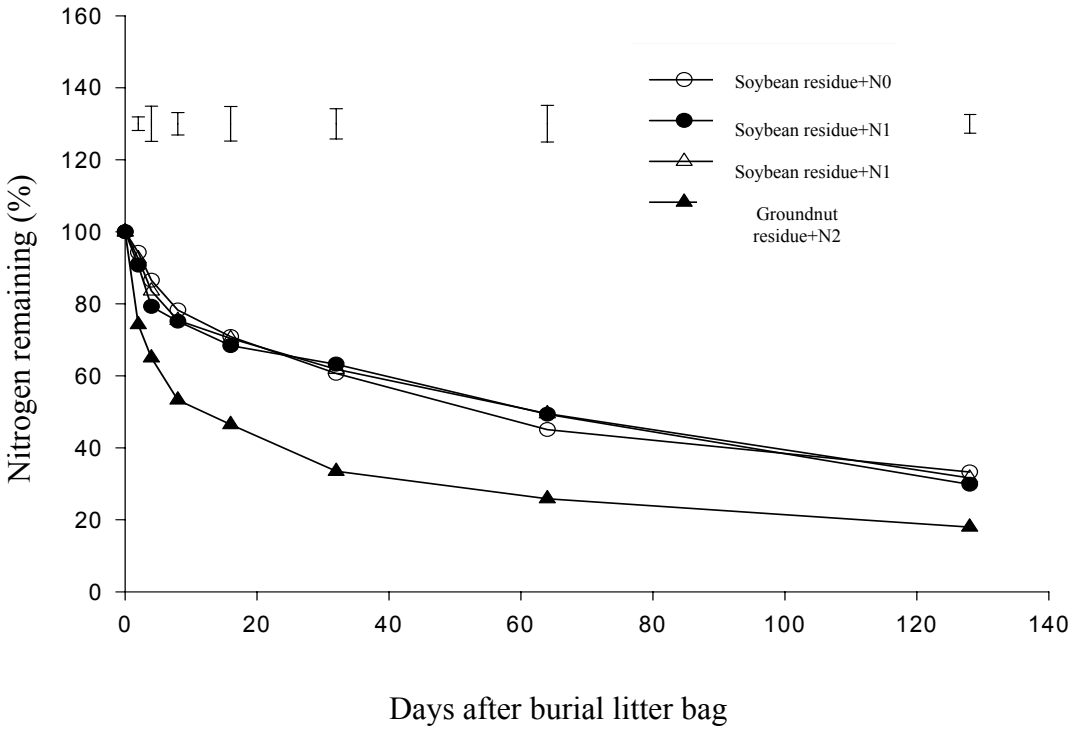

Fig. 3.4 Nitrogen remaining of soybean and peanut residues in litterbag.

Study 3-5. Effect of peanut stover application and weed management on growth and yield of maize in the next rainy season

Sukanya Promsakha na Sakonnakhon and Banyong Toomsan

This study consisted of two parts:

Study 3-5.1 Dry season groundnut stover management practices determine nitrogen cycling efficiency and subsequent maize yields

In the rainfed upland area, most farmers can grow only one crop per year and soils are left fallow about 6-8 months. It is not known whether (or not) peanut stover, when kept over this long fallow period, can still maintain and supply sufficient nutrients to benefit the succeeding crop. The objective of this study was to investigate the effects of peanut stover managements over the dry season on maize yield and nutrient use efficiency in the next rainy season.

Materials and methods

The experiment consisted of three parts, i.e., (i) preceding peanut crop, (ii) groundnut stover management over the dry season, and (iii) two succeeding maize crops. A randomized complete block design with four replicates was used in peanut stover management and succeeding crop experiments. The peanut cultivar Khon Kaen 60-3 was grown as a preceding crop during June to October 2001. At maturity, peanut was harvested on October 19-20, 2001. The remaining stover of peanuts was weighted and sub-samples were taken to determine dry matter and nutrient contents. The peanut stover management consisted of four treatments, i.e., (i) surface application, (ii) incorporation, (iii) initial removal, storage and reapplication (incorporation) before the following maize crop, and (iv) complete removal. In order to assess the fate of nitrogen under the different stover management options and dynamics of residue decomposition, mineral N, N_2O emissions and the microbial biomass were monitored. The use of ^{15}N labeled peanut stover further provided information regarding the efficiency of crop residue N recovery and total residue N losses from the system.

Results

At groundnut harvest, the total dry matter of peanut was 6,756 kg ha^{-1} with a harvest index of 30%. The total nitrogen recycled amounted to 100 kg N ha^{-1}, corresponding to about 60% of total nitrogen yield. The peanut stover had a C:N ratio of 23:1 with 8.5% lignin and 2.3% total extractable polyphenols. At the end of the dry season, soil organic matter was higher where stover was recycled compared to where stover was removed. However, no significant differences in soil pH and total nitrogen in the topsoil were observed due to stover management. During the early part of the dry season, dry matter disappearance of stover in litter bags was slow but similar between surface application and incorporation treatments. With the onset of the first rains, however, dry matter loss was initially faster when stover was incorporated. Nitrogen remaining in peanut residues showed a similar decomposition pattern with surface applied residues retaining more nitrogen than incorporated ones (Figure 3.5).

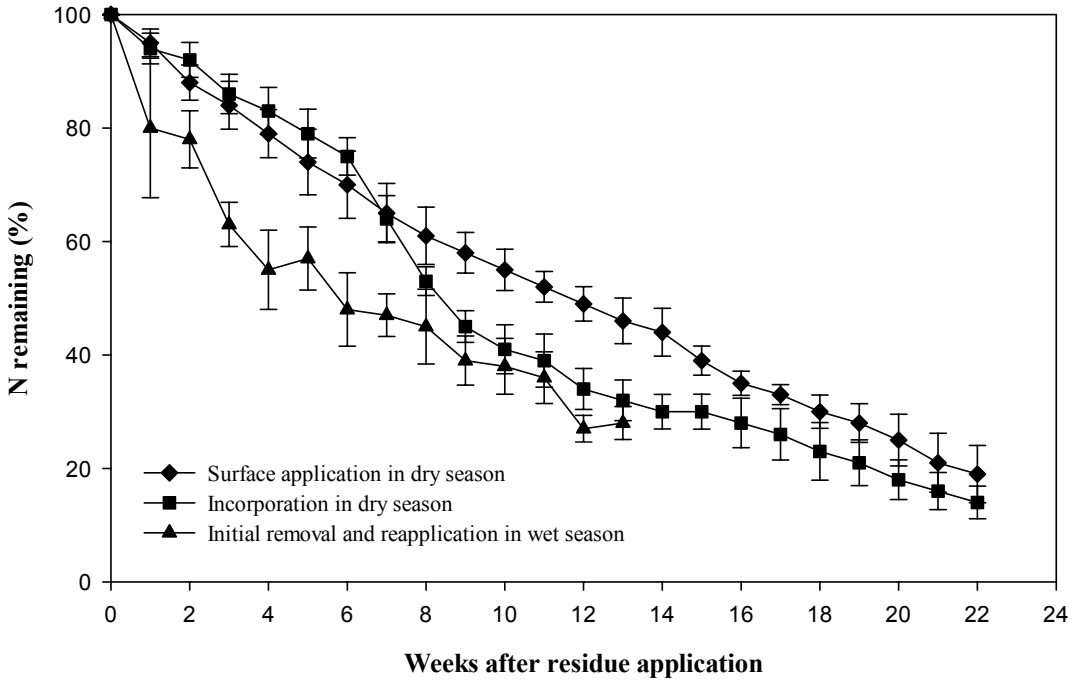

Figure 3.5 Comparison of N remaining of surface or incorporated residues during the dry season and of incorporated stover during the rainy season. Vertical bars represent SEM.

During the maize growing cycles, mineral N in topsoil and subsoil layers remained low in both treatments where residues were applied at the beginning of the dry season. On the other hand, removing and storing stover until the wet season and then incorporating stover before the maize crop resulted in a significant (P<0.01) increase in mineral N availability during the first maize crop in both topsoil and subsoil. Before the first maize crop, microbial biomass was consistently higher where residues were incorporated compared to surface application. However, after residues incorporation at the beginning of the first maize season, the trend was reversed and microbial biomass in the surface applied stover treatment was mostly higher than where incorporated at the beginning of the dry season. Economic yield of the first maize crop was highest (2,512 kg ha^{-1}) in the treatment where stover was initially removed and reapplied before the maize crop. Maize yield was lowest where stover was completely removed from the field. Soil microbial biomass during early maize development was closely related to maize N yield (R^2=0.99; Figure 3.6).

Surface application of labeled peanut residues led to a significantly lower ^{15}N recovery in the first maize crop compared to the incorporation treatments. The highest isotopic recovery in maize was observed in the treatment where stover was initially removed and reapplied before the maize crop. However, isotopic recoveries in the second maize crop were not significantly different between treatments. Residue N recoveries in soil after the second maize crop were less than 50% in the top 100 cm in all treatments. Results also suggested a better isotopic recovery in soil where peanut stover was immediately incorporated compared to surface application or removed and applied later but the effect was only significant at P<0.10 (Table 3.11).

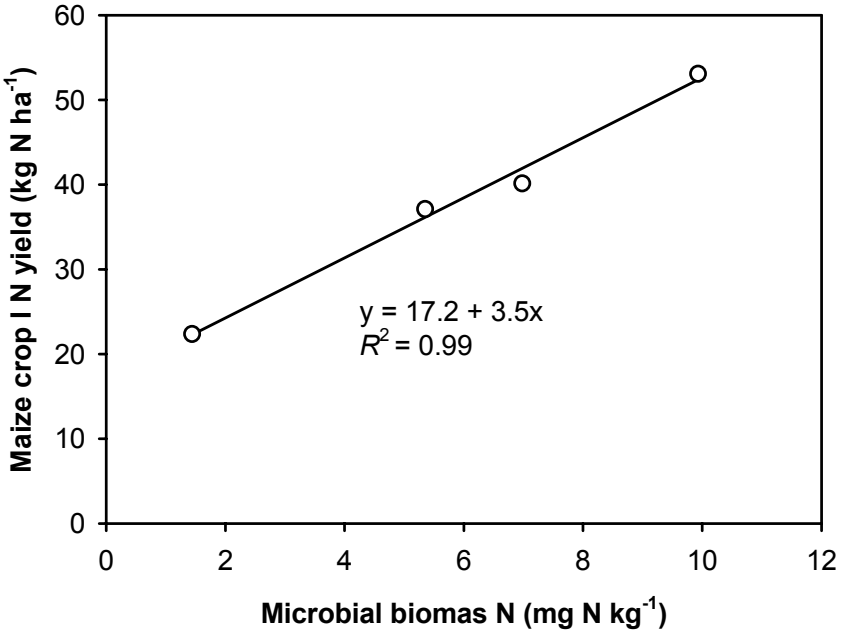

Figure 3.6 Relationship between soil microbial biomass 5 weeks after planting first maize crop and maize N yield of first crop.

