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Determination of adaptive responses of peanut genotypes and patterns of genotype × location interaction using the CSM-CROPGRO-Peanut model

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Abstract

The adaptive responses of crop genotypes and patterns of genotype x location (G x L) interaction are important to crop improvement as they are the basis for selection for specific adaptation and for elucidation of the causes of G x L interaction. Their legitimate assessment, however, requires yield data for the test genotypes for a large number of sites and over multiple years. Such data are seldom available from actual trials but could be provided by a crop simulation model. The objectives of this study were to assess the adaptive responses of a set of diverse peanut genotypes and to determine the various patterns of G x L interaction between pairs of these genotypes using a modeling approach. Pod yield of 17 peanut lines was simulated for 112 locations covering all peanut production areas in Thailand over three seasons and 30 years with the Cropping System Model (CSM) CROPGRO-Peanut. The data were analyzed for the adaptive response to locations of each peanut genotype with linear regression. Patterns of G x L interaction for the individual pairs of genotypes were determined. The results showed that the test genotypes could be classified into five groups based on mean yield and adaptive response, i.e., average yield with a low (<1.00) regression coefficient (Entries 5, 6, 8), above average yield with an average (=1.00) regression coefficient (Entries 3, 7, 10, 11, 12), above average yield with a high (>1.00) regression coefficient (Entries 13, 15, 17), below average yield with a low regression coefficient (Entry 1), and below average yield with an average regression coefficient (Entries 2, 4, 9, 14, 16). These characteristics are the basis for selection for either broad or specific adaptation. All three patterns of G x L interaction, i.e., no interaction, non-crossover interaction and crossover interaction, were also identified. Further analysis of these interaction patterns is recommended to elucidate the crop characters and environmental factors that are the causes of G x L interaction. The results indicate the potential of using crop simulation models as a tool to analyze adaptation of crop genotypes and to determine the pattern of G x L interaction for the individual genotype pairs.

Keywords: Crop breeding; Peanut; G x E interaction; Crop simulation model.

Introduction

Crop yield is a quantitative trait that generally exhibits large genotype by environment (G x E) interactions. Consequently, differences in yield performance between genotypes vary widely among environments (DeLacy, et al., 1990; Annicchiarico, 1997). The occurence of G x E interactions complicates the selection of genotypes with superior performance, as performance ranking of the test genotypes may change at different environments (Kang, 1990; Cooper and DeLacy, 1994; DeLacy et al., 1996; Annicchiarico, 2002a, b). Generally, G x E interactions are considered a hindrance to crop improvement in a target region (Kang, 1998), but they can be viewed as a reflection of the differences in genotype adaptation, which may be exploited by selection and/or by adjustments of the testing strategy (Basford et al., 1996). Multi-environmental trials (METs) are widely used by plant breeders to evaluate the relative performance of crop breeding lines for target environments. The information provided by these trials may also help breeding programs in gaining a better understanding of the type and size of G x E interactions that can be expected in a given region and in defining a breeding strategy to cope with them successfully (Annicchiarico, 2002a).

The effects of G x E interaction together with environmental effects contribute to the temporal and spatial instability of crop yield. To deal with each type of instability appropriately, the concept of yield stability has been used to define consistency of genotype performance across seasons/years (temporal stability), while adaptability has been used to define consistency across locations (spatial stability) (Barah et al., 1981; Lin and Binns, 1988; Evans, 1993). Information on stability is generally obtained from the analysis of METs that are conducted over multiple locations and years. The genotype x location (G x L) interaction indicates the spatial stability or adaptability, while the interaction of genotype with year (G x Y interaction) reflects the temporal stability. The former is especially important for breeding as this portion of G x E interaction that is repeatable and can be exploited by breeding for cultivars that are adapted to local conditions or that are widely adapted (Annicchiarico, 2002a). Concentrating on the G x L interaction also greatly simplifies the analysis of adaptation (Annicchiarico, 1997). The adaptation analysis will not only reveal the adaptive responses of the test genotypes for which the selection for a specific adaptation could be made but may identify patterns of G x L interaction for further analysis of their genotypic and environmental causes. The latter is quite important, as it could lead to the identification of crop characters that contribute to a superior genotype and the environmental factors that can be managed for a more effective cultivar evaluation (Yan and Hunt, 2001).

Generally, the adaptive response of a genotype is assessed with respect to other genotypes utilizing MET data (Annicchiarico, 2002a). To capture much of the G x L interaction that exists in the target area and to be able to separate it from season to season variation, data are needed on yield performance of the test genotypes for a large number of sites that cover the entire target area and for multiple years. Such data are seldom available from field trials, as there are practical limits to the number of sites and years in which METs can be conducted.

Physiologically-based crop simulation models have been developed as multipurpose tools for applications in agricultural research (Boote et al., 1996; Jone et al., 1998;

Hoogenboom et al., 1999; Hoogenboom et al., 2004). The ability of these models to simulate growth and yield of individual cultivars under different environmental and management conditions provides great opportunity for their use in studying the nature of G x E interactions (Aggarwal et al., 1997; White, 1998; Piper et al., 1998). With crop models, the yield of genotypes can be simulated for large numbers of test sites and years providing that the required input data are available. For peanut, the CSM-CROPGRO-Peanut is provided in the Decision Support System for Agrotechnology Transfer (DSSAT) software (Tsuji et al., 1994; Jone et al., 2003; Hoogenboom et al., 2004). The model has been evaluated extensively in Thailand, particularly for assisting with multi-environment evaluation of peanut breeding lines (Banterng et al., 2004; Banterng et al., 2006; Suriharn et al., 2007). The model has been shown to capture the differential responses of peanut genotypes to environmental conditions in different locations (Banterng et al., 2006). It has also been used to study the dynamic components of G x E interaction for pod yield of peanut (Phakamas et al., 2008) and to determine mega-environments for targeting peanut breeding in Thailand (Putto et al., 2008). It is, thus, a potential tool for assessing the adaptive response of peanut genotypes for a large number of sites and over multiple years that could capture the complete G x L interaction in a target region. The objectives of this study were to assess the adaptive response of a set of diverse peanut genotypes across peanut production areas in Thailand over multiple years and to determine the patterns of G x L interaction between pairs of these genotypes using the CSM-CROPGRO-Peanut model.

Materials and Methods

Simulation of multi-environment trial (MET) data

This study utilized simulated MET data from a previous study (Phakamas et al., 2008) that included simulated pod yield of 17 diverse peanut lines for all peanut production areas of Thailand. For each location, peanut yield was simulated for three growing seasons that included early-rainy, mid-rainy and dry seasons, over 30 years. To determine the specific peanut production locations in Thailand, statistical data by district for peanut production for the 2002-2003 cropping year were obtained from the Thai Department of Agricultural Extension. Forty-three districts, each with a considerable growing area of peanut, were selected. They were located in 24 provinces that extended from 12º 27´N to 19º 57´N latitude and 98º 33´E to 104º 43´E longitude. Eleven provinces are in the Northeast, one in the West, nine in the North, one in the East and two in the Central region of Thailand. Questionnaires were then sent to the district extension agents to obtain information on the main peanut producing villages in each district. The management and environmental information that was requested included the different growing seasons, the range of planting dates, the local soil characteristics and the irrigation practices. Once the production villages in the individual districts were identified, the soil types in the villages were determined based on the soil map and associated database of the Thai Department of Land Development. The weather station located in or closest to each growing area (41 total) were identified. The basic units for simulation, designated as locations, were then determined based on the combinations of weather stations and soil types. This was done by overlaying

the areas of the weather stations as determined by Thiessen polygons onto the soil series map (Hartkamp et al., 1999), resulting in 112 unique locations.

The 17 peanut lines were selected to represent the diverse breeding lines in early stage of yield testing in a peanut breeding program. Among them, 13 were breeding lines selected from preliminary yield trials of the Peanut Improvement Program of Khon Kaen University to provide diversity in yield level, plant type and maturity duration, and four were cultivars that have been released in Thailand (Table 1).

Table 1. Peanut lines and cultivars used in this study.