Table 3.11 ^{15}N recoveries (% of applied) in first (I) and second (II) maize crops and in weeds as well as ^{15}N recoveries in soil (0-100 cm) at end of second maize crop in relation to peanut stover management at the beginning of the previous dry season.

Stover management	Maize I	Maize II	Weed I	Weed II	Soil total	Total recovery	Losses[1/]
				(% of applied)			
Surface application	2.4	1.3	0.3	0.2	38.7	42.9	57.1
Incorporation	6.0	0.8	0.2	0.4	46.6	54.0	46.0
Initial removal and reapplication	10.3	1.5	0.5	0.4	40.2	52.9	47.1
SED	2.01*	0.31^{ns}	0.10^{ns}	0.14^{ns}	3.55**	5.42**	5.42**
C.V. (%)	54	34	39	52	12	15	15

[1/] N applied minus total recovery.

SED = Standard error of the differences between means.

^{ns,*,**} Non-significant and significantly different at $P \leq 0.05$ and $P \leq 0.01$, respectively.

Conclusions

The potential maize yield benefits from recycled peanut stover are dependent on the residue management method during the dry season and timing of stover application. Results from this experiment suggest that the peanut stover management method that supported the highest maize yield was initial stover removal at peanut harvest and reapplication before the following maize crop in the rainy season. This was due to a better N supply to the maize crop but did not lead to a better recycling efficiency, as N losses were equal to the other treatments due to an asynchrony in N release and demand. Although stover storage and reapplication before maize crop could greatly increase maize yields, this method is difficult to implement for smallholder farmer in the tropics because of the storage facility and labour requirements for transporting the stover. Even though, early incorporation of peanut residue resulted in a more efficient recycling of N, it led only to small increases in economic yield compared to the surface application. Therefore, in practice the preferred method for smallholder farmer will remain surface application of stover as there is no economic value attached to the reduced N losses when the stover is incorporated.

Study 3-5.2 The role of weed composition on stover nutrient recycling efficiency

In the upland soils of Northeast Thailand, most farmers can grow only one crop per year and soils are left fallow until the next crop, leading to the establishment of a native weed population. Additionally, these areas are often very sandy thus posing a high risk of nitrogen leaching during late or erratic and early rains occurring during the fallow period. The objective of this study was to assess the impact of weeds and weed composition, i.e. native weed mixture, grass or legume/broadleaf dominated weed fallows over the dry season on nutrient recycling of peanut stover, i.e. mineral N and microbial biomass N dynamics, ^{15}N pre-crop residue recovery and subsequent effects on maize yield.

Materials and methods

The experiment consisted of three parts, i.e., (i) preceding peanut crop, (ii) weed management over the dry season, and (iii) two succeeding maize crops. A randomized complete block with four replicates was used in weed management and succeeding crop experiments. The plot size was 6m x 8m and the harvest area was 4.5m x 6m. It was part of a larger experiment exploiting peanut residue management options during dry season. Weed management consisted of six treatments: (i) no weeds, i.e. weeds were hand-weeded during the dry season; (ii) mixed weed population, i.e. naturally emerging weeds were allowed to grow undisturbed; (iii) grass weeds only, i.e. all broadleaf weeds were hand-weeded weekly; (iv) legume/broadleaf weeds only, i.e. all grasses were hand-weeded weekly; (v) mixed weed population + topdressing with N fertilizer at 40 days after planting maize (Nt, 31 kg N ha^{-1}); (vi) mixed weed population + N fertilizer application 14 (Np, 47 kg N ha^{-1}) and 40 days (Nt) after planting maize. In order to assess the impact of weeds and weed composition over the dry season on nitrogen conservation dynamics of mineral N, N_2O emissions and the microbial biomass were monitored. The use of ^{15}N labeled peanut stover further provided information regarding the efficiency of crop residue N recovery and total residue N losses from the system.

Results

Grass and mixed weed treatments produced significantly more dry matter than the legume/broadleaf weed treatment (4,420 and 4,422 versus 3,372 kg dry matter ha^{-1}, respectively). There were no significant difference between grass weed and mixed weed treatments. The legume/broadleaf weed treatment accumulated more N than the other treatments. Grass and mixed weeds had higher C/N ratio and acid-detergent fibre (ADF) content than legume/broadleaf weed residues while the later had marginally higher lignin and polyphenol contents. During the dry season fallow period, mineral N in topsoil of the no weed treatment was significantly higher than that of the other treatments. Among the weed treatments, the broadleaf weed treatment had among the highest mineral N content during the fallow period, while grass and mixed weed treatments were lowest for both top and lower soil depths. During the fallow period, soil microbial biomass N was not significantly different between the no weed and mixed weed treatments. Soil microbial biomass N was highest in mixed weed treatments particularly where N fertilizer was applied at planting and as topdressing. From week 33 onwards, microbial biomass was smaller in the legume/broadleaf weed treatment compared to grass and mixed weed treatments for most of time. Towards the end of the maize cycle, microbial biomass declined during both maize crop cycles (Figure 3.7).

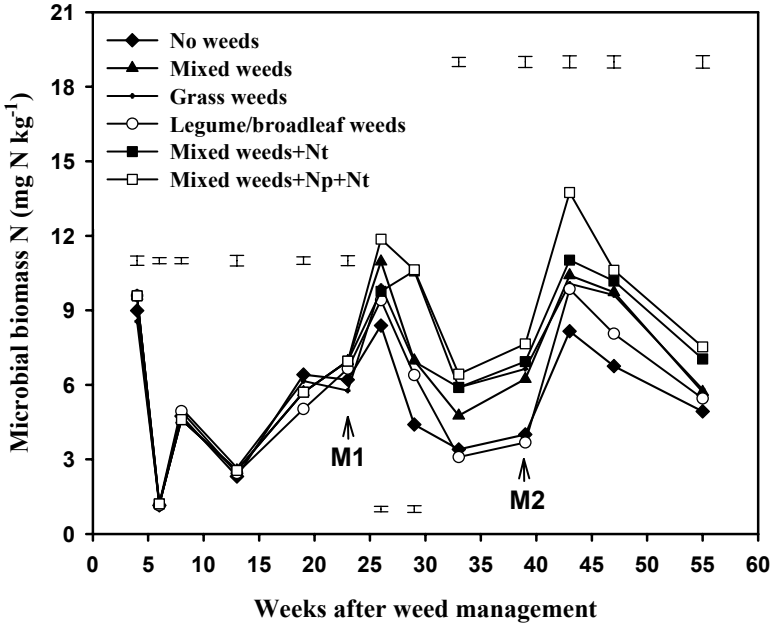

Fig. 3.7 Effect of weed management on microbial biomass N (0-15 cm soil depth) dynamics during dry season fallow period (0-23 weeks) and subsequent maize cycles (M1/2). Vertical bars represent SED.

Final yield components of the first maize crop were significantly higher after the legume/broadleaf weed fallow compared to the grass and mixed weed fallow treatments without N fertilizer apart from the cob component. The best maize seed yield was achieved after mixed weed fallow supplied with N after planting and

topdressing but that was not significantly different from the legume/broadleaf treatment. Applying topdressing N fertilizer significantly increased yield after the mixed weed fallow but was not sufficient to achieve maize yield potential. N fertilizer treatments led to a significant higher harvest index compared with the no weed treatment (Table 3.12).

Table 3.12 Maize dry weight (kg ha^{-1}) and harvest index (HI) at final harvest of first and second maize crop.

Treatments	Dry weight (kg ha^{-1})				
	Seed	Cob	Stover	Total	HI
			First crop		
No weed	2323 ^{cd}	492 ^{b}	5353 ^{bc}	8168 ^{b}	0.27 ^{c}
Mixed weed	1911 ^{d}	377 ^{b}	3528 ^{d}	5816 ^{b}	0.33 ^{ab}
Grass weed	1705 ^{d}	360 ^{b}	3750 ^{cd}	5814 ^{b}	0.30 ^{bc}
Legume/broadleaf weed	3731 ^{ab}	529 ^{b}	6630 ^{ab}	10889 ^{a}	0.34 ^{ab}
Mixed weed + Nt	2984 ^{bc}	537 ^{b}	4658 ^{cd}	8179 ^{b}	0.36 ^{a}
Mixed weed + Np + Nt	4532 ^{a}	802 ^{a}	7295 ^{a}	12630 ^{a}	0.36 ^{a}
F-test	**	**	**	**	**
C.V. (%)	22.5	23.8	21.7	20.3	9.6
			Second crop		
No weed	1229 ^{c}	280 ^{c}	3611 ^{c}	5120 ^{c}	0.24 ^{b}
Mixed weed	1209 ^{c}	316 ^{c}	3648 ^{c}	5173 ^{c}	0.23 ^{b}
Grass weed	1194 ^{c}	334 ^{bc}	3223 ^{c}	4751 ^{c}	0.25 ^{b}
Legume/broadleaf weed	1697 ^{bc}	447 ^{bc}	4852 ^{b}	6996 ^{b}	0.25 ^{b}
Mixed weed + Nt	2065 ^{b}	535 ^{b}	3731 ^{c}	6331 ^{bc}	0.33 ^{a}
Mixed weed + Np + Nt	3886 ^{a}	1082 ^{a}	8815 ^{a}	13783 ^{a}	0.28 ^{ab}
F-test	**	**	**	**	**
C.V. (%)	17.4	27.4	15.2	14.7	10.4

Treatment results in a column followed by a common letter are not significantly different at $P \leq 0.05$ by according to the Duncan Multiple Range Test.
*,** = significantly different at $P \leq 0.05$ and $P \leq 0.01$, respectively.

^{15}N recovery of groundnut stover in the no weeds treatment was significantly higher than in the mixed weed treatment at first maize crop but not in the second maize crop. Total stover N recoveries in the soil (0-100 cm) appeared to be higher in the mixed weed treatment but the effect was not significant (Table 3.13).

Table 3.13 ^{15}N recoveries (% of applied) of labeled groundnut residues in first (I) and second (II) maize crops as well as ^{15}N recoveries in soil (0-100 cm) at the end of second maize crop in relation to weed management at the beginning of the previous dry season. (Losses = N applied minus total recovery).

Weed management	Maize I	Maize II	Soil total	Total recovery	Losses
			% of applied		
No weeds	4.6 [a]	0.75	28.6	33.9	66.1
Mixed weeds	2.4 [b]	1.30	38.7	42.4	57.6
F-test	*	ns	ns	ns	ns
C.V. (%)	22	61	33	32	20

Treatment results in a column followed by a common letter are not significantly different at $P \leq 0.05$ by Duncan Multiple Range Test.
ns,* Non-significant and significant at $P \leq 0.05$, respectively.

Conclusions

Weeds grown during the dry season and incorporated during seed bed preparations suppressed maize yields but when weeds predominately consisted of native legumes and broadleaf species they significantly improved maize performance. Recycling grass dominated weed biomass resulted in a temporary nitrogen immobilization in the soil, thus such weeds should be incorporated well before maize planting or supplemented with fertilizer N to avoid competition for mineral N by the soil microbial biomass.

Our study showed that manipulating weed composition during the dry season was crucial to optimise benefits of recycled groundnut stover and minimise N losses. However, for practical applications this necessitates a better understanding of weed ecology, i.e. what factors determine weed composition and how can it be manipulated.

Published papers

Promsakha Na Sakonnakhon, S., B. Toomsan, G. Cadisch, E.M Baggs, P. Vityakon, V. Limpinuntana, S. Jogloy and **A. Patanothai**. 2005. Dry season groundnut stover management practices determine nitrogen cycling efficiency and subsequent maize yields. Plant and Soils 272:183-199.

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Sub-Project 4.

Application of Crop Simulation Model in Crop Breeding

Prof. Dr. Aran Patanothai

Sub-Project Leader

Physiologically-based crop simulation models have been developed as a multipurpose tool for application in agricultural research (Hoogenboom *et al*., 1992; Penning de Vries *et al*., 1993; Jones *et al*., 2003). As these models can simulate growth and yields of crop cultivars in response to environments, they can be used as a tool for the synthesis of research understanding on the interactions of genetics, physiology and environmental factors that influence crop growth and yield (de Wit, 1982; Whisler *et al*., 1986; Uehara, 1998). For peanut, the process-oriented Cropping System Model (CSM)-CROPGRO-Peanut has also been developed and included as a part of the Decision Support System for Agrotechnology Transfer (DSSAT) (Tsuji *et al*., 1994; Hoogenboom *et al*., 1999, 2004; Jone et al., 2003). The model is physiologically based and can simulate yields of peanut cultivars under various management and environmental conditions (Sing *et al*., 1994; Boote *et al*., 1998; Kaur and Hundal, 1999). Such ability of crop simulation models makes them an attractive tool for crop improvement and suggestions have also been made on their potential contributions to crop improvement process (Aggarwal *et al*., 1995; White, 1998; Matthews and Stephen, 2002). These include assisting with multi-location evaluation of crop breeding lines (Aggarwal *et al*., 1995), understanding the nature of genotype by environment (G x E) interactions (Hammer *et al*., 1996; Chapman *et al*., 2002), identification and evaluation of desirable traits or combination of traits leading to the design of a crop ideotype for a specific environment (Boote and Tollenaar, 1994; Aggarwal *et al*., 1995; Bastiaans *et al*., 1997; Boote *et al*., 2001). However, actual investigations on the applications of crop simulation models in plant breeding have been very limited.

During Phase I of the project, an investigation on the applicability of the CSM-CROPGRO-Peanut model in assisting with multi-environment evaluation of advanced peanut lines has been conducted. The results were very promising, but need to be confirmed in a diverse range of peanut lines. Determination of the genetic coefficients of new breeding lines is a major constrain for the utilization of crop simulation model as a breeding tool, as the recommended procedure is laborious and time consuming, and particularly required a considerable amount of seeds. Such procedure is not very practical for breeding lines at the early stages. Reduction in data collection is needed to make it practical for breeding programs.

In Phase II, a part of research was a continuation of work in Phase I, but new topics have also been investigated. Evaluation of the applicability of the CSM-CROPGRO-Peanut model in assisting with the multi-environment evaluation of peanut breeding lines was repeated. Attempts were made in exploring ways to reduce the data to be collected for deriving the cultivar coefficients of new breeding lines. The application of a crop simulation model in studying genotype x environment (G x E) interaction was investigated in various aspects, including mega-environment determination, dynamics of different components of G x E interaction over multiple years, and identification of crop characters and environmental factors determining G x

E interaction. Utilization of a crop simulation model in identification of desirable crop traits and in determining yield gap has also been investigated.

Seven studies were conducted under this sub-project:

4-1. Applicability of the CSM-CROPGRO-Peanut model for yield performance and stability evaluation of peanut breeding lines.

4-2. Determination of mega-environment for peanut breeding using the CSM-CROPGRO-Peanut model.

4-3. Dynamic patterns of components of genotype x environment interaction for pod yield of peanut over multiple years.

4-4. Designing peanut ideotype for a target environment using the CSM-CROPGRO-Peanut model..

4-5. Suitable planting dates for conducting the cultivar coefficient determination experiments.

4-6. Reduction in data collection for determination of cultivar coefficients for breeding applications.

4-7. Yield gap analysis of peanut using the CSM-CROPGRO-Peanut model.

Study 4-1. Applicability of the CSM-CROPGRO-Peanut model for yield performance and stability evaluation of peanut breeding lines

Bhalang Suriharn and Aran Patanothai

The model application that is of great interest to us and has been our main emphasis since the beginning is the use of crop simulation model in assisting the multi-environment evaluation of peanut breeding lines. This interest came from the fact that crop genotypes normally respond differently to different environmental conditions. Consequently, breeders are forced to evaluate new breeding lines in multi-environment trials (METs) over a set of sites and years to assess their yield performance and stability. METs, thus, have become a major activity in all crop breeding programs. This process is laborious, time consuming and expensive. Furthermore, it is not possible to evaluate promising breeding lines for the entire range of environments that correspond to local farmers' conditions in different production areas. It was anticipated that, if a simulation model could be used for this purpose, the efficiency of breeding lines evaluation would be greatly improved.

In Phase I of the project, the possibility of using the CSM-CROPGRO-Peanut model to evaluate yield performance and stability across a range of environments in Thailand of two groups of advanced peanut lines under testing at the regional yield trial stage was investigated (Banterng et al., 2006). The results showed that the model predicted the relative mean pod yields over the test environments of the test peanut lines and their relative yield responses to different environments reasonably well. However, more empirical evidence is needed before breeders are convinced that it can be used as a tool in their breeding program. The aim of this study was to confirm the findings of Banterng *et al*. (2006). The objective was to evaluate the potential application of the CSM-CROPGRO-Peanut model in assisting multi-environment and

yield stability evaluation for a set of diverse peanut breeding lines at the early stage of yield testing.

Materials and methods

Thirteen peanut lines selected from preliminary yield trials to provide a range of yield levels, seed types, and maturity durations, and four check cultivars were used. These lines were tested in farmers' fields and research stations in northeast and northern Thailand during 2002-2004, both in the rainy and the dry seasons for a total of 11 environments. Pod yield for the 17 peanut lines was simulated for the same 11 actual test environments and also 11 additional environments, using the CSM-CROPGRO-Peanut model.

Combined analyses of variance were conducted for the observed data from the 11 environments, and for the simulated data from the 11 actual test environments, the additional 11 environments, and all 22 environments. The evaluation of the model in yield performance evaluation was conducted by comparing means and ranks of the test entries based on observed and simulated pod yields, and by determining the number of lines in the top 52.9 %, i.e., 9 lines out of 17 lines, that were identified both by experimentation and model simulation.

Stability analyses were conducted with the GGE biplot method (Yan et al., 2000, 2001) both for observed and for simulated pod yields. For simulated data, separate analyses were conducted for the 11 actual test environments , for the additional 11 environments, and for all 22 environments. The applicability of the CSM-CROPGRO-Peanut model in assessing yield stability of the peanut lines was evaluated by comparing the GGE biplot results obtained from observed and simulated data.

Results

From a breeding perspective, the relative performances of the individual lines are of primary concern. Although the ranks of observed and simulated means for pod yield for the 11 actual test sites of the individual peanut lines were somewhat different, if the lines were divided into groups based on their yield performances, most lines would be classified into the same general group by both model simulation and actual testing, with the exceptions of a few lines. Nevertheless, the same six out of nine lines in the upper 52 % as well as the same top yielding line were identified by both simulation and experimentation. However, the means for simulated pod yield of the individual peanut lines for the 11 actual test sites and the 11 additional sites were highly correlated ($r = 0.90^{**}$). Thus, no gain was achieved in extending the range of the test environments with regard to relative mean performances of the test peanut lines.

Among the nine stable lines identified with observed pod yield, six were common with those identified by model simulation, i.e., Entries 1, 10, 11, 12, 15 and 16 (Fig. 4.1). These results indicated that the CSM-CROPGRO-Peanut model performed quite well in yield stability evaluation of these peanut breeding lines. However, there were still some lines that were identified as stable lines with the observed data but not with the simulated data, i.e., Entries 6, 8 and 14, and vice versa, i.e. Entries 9 and 13. Such discrepancies would be anticipated as the observed values represented the responses of the peanut lines to the variation in all environmental factors, both biotic and abiotic, while the simulated values only represented the responses of the lines to

varying soil and weather conditions to which the model is responsive. The differences between the observed and the corresponding simulated values, thus, indicated the effects of other stress factors and micro-variability not accounted for by the simulation model.

This study confirmed the findings of Banterng et al. (2006) in showing that the CSM-CROPGRO-Peanut model could be used in assisting yield performance and stability evaluation of peanut breeding lines.

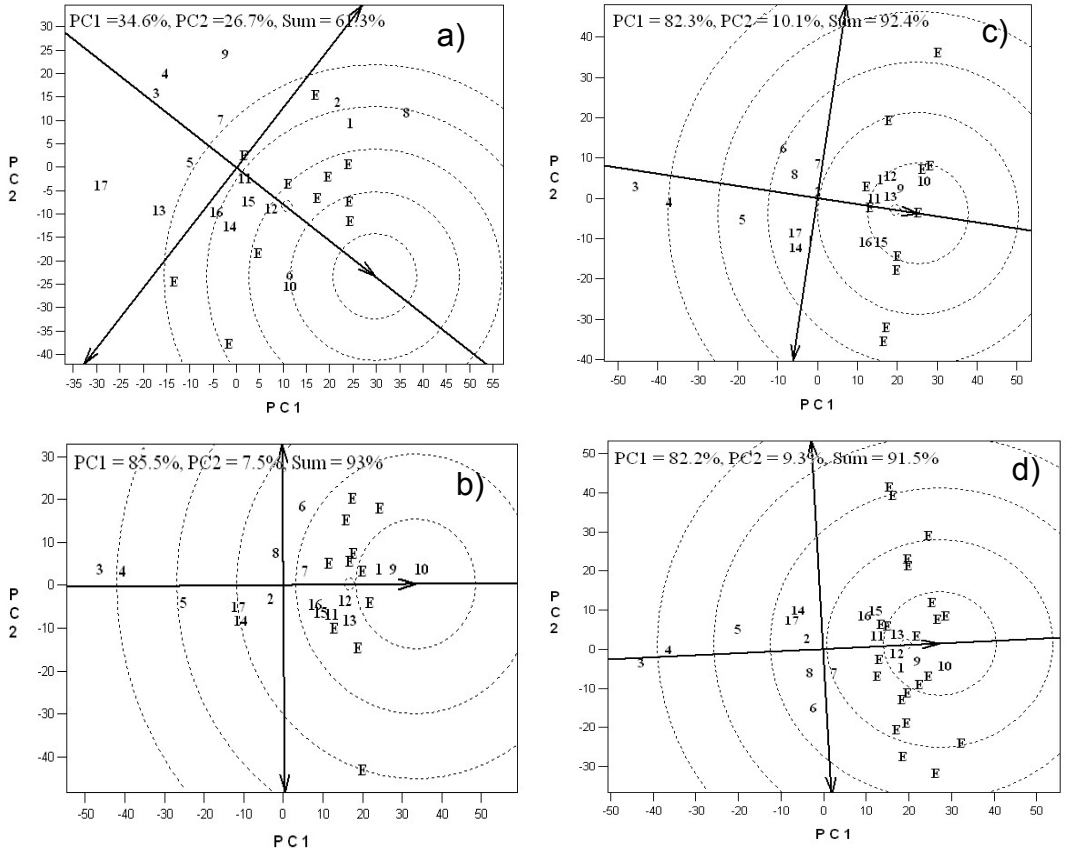

Fig. 4.1 GGE-biplot for mean pod yield of 17 peanut breeding lines (1-17) across the test environments (E): (a) observed yield from actual trials for 11 environments, (b) simulated yield for the same 11 environments as the observed data, (c), simulated yield for additional 11 environments, and (d) simulated yield for all 22 environments.