Entry no.	Genotype
	Early maturing lines
1	KKU1
2	KK5
3	(Luhua 11 x KK60-3)F6-15
4	(Luhua 11 x KK60-3)F6-22
	Medium maturing lines
5	(Luhua 11 x China 97-2)F6-11-3
6	((NC Ac.17090 x B_1)-25 x China 97-2)F5-14-8
7	((NC Ac.17090 x B_1)-25x China 97-2)F6-2-2
8	((NC Ac.17090 x B_1)-25 x China 97-2)F5-10-5
9	((NC Ac.17090 x B_1)-25 x Luhua 11)F5-14-2
10	((NC Ac.17090 x B_1)-25 x China 97-2)F6-7-1
11	(China 97-2 x Singburi)F6-13-1
	Late maturing lines
12	((NC Ac.17090 x B_1)-25 x China 97-2)F5-11-2
13	KKU 72-1
14	((NC Ac.17090 x B_1)-25 x KK60-3)F6-2-2
15	((NC Ac.17090 x B_1)-91 x China 97-2)F6-9-2
16	KK60-3
17	((NC Ac.17090 x B_1)-25 x China 97-2)F6-6-6

The CSM-CROPGRO-Peanut Model was used to simulate pod yield of each peanut genotype for the individual locations. The model requires input data that include local weather and soil conditions, cultivar coefficients and crop management information. The soil characteristics of each soil type were obtained from the database of the Thai Department of Land Development. The soil data included bulk density, percentage of sand, silt and clay, initial soil moisture, organic matter, pH, nitrate (NO_3^-) and ammonium (NH_4^+) concentrations, and exchangeable P and K. Historical weather data corresponding to the period from 1972 to 2002 were obtained from the Thai Department of Meteorology for the 41 weather stations. The weather data included daily maximum and minimum temperatures (^{o}C) and daily rainfall (mm). Daily solar radiation (MJ m^{-2} d^{-1}) was estimated based on the relationship between daily maximum and minimum temperatures and solar radiation using the procedure of Goodin et al. (1999) that was adapted for Thailand (Jintrawet et al., 2003). Crop management data for row spacing and plant population followed the standard procedure of the peanut yield trials, while the planting dates for each location were set according to the information obtained from the questionnaires. The cultivar coefficients for the 17 lines and cultivars were obtained from a previous study (Suriharn et al., 2007). In that study, data were collected on crop growth and development, crop management, and

soil and weather conditions as required for calibrating the cultivar coefficients (Hoogenboom et al., 1999) and calibrations were conducted following the procedures described by Boote (1999). The derived cultivar coefficients of these peanut lines were evaluated against an independent data set obtained from a separate experiment.

The simulation of pod yield for the 17 peanut lines was conducted with the seasonal analysis option of DSSAT (Thornton and Hoogenboom, 1994; Hoogenboom et al., 2004). For each of the 112 locations (basic units), pod yield of each line was simulated for 30 years (1972-2002) for three seasons, i.e., early-rainy, mid-rainy and dry seasons. A model feature called "automatic planting" was used to obtain the planting date for the rainy season, with planting condition requirements set to 80% of extractable soil moisture for the top 30 cm of the soil profile. The planting date ranged from May 1 to June 30 for the early-rainy season, and from July 1 to August 30 for the mid-rainy season. For the dry season, the crop was presumed to be irrigated, thus, the planting date was set to December 15. Nitrogen was assumed non-limiting, as peanut fixes nitrogen. Rainfed conditions were assumed for the early-rainy and the mid-rainy seasons, and full irrigation was used for the dry season. The harvest dates were based on the predicted time of maturity.

Determination of adaptive responses of peanut genotypes and patterns of G x L interaction

The combined analysis of variance for the full data set indicating the relative contributions of the various sources of variation was taken from Phakamas et al. (2008). The analysis was done in the conventional manner, in which years and locations were assumed to be random factors, while seasons and genotypes were considered as fixed factors (Gomez and Gomez, 1984).

In this study, the adaptive response of peanut genotypes to environmental conditions for the different locations was determined with a conventional linear regression model (Eberhart and Russell, 1966). Although multivariate techniques are thought to be more effective in explaining G x E interactions than linear regression models in general (Lin et al., 1986; Zobel et al., 1988; Nachit et al., 1992) and other methods for analyzing MET data are more popular [particularly the Additive Main Effects and Multiplicative Interaction (AMMI) and the genotype main effects and genotype x environment interaction biplot (GGE biplot) (Gauch, 2006; Yan et al., 2007)], we selected the linear regression model because it gives the adaptive responses to locations of the test genotypes and thus allows for the identification of patterns of G x L interaction, which are the primary objectives of this study. Furthermore, our preliminary analysis showed that the relationships between the means of the individual genotypes at different sites with site mean yields were essentially linear.