Publication

Suriharn, B. **A. Patanothai**, K. Pannangpetch, S. Jogloy, and G. Hoogenboom. 2007. Derivation of cultivar coefficients of peanut lines for breeding applications of the CSM-CROPGRO Peanut Model. Crop Science 47: 605-619.

Suriharn, B., A. Patanothai, K. Pannangpetch, S. Jogloy, and G. Hoogenboom. 2007. Applicability of the CSM-CROPGRO-Peanut model for yield performance and stability evaluation of peanut breeding lines. Crop Science. (Submitted).

Study 4-2. Determination of mega-environment for peanut breeding using the CSM-CROPGRO-Peanut model

Wanlaya Putto and Aran Patanothai

In a crop breeding program, the first strategy is to define the geographical areas that will be the target environments for newly-released cultivars. Normally, plant breeders try to develop broadly adapted cultivars for a wide target region. However, there is now an increasing interest to breed crop cultivars for a specific environment to take advantage of specific adaptations (Annicchiarico et al., 2005; Samonte et al., 2005). Breeding for a specific adaptation of a particular crop, however, requires a sub-division of all production areas into mega-environments that are the target environments for breeding. A mega-environment is a group of growing areas that are similar in terms of genotype response and show a repeatable relative performance of crop genotypes across years (Gauch and Zobel, 1997; Yan and Rajcan, 2002; Yan and Tinker, 2005). It is generally identified through the analysis of multi-environment trials (MET) of crop breeding lines. The process involves analyzing the environmental responses of the test genotypes and then grouping the test environments based on their similarity in genotypic responses.

In Thailand, peanut is grown in all regions across the country. However, so far it is unknown whether peanut production areas in Thailand are sufficiently diverse in environmental conditions to justify a sub-division into mega-environments for breeding purpose. To examine the above question, several years of MET data for all major production areas are required. This information is not readily available from actual variety trials but could be generated by the CSM-CROPGRO-Peanut model. The objective of this study was to investigate whether peanut production areas in Thailand could be sub-divided into mega-environments for specific adaptation breeding using yield data simulated witb a crop simulation model.

Materials and methods

The main procedure used consisted of the determination of peanut production areas in different regions of Thailand, gathering the required input data for model simulation, simulating pod yields of a selected set of peanut lines for all locations identified for 30 years, grouping the peanut production areas based on their similarity in genotypic responses, and evaluating whether the derived location-groups would justify the criteria of being different mega-environments.

Peanut production areas were identified through production statistics by district. A total of 44 districts in 25 provinces were selected. Questionnaires were sent to the district extension agents requesting the identification of the main peanut producing villages and information on agronomic management in the individual villages. Soil types of the identified villages were obtained from the soil map and associated database of the Department of Land Development. The weather station that was located in or adjacent to each growing area was also identified. The basic units for model simulation, designated as locations in this study, were then determined based on the combinations of weather stations and soil types. This resulted in 130 unique locations.

Seventeen peanut lines representing the typical breeding lines under yield testing in a peanut breeding program were used in this study. Yield simulations were

performed using the CSM-CROPGRO-Peanut model (Jones et al, 2003; Hoogenboom et al., 2004). For each of the 130 locations, pod yield for each line were simulated for 30 years (1972–2002). Simulated pod yield for all locations of the individual peanut lines were used in grouping the peanut production locations into sub-regions. These location groupings were doned for each of the 30 years from 1972 to 2001 and for combined 30 years. The GGE biplot technique as described by Yan (2000) was used for grouping the peanut production locations that were identified. The evaluation whether these location-groups could be considered as mega-environments was based on the consistency of location groupings and of the winning genotypes in the individual location-groups across years (Yan et al., 2000, 2007).

Results

With a GGE biplot, location grouping is conducted by connecting the markers of the vertex genotypes and drawing lines perpendicular to each side of the polygon that pass through the origin, forming different sectors. Locations that fall into the same sector will have the same winning genotype and are considered to be in the same group (Yan and Rajcan, 2002). The GGE biplot of the 1972 data showed that the 130 locations could be divided into only two groups. The GGE biplot of the 1974 data, on the other hand, classified the 130 locations into three groups, but only few locations were in the third group. Some changes in the locations within the two dominant groups from those in the year 1972 were also noted. Such differences were observed when the results of location grouping based on data for the individual years were compared, indicating that location grouping was inconsistent. The inconsistency of location grouping across years could also be seen by the differences in the winning genotypes for the individual location-groups in different years. These results indicated that there is no justification to subdivide the peanut growing areas in Thailand into different mega-environments.

The GGE biplot based on mean data over 30 years also divided the 130 peanut producing locations in Thailand into two groups. However, all the locations were clustered close to the line separating the two groups, with a very narrow angle between line vectors encompassing all the locations (Figure 4.2). According to Yan and Rajcan (2002), An angle of environmental vectors of 90^{o} or less would indicate the similarity in genotype discrimination of the enclosed environments. In this study, the maximum angle between the vectors encompassing all the 130 locations was much below 90^{o}, indicating that these locations would discriminate genotypes in a similar manner and should be considered as one mega-environment.

Publication

Putto, W., A. Patanothai, S. Jogloy, and G. Hoogenboom. 2007. Determination of mega-environment for peanut breeding using the CSM-CROPGRO-Peanut model. Crop Science. (Submitted).

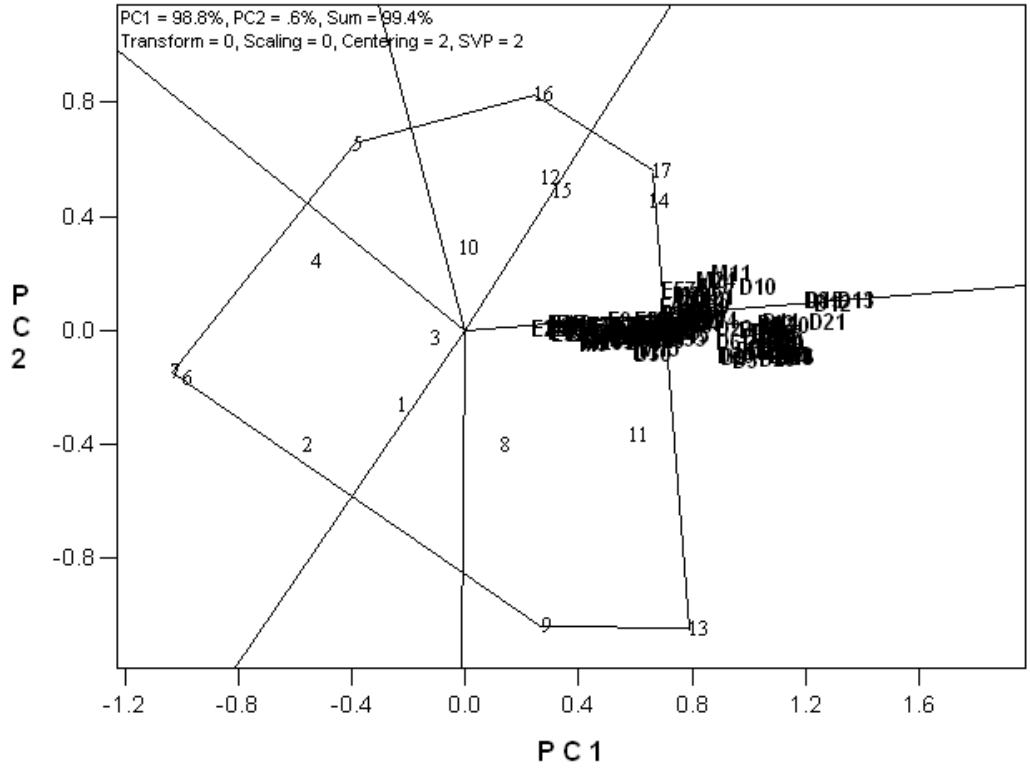

Fig. 4.2 GGE biplot for mean simulated pod yield over 30 years (1972-2001) of 17 peanut lines at 130 locations. The locations are identified by letter and numbers, e.g., E1, D1, M1, and the genotypes are represented by numbers ranging from 1 to 17.

Study 4-3. Dynamic patterns of components of genotype x environment interaction for pod yield of peanut over multiple years

Nittaya Phakamas and Aran Patanothai

Allocation of resources for testing is an important decision for breeders, as METs have become an essential part of all crop breeding programs. An understanding of the magnitudes of the components of G x E interaction is useful in this regard. Generally, an effective allocation of resources for testing of genotypes across locations and years is based on the relative importance of genotype x location (G x L), genotype x year (G x Y), and genotype x location x year (G x L x Y) interactions (Fehr, 1987). For a given target region, it is also not known how the relative importance of G x L, G x Y and G x L x Y interactions would change with increasing number of locations and years. Such information will have significant implication on the testing strategy of crop breeding lines. These information could be obtained from the analysis of data from METs that were conducted over multiple locations and years. To be reliable, the test genotypes should be relatively diverse, and the number of locations and years should be sufficiently large. In reality, such METs data are essentially not available. A crop simulation model can be used to simulate METs data for a large number of locations and years that are needed to examine the nature of the G x E interaction components.

The objective of the present study was to investigate the dynamic patterns of the G x Y, G x L and G x Y x L interactions for pod yield of peanut over multiple years using the CSM-CROPGRO-Peanut model.

Materials and methods

The METs data that were used for this study included simulated pod yield of 17 peanut lines at all peanut production areas of Thailand. A total of 112 unique locations were identified from combinations of soil types and weather stations as described in Study 4-2. The CSM-CROPGRO-Peanut Model was used for the simulation of peanut yield. At each location, peanut yield was simulated for three growing seasons, e.g., early-rainy, mid-rainy and dry seasons, over 30 years.

Combined analyses of variance for simulated pod yields of the 17 peanut lines at 112 locations over three seasons were done with the number of years incrementally increased from 2 to 30 years. Similar analyses were also done for the individual seasons with the number of years incrementally increased from 2 to 30. For each analysis, the contribution to total variation for each source of variation was calculated as the percentage of its sum of squares to the total sum of squares (% SS) in the combined analysis of variance. Percentages of sum of squares to total sum of squares for G, Y, L, G x Y, G x L and G x Y x L were determined for the combined three seasons and for the individual seasons, with the number of years incrementally increased from 2 to 30. The procedure was repeated four times, with four different starting years. The dynamic patterns of different components of G x E interaction were examined by the changes in their percentages of sum of squares to the total sum of squares as the number of years in the analysis of variance increased. Agreements in relative performances of the peanut lines between different numbers of testing years and between two contrasting years were also assessed by comparing simulated mean yield values and ranking of the individual peanut lines for the respective tests.