A regression coefficient was calculated for each peanut genotype by regressing the genotype mean for each location upon the mean of all genotypes for each location (site mean yield). Following Eberhart and Russell (1966), a regression coefficient value greater than 1.0 indicates the adaptability of the line to locations with favorable environments (high yielding locations), a value less than 1.0 indicates the adaptability to locations with unfavorable conditions (low yielding environments), while a value of 1.0 indicates an average adaptability across locations. The G x L interaction pattern was determined for each pair of genotypes based on the mean for simulated yield and the regression coefficient.

The difference between regression coefficients of the peanut lines in a pair was tested for significance with the t-test (Gomez and Gomez, 1984). Pairs of genotypes showing the three basic types of G x L interaction, i.e., no interaction, non-crossover interaction and crossover interaction, were also identified.

Results

The combined analysis of variance for the full data set as performed by Phakamas et al. (2008) showed that variations due to environments (year, season, location and their interaction) were predominant, accounting for 85.5% of the total variation in yield. Among these environmental factors, variation due to seasons was prominent, accounting for 40.0% of the total variation, followed by the variation due to locations (18.4% of total variation), while the yearly variation was relatively small, accounting for only 3.0% of the total variation. The genotypic variation was much lower than the environmental variation, contributing 7.6% to the total variation. The interactions of genotypes with environmental factors were all small, with the G x L interaction accounting for only 0.4% of the total variation (Phakamas et al., 2008).

The adaptive responses of the individual genotypes to location for simulated pod yield are illustrated in Figure 1. The relationship between mean yield and the regression coefficient of mean yield for each site against site mean yield for the individual genotypes is shown in Figure 2. Based on the values of mean yield and regression coefficient, the genotypes could be divided into five groups, i.e., average yield with a low (<1.00) regression coefficient (Entries 5, 6, 8), above average yield with an average ($=1.00$) regression coefficient (Entries 3, 7, 10, 11, 12), above average yield with a high (>1.00) regression coefficient (Entries 13, 15, 17), below average yield with a low regression coefficient (Entry 1), and below average yield with an average regression coefficient (Entries 2, 4, 9, 14, 16) (Figure 2). Following Eberhart and Russell (1966), Entries 3, 7, 10, 11, 12 were considered to have broad adaptability, as they have above average mean yield and a regression coefficient close to 1.0. Entry 7, the top yielding line, was the best in general adaptability, followed by Entry 10. Entries 13, 15 and 17 are adapted to high yielding environments as they have above average yield and regression coefficient greater than 1.00. On the other hand, Entries 5, 6 and 8 are adapted to the low yielding environment as they have a low value (<1.00) of the regression coefficient.