Results

The combined analyses of variance showed that the variation due to environments constituted the major proportion of the total yield variation, followed by the variation due to genotype, while the variation due to G x E interactions accounted for the smallest proportion. Among the environmental factors, the variation due to seasons (S) were most prominent, the variation due to location (L) were also substantial, but the variation due to year (Y) was much less. The relative contribution of these environmental factors changed as the number of years increased.

Generally, the year effect initially increased as the number of years increased until it reached a maximum and then gradually declined. The relative contribution of the location effect showed the opposite trend, being decreased as the number of years in the combined analysis increased, and then became more or less stable after reaching a certain number of years depending on the season and the starting year. The relative contribution of genotypic variation showed less fluctuation than those for year and location (Fig. 4.3).

The relative magnitude of the G x Y interaction increased as the number of years increased, and became more or less stable when the number of years was sufficiently large. Notable increases in the relative contribution of the G x Y interaction for the dry season were found to be associated with certain years.

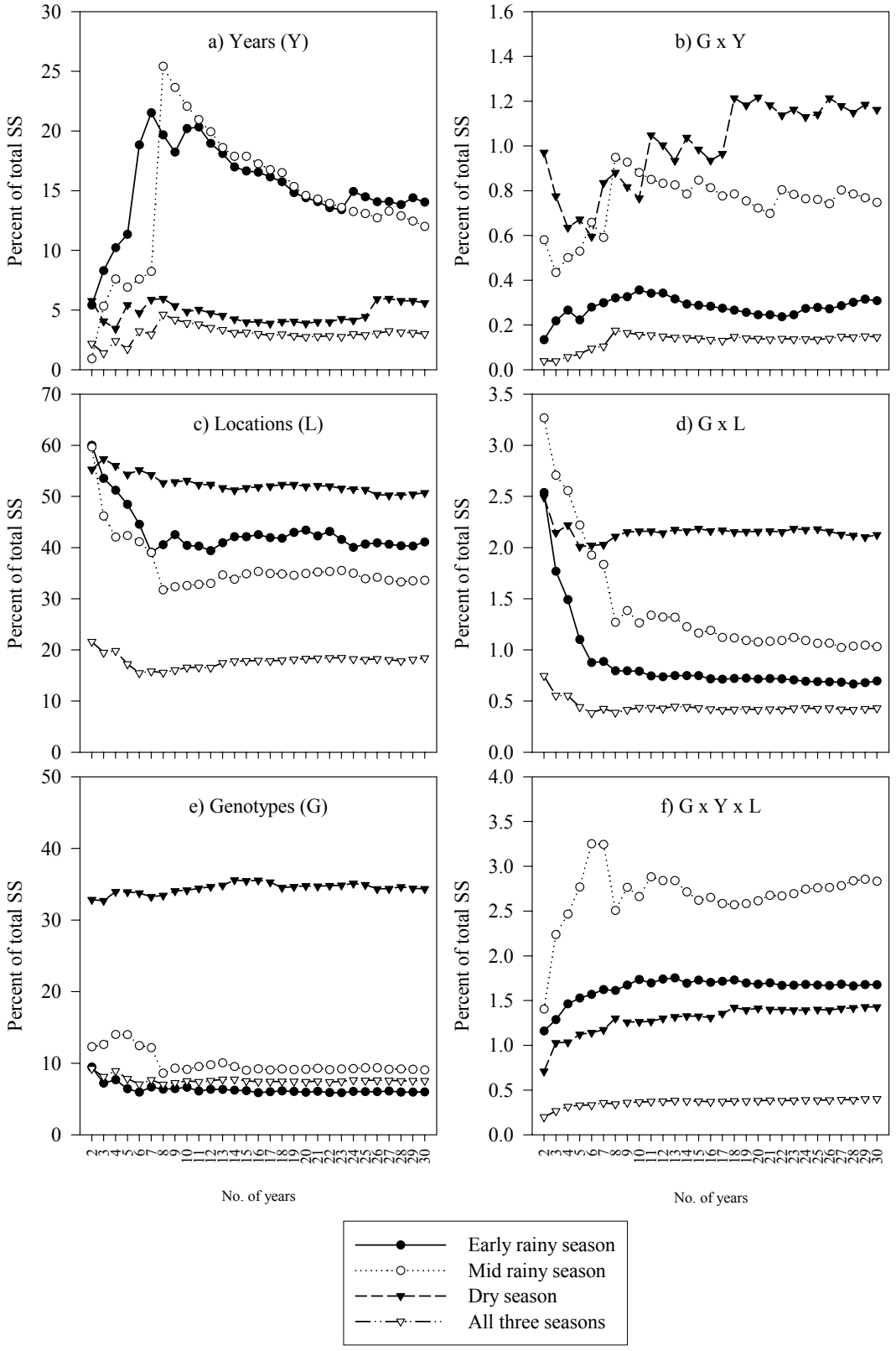

Fig. 4.3 Dynamic patterns of the contributions of the different sources of variation for simulated pod yield for the individual seasons and all seasons combined during the years 1972-2001 (30 years).

The relative contribution of the G x L interaction showed a sharp declining trend initially, but became more or less stable as the number of years increased (Fig. 4.3d). The trend was relatively smooth for all seasons, and became nearly stable in about 6 years, regardless of the starting year.

The relative contributions of the G x Y x L interaction showed the opposite trend as those of the G x L interaction, i.e., increasing initially and leveling off later as the number of years increased. The dynamic patterns for the different seasons were similar, and appeared to be more or less stable after about 6 years, regardless of the starting year in the combined analysis.

To examine how the G x Y interaction would affect the decision in breeding line selection, the mean and rank of the simulated pod yield of the 17 peanut lines over 112 locations and 3 seasons for 1, 2, 10 and 30 years were compared. Close agreements were observed between the means of the individual peanut lines over different numbers of years, both in terms of absolute value and ranking. However, when the mean performance of the peanut lines for the same 112 locations for two contrasting years were compared for the individual seasons, there was only a good agreement between the relative performance of the lines for the early-rainy season. A moderate correlation, however, was obtained for the mid-rainy season, in which cross over in ranking was found for several lines.

The 6 years required to stabilize the G x L interaction and the cross over in ranking of line performances in some contrasting years raise a question on the effectiveness of the strategy for using locations to replace years in varietal testing that is normally employed by breeders.

Publication

Phakamas, N., A. Patanothai, K. Pannangpetch, S. Jogloy and Gerrit Hoogenboom. 2007. Dynamic patterns of components of genotype x environment interaction for pod yield of peanut over multiple years: A simulation approach. Field Crops Research. (In press).

Study 4-4. Designing peanut ideotype for a target environment using the CSM-CROPGRO-Peanut model

Bhalang Suriharn and Aran Patanothai

High yield is generally a primary objective of all plant breeding programs (Fehr, 1987; Marshall, 1991). To date, breeding for higher yield has been done primarily based on empirical selection for yield *per se*. This approach, though, has been successful in increasing yields of various crops in the past, but further progress is becoming increasingly difficult (Araus et al., 2002). Great effort has gone to the identification of traits which breeders might select for in order to increase yield indirectly. Although a single trait may be of interest, a suit of traits representing a crop ideotype is often sought (Donald, 1968). Although the concept of plant ideotype has long been proposed, it has never been used directly (Rasmusson, 1991; Sedgley, 1991).

This was because the desired trait or combinations of traits have to be actually incorporated into a genotype to be able to evaluate their effects on yield performance (Mashall, 1991).

The ability of crop models to predict growth and yield as influenced by growing environment, agronomic practices and cultivar traits offers an opportunity to evaluate the effects on yield of a trait or a combination of traits by model simulation without actual incorporation of these traits into a genotype. With simulation models, effect of traits could be assessed in sensitivity analyses where the coefficients determining traits are varied, and the effects on simulated growth or yield observed (White, 1998). These models, thus, can be used to identify a desirable trait or a combination of traits leading to the designing of a crop ideotype for a specific environment. The objective of this study was to design a peanut ideotype with high yield potential under the growing environments of Khon Kaen province in northeast Thailand using the CSM-CROPGRO-Peanut model.

Materials and methods

A sensitivity analysis using the CSM-CROPGRO-Peanut model was employed in designing and evaluating the peanut ideotype. The CSM-CROPGRO-Peanut model uses 15 cultivar coefficients that define the growth and development characteristics or traits of a peanut cultivar as a model input. The sensitivity analysis was performed by first defining the target environment and management practices and selecting the initial values of the genetic coefficients to be used for model simulation, then changing the values of a particular genetic coefficient defining a particular trait within a certain limit for consecutive runs of model simulation over seasons and years. The resulting simulated final biomass and pod yields were compared to determine the yield responses to changing values of that particular trait parameter. The value that gave the highest average biomass or pod yield over a specified number of seasons and years in the target area was selected to represent the best value for that particular trait parameter. The sensitivity analysis was done sequentially by first adjusting the durations of developmental stages to obtain the maximum pod yield, then adjusting growth parameters to obtain the maximum biomass, and finally adjusting the partitioning parameters to obtain the maximum pod yield. The final outcome was a set of values for the trait parameters characterizing the peanut ideotype for the target environment. The designed ideotype was then evaluated for yield improvement over the current peanut cultivars.

The following steps were employed in the design and evaluation of the peanut ideotype: (1) defining the target environment and management practices, (2) selecting the initial cultivar genetic coefficients (GCs), (3) defining the desired crop duration and adjusting the durations of developmental stages, (4) adjusting growth parameters to obtain the maximum biomass, (5) adjusting partitioning parameters to obtain the maximum pod yield, and (6) evaluation of the designed peanut ideotype.

Results

Three peanut lines with different maturity durations were selected for utilizing their genetic coefficients as initial values. The resulting ideotypes have the same values of the individual GCs except the values of FLSH and FLSD for which adjustment have not been made. The characteristics of the designed peanut ideotype are early flowering, moderate to high leaf area and SLA, high leaf photosynthesis rate, determinate growth

habit and high partitioning of assimilates to pods and seeds, and short pod adding and moderate seed filling durations.

Substantial yield improvements were shown for all ideotypes and in all seasons (Table 4.1). Averaging over the three seasons, pod yields of the EM-ideotype, the MM-ideotype and the LM-ideotype were 65.5 %, 92.5 % and 52.1 % higher than their respective original lines. Averaging overall genotypes, the designed peanut ideotypes gave pod yield 70.3 % higher than the original peanut lines. However, the designed ideotypes gave slightly lower biomass than those of the original lines. Apparently, the designed ideotypes were much more effective in the reproductive growth than the original peanut lines.

The results of this study have demonstrated that the CSM-CROPGRO-Peanut model could be used in investigating the effects of different traits on performance of the peanut genotype and in designing peanut ideotype for a target environment. Among all these traits, adjusting PODUR and SFDUR appeared to give the highest impact on yield improvement. While combining all these desirable traits into a single genotype will take a long time, greater attentions should be given to selection for these two traits in breeding peanut for higher yield.

Table 4.1 Means over 20 years for pod yield and biomass of the original lines and the designed ideotypes in the early-rainy, the mid-rainy and the dry seasons, and percentages of yield improvements.

Category	Early-rainy season	Mid-rainy season	Dry season	Mean
Pod yield				
EM (kg ha^{-1})	1500	2248	1898	1882
EM-ideotype (kg ha^{-1})	2499	3377	3429	3102
Improvement (%)	*66.6*	*50.2*	*80.7*	*65.8*
MM (kg ha^{-1})	1235	1946	1478	1553
MM-Ideotype (kg ha^{-1})	2281	3286	3309	2959
Improvement	*84.6*	*68.9*	*123.9*	*92.5*
LM (kg ha^{-1})	1526	2383	1854	1921
LM-ideotype (kg ha^{-1})	2197	3286	3263	2915
Improvement (%)	*44.0*	*37.9*	*76.0*	*52.6*
Biomass				
EM (kg ha^{-1})	6908	8393	8169	7823
EM-ideotype (kg ha^{-1})	6227	7455	7728	7137
Improvement (%)	*-9.9*	*-11.2*	*-5.4*	*-8.8*
MM (kg ha^{-1})	6549	7990	7804	7448
MM-Ideotype (kg ha^{-1})	6079	7209	7603	6964
Improvement	*-7.2*	*-9.8*	*-2.6*	*-6.5*
LM (kg ha^{-1})	6393	7793	7151	7112
LM-ideotype (kg ha^{-1})	6004	7051	7488	6848
Improvement (%)	*-6.1*	*-9.5*	*4.7*	*-3.6*

EM = early maturing, MM = medium maturing, LM = late maturing.

Study 4-5. Suitable planting dates for determination of cultivar coefficients of peanut lines for application of a peanut model

Sukanya Sujariya and Aran Patanothai

Application of the CSM-CROPGRO-Peanut model requires cultivar-specific genetic coefficients (GCs) as an input (Tsuji et al., 1994; Boote et al., 1998). These GCs are crop characters that define the development, vegetative growth, and reproductive growth of individual genotypes (Hunt et al., 1993). They are normally not available for breeding lines or new crop cultivars. Determination of GCs of crop genotypes is normally done based on data collected in experiments that are conducted under optimum conditions over several environments (Hoogenboom et al., 1999). Data collection is also elaborate and intensive (IBSNAT, 1988). This poses a restriction on breeding and other applications of the model where time and resources are restricted. However, the studies of Banterng et al. (2004) and Suriharn et al. (2007) have shown that experimental data for two seasons are sufficient for the determination of GCs of peanut lines for breeding applications of the CSM-CROPGRO-Peanut model. In these studies, the GC determination experiments were conducted in two contrasting environments, i.e. rainy and dry seasons. It was noted that, in model calibration, the GCs that gave the best fit for the individual season data were some what different, particularly the phenological development parameters, forcing the GCs values that gave the best fit for both data sets to be between those for the individual seasons. This raises a question whether experimental data from two planting dates in the same season, e.g. early and mid-rainy seasons, would provide information for model calibration equivalent to those data from two contrasting seasons, e.g. rainy and dry seasons. The overall goal of this study was to investigate the predictability of the GCs of peanut lines that were derived from data for individual planting dates of a serial-planting-date experiment. Specific objectives were to determine the suitable planting dates for conducting field experiments for the determination of GCs of peanut lines for application of the CSM-CROPGRO-Peanut model.

Materials and methods

Six peanut lines/cultivars were used in this study. These lines/cultivars were grown in a serial-planting-date trial at the Khon Kaen Field Crops Research Center located in Khon Kaen, Thailand. The planting dates were (1) 4 December 2000, (2) 4 January 2001, (3) 4 February 2001, (4) 6 March 2001, (5) 4 April 2001, (6) 21 May 2001, (7) 13 June 2001 and (8) 13 July 2001. For each date, a randomized complete block design with three replicates was used. The trial was well managed to obtain optimum conditions for plant growth, avoiding drought, nutrient and biotic stresses as much as possible.

The experimental data collection followed the procedures described in IBSNAT (1988) and Hoogenboom et al. (1999). To determine the GCs of the test peanut lines, the minimum data set collected from the experiment was used according to the standard format of DSSAT Version 3.5. The GCs of individual peanut lines were calibrated to fit the measured data from each planting date following the procedures described by Boote (1999). The accuracy of the procedure used to estimate the cultivar coefficients was determined by comparing the simulated values of development and growth characteristics with their corresponding observed values, and by the values of the index of agreement (d) (Willmott, 1982).

The independent data sets for evaluating the model performance of the GCs for each planting date were data from the remaining 7 planting dates that were not used in deriving the GCs of the peanut lines. To evaluate model performance, the GCs of the individual peanut lines obtained from model calibration of data for a particular planting date were used to simulate growth and development of the same peanut lines for the remaining 7 planting dates. Model evaluation was conducted by comparing the simulated values of development and growth characteristics of the individual peanut lines with their corresponding observed values, and by obtaining the values for *d* statistic.

Results

The results from model calibration using data from individual planting dates showed that the simulated values for development and growth traits were in good agreement with their corresponding observed values for all peanut lines and all planting dates. This indicated that the experimental data obtained were reasonably good and model calibrations were done well. Although there were considerable discrepancies between simulated and observed values for some developmental stages of some of the peanut lines, particularly days to first pod and days to first seed, they were considered within the range of deviations possibly encountered in field observations.

In principle, the estimates of a particular GC that are derived from data of a field experiment planted in different dates should be the same or close together. In this study, it was evident that the values of the GC estimates varied considerably for the different planting dates. These variations could possibly be accounted for by the variations in temperature and solar radiation for the different planting dates. It was also noted that, in many cases, the GCs that were derived from the planting dates in the dry season were somewhat different from those that were derived from the planting dates during other times of the year. The results of model evaluation with independent data sets also showed different predictability of the GCs that were derived from data for individual planting dates. The GCs derived from planting dates in the cool and rainy seasons could well predict other planting dates in the cool and rainy seasons. Similarly, the GCs derived from planting dates in the dry season could only provide a good prediction for other planting dates of the dry season (Table 4.2). Examination of the weather conditions of the individual planting dates revealed that during the period from late-March to early-July the maximum temperature was generally higher than 35^{o}C. The optimum temperatures for peanut were found to range from 25 to 28^{o}C for vegetative growth and from 20 to 25^{o}C for reproductive growth (Vara Prasad et al., 2000). Higher or lower temperatures than the optimum were found to affect both growth and development of the peanut crop (Wynne et al. 1973; Cox 1979; Ketring 1984). It is possible that the temperature response function in the current CSM-CROPGRO-Peanut model could not account for such a high temperature during the dry season in Thailand, making the predictability of the GCs derived from this high temperature period differ from those derived from other periods. We also suspect that the current temperature response function in the model might not be sufficiently accurate to make the GCs derived from different planting dates more or less the same as would be expected theoretically.

The results from model evaluation indicated that the GCs that were derived from different planting dates could be divided into two groups (Table 4.2). The first group consists of the CGs from Planting dates 3 (Feb.), 4 (Mar.) and 5 (Apr.), which

were in the dry season. The second group includes the GCs from Planting dates 1 (Dec.), 2 (Jan.), 6 (May), 7 (Jun.) and 8 (Jul.) which were in the cool and rainy seasons. For both groups, the GCs form a particular planting date could predict the development and growth of peanut lines for the other planting dates in the same group quite well, but not for the other group. In Thailand, however, peanut is normally grown in three seasons, i.e., the early-rainy season, the mid-rainy season and the dry season. For the early-rainy season, the crop is planted during mid-April to the end of May, while it is planted during July to August for the mid-rainy season, and during December to January for the dry season. Planting dates in the first group, i.e., Planting dates 3, 4 and 5, are in the period from February to early-April which are not the regular planting periods of peanut in Thailand. Thus, in practice, the GC determination experiment would not be planted during this period. The other planting dates, on the other hand, are the normal peanut planting periods in Thailand. As the GCs derived from these dates could predict growth and development well for the peanut crop for other dates, they were considered suitable planting dates for GC determination experiments. It was concluded that the GC determination experiment could be planted at any time of the year except during the period from February to early-April.

Table 4.2 Summary of agreements between observed and simulated values for different characters of six peanut lines in model evaluation using cultivar coefficients derived from experimental data of a planting date in simulating peanut characters for another seven planting dates.

Evaluation	Calibration Planting Date							
Planting Date	3. Feb	4. Mar	5. Apr	6. May	7. Jun	8. July	1. Dec	2. Jan
3. Feb	G*	P	P	P	P	P	P	P
4. Mar	P	G*	G	P	P	P	P	P
5. Apr	P	G	G*	P	P	P	P	P
6. May	P	P	P	G*	G	G	G	G
7. Jun	P	P	P	G	G*	G	G	G
8. Jul	P	P	P	G	G	G*	G	G
1. Dec	P	P	P	G	G	G	G*	C
2. Jan	G	P	P	G	G	G	G	G*

*Calibration; G = Good, P = Poor.

Publication

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Study 4-6. Reduction in data collection for determination of cultivar coefficients for breeding applications

Jakarat Anothai and Aran Patanothai

The use of a crop simulation model in assisting the multi-environment evaluation of crop breeding lines would be more useful if it could be done during the early stages of line evaluation, because actual yield testing is normally done in only a few environments. A major difficulty, however, is the estimation of the GCs of new breeding lines which are required for model simulation. Typically, data of each line needs to be sampled several times throughout its life cycle on field experiments conducted over several environments (Hoogenboom et al., 1999). This recommended procedure is not very practical for plant breeding programs that have large numbers of breeding lines. Research is needed to reduce the intensity of data collection required for the determination of cultivar coefficients to make such an application practical. The objective of this study was to determine the minimum data to be collected for estimation of cultivar coefficients of peanut breeding lines for breeding applications of the CSM-CROPGRO-Peanut model.

Materials and methods

Data on growth and development of nine peanut lines in the present study were obtained from Suriharn et al. (2007). They were derived from an experiment designed specifically for determining the cultivar coefficients of these peanut lines. The data collected following the procedures described by IBSNAT (1988) and Hoogenboom *et al*. (1999), called "full data", involved five times of plant sampling for growth analysis and determination of nine developmental stages. Twenty alternative types of reduced data collection were designed from combinations of five types of growth sampling and four types of phenological stage determination. These and the full data set were used for model calibration to derive the cultivar coefficients of the nine peanut lines. The accuracy of model calibration was determined by comparing the simulated values of development and growth characteristics with their corresponding observed values, and by the values of the index of agreement (*d*) (Wilmott, 1982) and the values of the normalized root mean square error (RMSEn).