Figure 3 shows patterns of genotypic responses for six selected pairs of genotypes. Lack of interaction was shown for the Entry pairs 3-4 and 9-10, as indicated by their regression lines being parallel and statistically non-significant ($P>0.05$) (Figures 3a, 3b). The non-crossover interaction pattern was observed for the Entry pairs 1-7 and 10-16, as shown by difference in slopes ($P<0.05$), but no cross over of the regression lines between the two genotypes in a pair (Figures 3c, 3d). A crossover interaction was shown for the Entry pairs 5-8 and 3-15, indicated by differences in slopes ($P<0.05$) and cross over of the regression lines between the two genotypes in a pair. In fact, the patterns of G x L interaction could be determined for all pairs of the test genotypes. Apparently, the adaptive responses to location of the test peanut genotypes and all patterns of G x L interaction could be determined by the use of the CSM-CROPGRO-Peanut model.
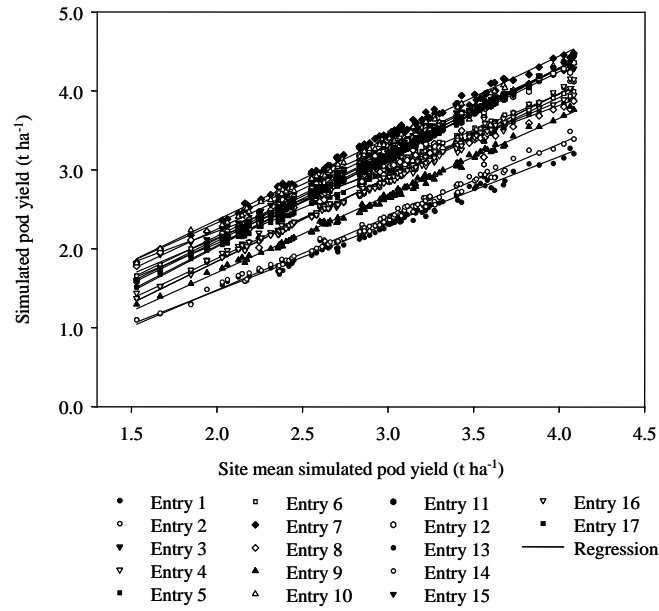
Figure 1. Adaptive response to location for simulated pod yield of peanut genotypes (see Table 1 for entry description).
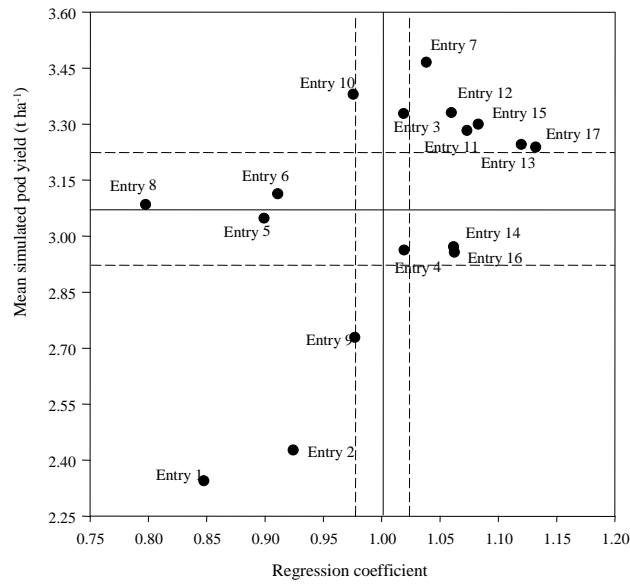

Figure 2. Relationship between mean simulated pod yield and the regression coefficient of the individual peanut genotypes; dotted lines indicate $\pm$ 2 standard errors (see Table 1 for entry description).
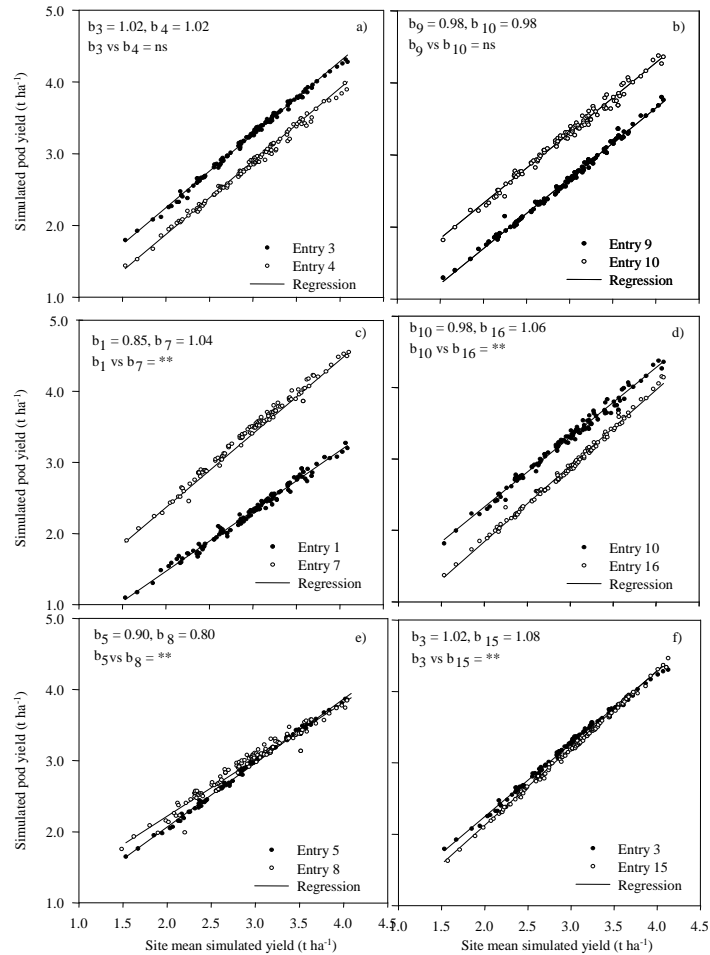
Figure 3. Patterns of genotype x location (G x L) interaction expressed by different pairs of selected genotypes: no interaction (a and b), non-crossover interaction (c and d), crossover interaction (e and f) (see Table 1 for entry description).

Discussion

The basis for a legitimate adaptability analysis of peanut genotypes is that the G x L interaction should cover a broad range of locations and multiple years. In this study, pod yield was simulated for 17 peanut genotypes at 112 locations over three seasons for 30 years with the CSM-CROPGRO-Peanut model in order to capture the G x L interaction encompassing all peanut production areas in Thailand. To obtain such a large number of yield data for a very broad scope of environments and management scenarios is impossible with actual experimentation.

The CSM-CROPGRO-Peanut model is responsive to only certain abiotic factors that include air temperature, solar radiation, rainfall and irrigation, and soil characteristics related to water availability in the profile and soil nitrogen. The model, however, does not respond to biotic factors such as diseases, insects, and weeds, and other abiotic factors such as phosphorus, potassium, water logging and microvariability within a field (Boote et al., 1996; Hoogenboom et al., 1999; Jone et al., 2003). The G x L interaction in the present study, therefore, represents only the interaction of the test genotypes with the weather and soil factors that were accounted for by the CSM-CROPGRO-Peanut model. However, it is the genotypic response to these environmental factors that are of concern to breeders as they would reflect the adaptability of genotypes to the inherent and persistent natural environments of the different production areas.

The results of the present study have demonstrated that with the use of a crop simulation model, the adaptive responses to location of the test genotypes as well as the different patterns of G x L interaction over a broad range of locations could be determined. The adaptive responses can be used for selecting lines with a broad or specific adaptation depending on the strategy of the breeding program; while the patterns of G x L interaction can be used for further analysis, particularly by a crop simulation model, to elucidate the causes of the G x L interaction. This information is very valuable as it could help develop an understanding of the genotypic characteristics that contribute to a superior genotype and the environmental factors that could be managed to facilitate cultivar evaluation (Yan and Hunt, 2001). The procedure could be extended to other regions and to other crops for which the crop simulation models are available. The difficulty would be the availability of the cultivar coefficients for a range of genotypes that are required for model simulation, as they are normally not available and their determination with the standard procedure requires specific field experiments with intensive data collection (Hoogenboom et al., 1999). However, a recent study by Anothai et al. (2008a) demonstrated that the minimum data required for the determination of the cultivar coefficients of the CSM-CROPGRO-Peanut model could be much reduced without sacrificing the accuracy of the estimates. (Mavromatis et al., 2001, 2002) and Anothai et al. (2008b) have also shown that cultivar coefficients for soybean and peanut lines, respectively, could be derived from crop performance trials. These procedures provide the opportunity for deriving the cultivar coefficients of crop genotypes from more readily available data that can then be used for generating the required data for subsequent analysis.

Investigating the genotypic characteristics and environmental factors causing G x L interaction is a big challenge for plant breeders. The present study was successful in obtaining the required data and identifying different patterns of G x L interaction among pairs of peanut genotypes with the use of the CSM-CROPGRO-Peanut model. The next step is further analysis to elucidate the causes. This can be done by conducting sensitivity analysis on pairs of genotypes with different patterns of G x L interaction using the CSM-CROPGRO-Peanut model. The procedure can be used to determine both the plant characters and the environmental factors that cause the G x L interaction.

Conclusion

Based on the results of the present study, it can be concluded that the adaptive response of peanut genotypes across a wide range of production environments and over multiple years and the patterns of G x L interaction between pairs of these genotypes can be

determined with the use of the CSM-CROPGRO-Peanut model. The approach can also be extended to other crops in which the crop simulation model and the required input data are available.