The cultivar coefficients derived from the different reduced data sets were evaluated by three methods, i.e., (i) by comparing the values of the cultivar coefficients derived from the full data and from reduced data sets; (ii) by comparing the agreements between the simulated values of development and growth characteristics obtained from the cultivar coefficients derived from the full and the reduced data sets with their corresponding observed values from which these cultivar coefficients were derived (the 2002 rainy and 2003 dry season data) as indicated by the *d* and RMSEn values; and (iii) an independent evaluation of the cultivar coefficients derived from the full data and various types of reduced data by comparing the agreements between the simulated values of development and growth characteristics with their corresponding observed values from an independent data set (the 2004 dry season data) as indicated by the *d* and RMSEn values.

Results

The results showed that (i) different types of reduced phenological data resulted in the same values of the cultivar coefficients; (ii) cultivar coefficients derived from some reduced growth data sets were as good as those derived from full data collection; (iii) model calibration of cultivar coefficients derived from various types of reduced data collection worked well for all development characteristics and fairly well for the normalized root mean square error (RMSEn) values of the plant growth characteristics; and (iv) model evaluation showed good agreements between observed and simulated values for all growth and development characteristics (Table 4.3). These results showed that it is possible to reduce the data collection for cultivar coefficients determination. The minimum data suggested is to determine two developmental stages, i.e., first flowering (R1) and harvest maturity (R8), and three plant samplings for growth analysis, i.e., around the stages of full seed (R6), physiological maturity (R7) and harvest maturity (R8).

Table 4.3 Mean and range for the normalized root mean square error (RMSEn) and index of agreement (*d*) for crop characters of nine peanut breeding lines in model evaluation with an independent data set

Types/ times of data collection	RMSEn (%)		*d*	
	Mean	Range	Mean	Range
		Biomass		
3	25.7	16.5-43.5	0.94	0.84-0.98
3′	26.9	14.8-40.0	0.93	0.87-0.99
3″	26.0	12.4-41.7	0.94	0.86-0.99
4	26.2	12.3-41.1	0.94	0.86-0.99
5	26.3	12.0-41.4	0.93	0.86-0.99
5′ (full data)	25.9	12.3-41.6	0.94	0.86-0.99
		Pod		
3	30.7	16.7-63.1	0.95	0.89-0.98
3′	27.0	14.3-50.4	0.94	0.74-0.99
3″	26.3	13.9-53.1	0.94	0.74-0.99
4	25.9	13.7-45.3	0.94	0.74-0.99
5	26.4	13.6-56.5	0.94	0.74-0.99
5′ (full data)	26.9	13.7-49.4	0.94	0.75-0.99
		Seed		
3	25.4	9.4-64.8	0.87	0.70-0.99
3′	26.5	8.8-64.2	0.87	0.71-0.99
3″	27.2	8.6-61.8	0.87	0.74-0.99
4	27.0	9.0-62.9	0.88	0.74-0.98
5	26.9	8.4-63.8	0.87	0.73-0.99
5′ (full data)	27.7	7.9-54.6	0.87	0.75-0.99

Publication

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Study 4-7. Determination of yield gap in a peanut production area

Preecha Kapetch, Aran Patanothai and Taksina Sansayavichai

In actual production, crop yield obtained is generally lower than what would be attainable as the crop always faces with some kinds of stress. The magnitude of this yield gap will indicate the chance of raising the actual yield level, and if the causes are known appropriate strategies for yield improvement could be determined. Previous yield gap analyses often used crop yield at a research station as attainable yield and taking observed yield from survey data or reported statistics. These yield gap estimates faced a lot of criticisms on their accuracy. Currently, crop growth models are available that can provide a good estimate of attainable yield from model simulation, and also can be used to identify certain causes of yield gap. The aim of this study was to evaluate the effectiveness the CSM-CROPGRO-Peanut model in estimating yield gap of peanut in a production area and identifying the associated causes.

Materials and methods

A peanut production area in Udon Thani province in Northeast Thailand was selected for this study. An initial survey was done to understand the production system and farmers' practices in the area. In the dry season, peanut is grown in paddy fields with irrigation in two soil series, while the rainy season crop is grown in upland areas without irrigation in three soil series. The area was, thus, divided into 5 zones or "basic simulation units" based on planting season and soil type. In each unit, 9 fields were harvested to determine biomass and pod yield, each with 4 samples of 4 rows x 4 m long. The average yield over these 9 fields was used to represent the actual yield of that unit. For each basic unit, yields of 6 released cultivars were simulated at different planting dates within a possible range, and over different plant populations, using the CSM-CROPGRO-Peanut model with soil and climatic data collected at the site and genetic coefficients of the peanut cultivars from other studies. The maximum yield from all combinations of cultivars x planting dates x plant populations was taken as the attainable yield of that particular basic unit, and yield gap was then calculated for each basic unit.

Results

Yield gaps of all units were considerably large, varying from 1,310 to 2,594 kg ha^{-1} or 40.7-69.6% in the different zones (Table 4.4). Within a basic unit, observed yields from individual fields also varied considerably. From field observations, the main factor reducing peanut yield in the dry season was water deficit, while poor soil preparation and low soil fertility were the major limiting factors in the rainy season. Drawing from the results of model simulation, in the dry season, a yield reduction of about 11.0% was from delayed planting and about 5.0% was from low plant population. In rainy season, however, inappropriate crop cultivar is main cause of yield reduction (12.9%), while late planting and low plant population accounted for only 1.6% and 7.1% of yield reduction, respectively (Table 4.5). It was concluded that the CSM-CROPGRO-Peanut model could effectively be used in estimating yield gaps and identifying associate causes, and can be applied in other sites.

Table 4.4 Yield gaps of peanut (kg ha^{-1}) in each zone.

Zone	Attainable yield (kg ha^{-1})	Farmer's yield	Yield gap	
			Kg ha^{-1}	%[1]
1	3,219	1,909	1,310	40.7
2	3,269	1,433	1,836	56.1
3	3,694	1,139	2,555	69.2
4	3,706	1,394	2,312	62.4
5	3,725	1,131	2,594	69.6

[1] Percent of attainable yield

Table 4.5 Percentage of yield increase from changing cultivar, planting date and plant population currently used to those that gave maximum simulated yields.

Management			Yield increase (%) *						
			Dry season			Rainy season			
Cultivar	Planting date	Plant density	Zone 1	Zone 2	Mean	Zone 3	Zone 4	Zone 5	Mean
√	√	√	30.8	27.1	29.0	25.1	18.7	19.0	20.9
√	√	×	27.7	22.5	25.1	18.0	13.9	16.2	16.0
√	×	√	3.5	7.3	5.4	16.3	16.6	16.5	16.5
√	×	×	1.0	6.2	3.6	10.4	14.5	13.9	12.9
×	√*	√*	17.5	15.3	16.4	17.0	10.9	13.2	13.7
×	√*	×	10.8	11.1	11.0	3.3	0.6	0.9	1.6
×	×	√*	5.5	4.4	5.0	1.6	10.0	9.7	7.1

√ Change to the cultivar, planting date or plant density that gave maximum simulated yields.

× Use the current cultivar, planting date or plant density.

√* Change to planting date and plant density that gave maximum simulated yield of the cultivar currently used.

* Average of 9 farmers' fields in each zone.

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Project outputs

1) Capacity building of researchers

Research team:

Number of researchers: 10

Number of Ph.D. students: 11

Number of M.S. students: 8

Number of research assistants: 3

Improved research capacity of researchers

Researchers in the team have gained their experiences in conducting quality research and in supervising thesis research of graduate students both at the M.S. and Ph.D. levels.

All of the researchers in the team have the capability of seeking their own research funds, and have their own projects in which they are the project leaders. All of them have research projects that received supports from the government budget through their research systems of their organizations, e.g., the university or the Department of Agriculture of the Ministry of Agriculture and Cooperatives. In additions, Dr. Sanun Jogloy also have projects supported by the Thailand Research Fund, the National Research Council and some private enterprises; Dr. Chutipong Akkasaeng and Dr. Napaporn Tantisuwichwong each has a project supported by the National Center for Genetic Engineering and Biotechnology; and Dr. Sanun Jogloy, Dr. Banyong Toomsan and Dr. Chutipong Akkasaeng also are grantees of the RGJ-PhD program of the TRF.

Training of graduate students

Eleven Ph.D. and 8 M.S. students are trained under the project. Two of the Ph.D. students have finished their program, and 9 are still on going. All of the M.S. students have graduated. Names of students and their current status are listed below:

No.	Degree	Name of student	Major advisor	Expected date of completion
1	Ph.D.	Mr. Bhalang Suriharn	Dr. Aran Patanothai	Graduated
2	Ph.D.	Miss Nittaya Phakamas	Dr. Aran Patanothai	December 2007
3	Ph.D.	Mr. Samran Pimrach	Dr. Aran Patanothai	February 2008
4	Ph.D.	Mr. Jakarat Anothai	Dr. Aran Patanothai	April 2008
5	Ph.D.	Miss Walaya Phutto	Dr. Aran Patanothai	April 2008
6	Ph.D.	Mr. Patcharin Songsri	Dr. Sanun Jogloy	October 2008
7	Ph.D.	Mr. Teerayuth Kerdthai	Dr. Sanun Jogloy	December 2008
8	Ph.D.	Miss Sukanya Promsakha Na Sakonnakhon	Dr. Banyong Toomsan	Graduated
9	Ph.D.	Ms. Srisuda Thippayarags	Dr. Banyong Toomsan	April 2008
10	Ph.D.	Miss Saowakon Hemwong	Dr. Banyong Toomsan	April 2008
11	Ph.D.	Miss Wanwipa Kaewpradit	Dr. Banyong Toomsan	April 2008

No.	Degree	Name of student	Major advisor	Expected date of completion
1	M.S.	Miss Sukanya Sujariya	Dr. Aran Patanothai	Graduated
2	M.S.	Mr. Preecha Kapetch	Dr. Aran Patanothai	Graduated
3	M.S.	Miss Ratchanok Meekaew	Dr. Sanun Jogloy	Graduated
4	M.S.	Miss Daungsamorn Jeeracheewanan	Dr. Sanun Jogloy	Graduated
5	M.S.	Mr. Saengjan Aekwisate	Dr. Sanun Jogloy	Graduated
6	M.S.	Miss Kanokwan Niyomsil	Dr. Sanun Jogloy	Graduated
7	M.S.	Mr. Chatchai Somee	Dr. Banyong Toomsan	Graduated
8	M.S.	Miss Prakobkit Phuthaisong	Dr. Poramate Banterng	Graduated

2) Published papers in accredited journals (as of 22 October 2007):

2.1 Number of published or accepted papers: 19.

(1) Promsakha Na Sakonnakhon, S., B. Toomsan, G. Cadisch, E.M Baggs, P. Vityakon, V. Limpinuntana, S. Jogloy and **A. Patanothai**. 2005. Dry season groundnut stover management practices determine nitrogen cycling efficiency and subsequent maize yields. Plant and Soils 272:183-199. (Impact factor 2006 = 1.495).

(2) Banterng, P., **A. Patanothai**, K. Pannangpetch, S. Jogloy and G. Hoogenboom. 2005. Yield stability evaluation of peanut lines: A comparison of an experimental versus a simulation approach. Field Crop Research 96: 168-175. (Impact factor 2006 = 1.634).

(3) Suriharn, B., **A. Patanothai** and S. Jogloy. Gene effects for specific leaf area and harvest index in peanut (*Arachis hypogaea* L.). Asian Journal of Plant Science 4(6): 667-672. (No impact factor).

(4) Promsakha Na Sakonnakhon, S., G. Cadisch, B. Toomsan, P. Vityakon, V. Limpinuntana, S. Jogloy and **A. Patanothai**. 2006. Weeds – friend or foe? The role of weed composition on nutrient recycling efficiency. Field Crop Research 97:238-247. (Impact factor 2006 = 1.634).

(5) Suriharn, B. **A. Patanothai**, K. Pannangpetch, S. Jogloy, and G. Hoogenboom. 2006. Derivation of cultivar coefficients of peanut lines for breeding applications of the CSM-CROPGRO Peanut Model. Crop Science 47: 605-619. (Impact factor 2006 = 1.153).

(6) Ekvised S., S. Jogloy, C. Akkasaeng, M. Keerati-kasikorn, T. Kesmala, I. Buddhasimma and **A. Patanothai**. 2006. Field evaluation of screening

procedures for thrips resistance in peanut. Asian J. Plant Sci. 5(5): 838-846. (No impact factor).

(7) Dangthaisong, P., P. Banterng, S. Jogloy, N. Vorasoot, **A. Patanothai** and G. Hoogenboom. 2006. Evaluation of the CSM-CROPGRO-Peanut model in simulating responses of two peanut cultivars to different moisture regimes. Asian J. Plant Sci. 5(6): 923-931. (No impact factor).

(8) Ekvised S., S. Jogloy, C. Akkasaeng, M. Keerati-kasikorn, T. Kesmala, I. Buddhasimma and **A. Patanothai**. 2006. Heritability and correlation of thrips resistance and agronomic traits in peanut. Asian J. Plant Sci. 5(6): 923-931. (No impact factor).

(9) Daengpuang, N., S. Jogloy, S. Wongkaew, B. Toomsan, T. Kesmala and **A. Patanothai.** 2006. Combining ability of peanut bud necrosis virus (PBNV) resistance in peanut. Thai J. Agric. Sci. (In press). (No impact factor).

(10) Niyomsil, K., S. Jogloy, M. Keeratikasikorn, C. Akkasaeng, T. Kesmala and **A. Patanothai**. 2006. Generation means analysis for thrips (*Thysanoptera*: *thripidae*) number and leaf damage by thrips feeding in peanut. Asian J. Plant Sci. (In press). (No impact factor).

(11) Kesmala, T., S. Jogloy, S. Wongkaew, C. Akkasaeng and **A. Patanothai**. 2006. Evaluation of ten peanut genotypes for resistance to *Peanut bud necrosis virus* (PBNV). Songklanakarin J. Sci. Technol. 28 (3): 459-467. (No impact factor). (No impact factor).

(12) Tonsomros, Y., S. Jogloy, S. Wongkaew, C. Akkasaeng, T. Kesmala and **A. Patanothai**. 2006. Heritability, phenotypic and genotypic correlations of *Peanut bud necrosis virus* (PBNV) reaction parameters in peanut. Songklanakarin J. Sci. Technol. 28 (3): 469-477. (No impact factor).

(13) Phudenpa, A., S. Jogloy, B. Toomsan, S. Wongkaew, T. Kesmala and **A. Patanothai**. 2006. Combining ability analysis for traits related to N_2-fixation and agronomic traits in peanut (*Arachis hypogaea* L.). Songklanakarin J. Sci. Technol. 28 (3): 449-457. (No impact factor).

(14) Poledate, A., S. Laohasiriwong, P. Jaisil, N. Vorasoot, S. Jogloy, T. Kesmala and **A. Patanothai**. 2007. Gene effects for parameters of *Peanut bud necrosis virus* (PBNV) resistance in peanut. Pakistan Journal of Biological Sciences 10(9): 1501-1506. (No impact factor).

(15) Akkasaeng, C., N. Tantisuwichwong, I. Chairam, N. Prakronrak, S. Jogloy and **A. Patanothai.** Isolation and identification of peanut leaf proteins regulated by water stress. Pakistan Journal of Biological Science 10(10): 1611-1617. (No impact factor).

(16) Thippayarugs, S., B. Toomsan, P. Vitayakon, V. Limpinuntana, **A. Patanothai** and G. Cadisch. Interactions in decomposition and N mineralization between tropical legume residue components. Agroforestry Systems. (In press) (Impact factor 2006 = 0.921).

(17) Anothai, J., **A. Patanothai**, K. Pannangpetch, S. Jogloy, G. Hoogenboom, and K. J. Boote. Reduction in data collection for determination of cultivar

coefficients for breeding application. Agricultural Systems (In press) (Impact factor 2006 = 1.378).

(18) Phakamas, N., **A. Patanothai**, K. Pannangpetch, S. Jogloy and Gerrit Hoogenboom. 2007. Dynamic patterns of components of genotype x environment interaction for pod yield of peanut over multiple years: A simulation approach. Field Crops Research. (In press). (Impact factor 2006 = 1.634).

(19) Pimratch, S., S. Jogloy, **A. Patanothai**, N. Vorasoot, B. Toomsan and C.C. Holbrook. Effects of Water Stress on Nitrogen Fixation in Peanut Genotypes with Different Levels of Drought Tolerance. Journal of Agronomy and Crop Science. (In press). (Impact factor 2006 = 1.046)

2.2 Number of submitted papers with revision: 4.

(1) Phakamas, N., **A. Patanothai**, K. Pannangpetch, S. Jogloy and G. Hoogenboom. Seasonal responses and genotype-by-season interactions for the dynamic growth and development traits of peanut. Submitted to Journal of Agricultural Science (Impact factor 2006 = 0.861).

(2) Phakamas, N., **A. Patanothai**, K. Pannangpetch, S. Jogloy and G. Hoogenboom. Physiological determinants for pod yield of peanut lines. Submitted to Annals of Applied Biology (Impact factor 2006 = 1.379).

(3) Songsri, P., S. Jogloy, N. Vorasoot, C. Akkasaeng, **A. Patanothai** and C.C. Holbrook. Responses to two levels of drought stress on reproductive characters of drought tolerant peanut. Submitted to Journal of Agronomy and Crop Science. (Impact factor 2006 = 1.046).

(4) Hemwong, S., G Cadisch, B. Toomsan, V. Limpinuntana, P. Vityakon and **A. Patanothai.** 2007. Dynamics of residue decomposition and N_2 fixation of grain legumes upon sugarcane stover retention instead of burning. Submitted to Soil and Tillage Research. (Impact factor 2006 = 1.619).

2.3 Number of first-submitted papers: 6.

(1) Suriharn, B., **A. Patanothai**, K. Pannangpetch, S. Jogloy and G. Hoogenboom. Applicability of the CSM-CROPGRO-Peanut model for yield performance and stability evaluation of peanut breeding lines. Submitted to Crop Science. (Impact factor 2006 = 1.153).

(2) Sujariya, S., **A. Patanothai**, T. Sansayavichai, K. Pannangpetch and G. Hoogenboom. Suitable planting dates for determination of cultivar coefficients of peanut lines for breeding applications. Submitted to Agronomy Journal (Impact factor 2006 = 1.272).

(3) Putto, W., **A. Patanothai** ,S. Jogloy, K. Pannangpetch and G. Hoogenboom. Determination of target environments for peanut breeding using the CSM-CROPGRO-Peanut model. Submitted to Crop Science. (Impact factor 2006 = 1.153).

(4) Pensuk, V., Jogloy, S., and **Patanothai, A**. 2006. Factors influencing the efficacy of mechanical inoculation of *Peanut bud necrosis tospovirus* in

Peanut (*Arachis hypogaea* L.). Submitted to Plant Disease (Impact factor 2006 = 1.795)

(5) Arunyarark, A., C. Akkasaeng, N. Vorasoot, S. Jogloy, N.R. Rachaputi, G.C. Wright and **A. Pathanothai**. Chlorophyll stability as indicator of drought toleranee in peanut. Submitted to Journal of Agronomy and Crop Science. (Impact factor 2006 = 1.046).

(6) Kaewpradit, W., B. Toomsan, G. Cadisch, P. Vitayakon, V. Limpinuntana, P. Sanjun, S. Jogloy and **A. Patanothai**. N dynamics of groundnut residues and rice straw management, its effect on growth and yield of KDML rice. Submitted to Field Crop Research. (Impact factor 2006 = 1.634).

3) Annual technical seminars

Three annual seminar had been held during the period of the project. All of these had been organized together with the Senior Research Scholar projects of Prof. Dr. Peerasak Srinives of Kasetsart University and Prof. Dr. Benjawan Rerkasem of Chiang Mai University.

The first one was held at the Imperial Phukaew Hill Resource, Petchaboon, during 6-7 May 2004.

The second was held at Hin Souy Nam Sai hotel, Rayong, during 26-27 October 2005.

The third was held at the Agricultural Research and Training Center of Chiang Mai University, Chiang Mai, during 3-4 December 2006.

4) Linkages with foreign institutes

Linkages have been established and collaborative research on peanut has been undertaken with the following foreign researchers at different institutes:

4.1 Dr. C.C. Holbrook, Crop Genetics and Breeding
Institute: USDA-ARS
Address: USDA-ARS, Coastal Plain Experiment Station
P.O. Box 748, Tifton, Georgia 31793 USA
E-mail : Holbrook@tifton.usda.gov

4.2 Dr. G.C. Wright, Principle Scientist (Agronomy)
Dr. N.C. Rachaputi, Senior Research Agronomist
Institute: Queensland Department of Primary Industies
Address: Queensland Department of Primary Industies
P.O. Box 23 Kingaroy Q4610, Australia
E-mail : Graeme.wright@dpi.gld.gov.au
E-mail : Rao.Rachaputi@dpi.gld.gov.au

4.3 Dr. G. Hoogenboom, Professor
Institute: University of Georgia
Address: Department of Biological and Agricultural Engineering
University of Georgia 165 Gordon Fotral Court Griffin,
Georgia 30223-1797, USA.
E-mail : gerrit@griffin.uga.edu

4.4 Dr. K.J. Boote, Professor
Institute: University of Florida
Address: Agronomy Department, University of Florida, Gainesville, FL 32611-0500, USA.
E-mail : kjb@mail.ifas.ufl.edu

4.5 Dr. R.K. Varshney : Senior Researcher
Institute: International Crop Research Insitute for the Semi-arid Tropic (ICRISAT)
Address: Applied genomic lab, International Crops Research Institute for the Semi-arid Tropics (ICRISAT),
Patancheru 502324 Andar Pradesh, India.
E-mail : r.k.varshney@cgiar.org, varshney.raj@gmail.com

4.6 Dr. George Cadisch, Professor
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University of Hohenheim
Address: 70593 Stuttgard, Germany
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