Acknowledgments

References

Aggarwal, P.K., Kropff, M.J., Teng, P.S., Khush, G.S., 1997. The challenge of integrating systems approach in plant breeding: opportunities, accomplishments and limitations. In: Kropff, M.J., Teng, P.S., Aggarwal, P.K., Bouman, B.A.M., Jones, J.W., van Laar, H.H. (Eds.), Applications of Systems Approaches at the Field Level. Kluwer Acadamic Publishers, Dordrecht, Pp: 1-23.

Annicchiarico, P., 1997. Additive main effects and multiplicative interaction (AMMI) of genotype-location interaction in variety trials repeated over years. Theor. Appl. Genet. 94: 1072-1077.

Annicchiarico, P., 2002a. Genotype x environment interactions: Challenges and opportunities for plant breeding and cultivar recommendations. FAO plant production and protection paper No. 174. FAO, Rome.

Annicchiarico, P., 2002b. Defining adaptation strategies and yield-stability targets in breeding programmes. In: Kang, M.S. (Ed.), Quantitative Genetics, Genomics and Plant Breeding. CABI Publishing, Wallingford, Pp: 365-383.

Anothai, J., Patanothai, A., Pannangpetch, K., Jogloy, S., Hoogenboom, G., Boote, K.J., 2008a. Reduction in data collection for determination of cultivar coefficients for breeding applications. Agr. Syst. 96: 195-206.

Anothai, J., Patanothai, A., Pannangpetch, K., Jogloy, S., Hoogenboom, G., Boote, K.J., 2008b. A sequential approach for determining the cultivar coefficients of peanut lines using end-of-season data of crop performance trials. Field Crops Res. 108: 169-178.

Banterng, P., Patanothai, A., Pannangpetch, K., Jogloy, S., Hoogenboom, G., 2004. Determination and evaluation of genetic coefficients of peanut lines for breeding applications. Eur. J. Agron. 21: 297-310.

Banterng, P., Patanothai, A., Pannangpetch, K., Jogloy, S., Hoogenboom, G., 2006. Yield stability evaluation of peanut lines: A comparison of an experimental versus a simulation approach. Field Crops Res. 96: 168-175.

Barah, B.C., Binswanger, H.P., Rana, B.S., Rao, G.P., 1981. The use of risk aversion in plant breeding: concept and application. Euphytica. 30: 451-458.

Basford, K.E., Williams, E.R., Cullis, B.R., Gilmour, A., 1996. Experimental design and analysis of variety trials. In: Cooper, M., Hammer, G.L. (Eds.), Plant Adaptation and Crop Improvement. CABI Publishing, Wallingford, Pp: 125-138.

Boote, K.J., 1999. Concepts for calibrating crop growth models. In: Hoogenboom, G., Wilkens, P.W., Tsuji, G.Y. (Eds.), DSSAT v3. Vol. 4. Univ. of Hawaii, Honolulu, Hawaii, Pp: 179-200.

Boote, K.J., Jones, J.W., Pickering, N.B., 1996. Potential uses and limitations of crop models. Agron. J. 88: 704-716.

Cooper, M., DeLacy, I.H., 1994. Relationships among analytical methods used to study genotypic variation and genotype-by-environment interaction in plant breeding multi-environment experiments. Theor. Appl. Genet. 88:561-572.

DeLacy, I.H., Eisemann, R.L., Cooper, M., 1990. The importance of genotype by environment interaction in regional variety trials. In: Kang, M.S. (Ed.), Genotype-by-Environment Interaction and Plant Breeding. Louisiana State Universitry, Baton Rouge, Louisiana, Pp: 189-213.

DeLacy, I.H., Basford, K.E., Cooper, M., Bull, J.K., McLaren, G.C., 1996. Analysis of multi-environmrnt trials-an historical perspective. In: Cooper, M., Hammer, G.L. (Eds.), Plant Adaptation and Crop Improvement. CAB International, Wallingford, Pp: 39-103.

Eberhart, S.A., Russell, W.A., 1966. Stability parameters for comparing varieties. Crop Sci. 6: 36-40.

Evan, L.T., 1993. Crop Evolution, Adaptation and Yield. Cambridge University Press, New York.

Gomez, K.A., Gomez, A.A., 1984. Statistical Procedures for Agricultural Research. John Wiley & Sons, New York.

Goodin, D.G., Hutchinson, J.M.S., Vanderlip, R.L., Knapp, M.C., 1999. Estimating solar irradiance for crop modeling using daily air temperature data. Agron. J. 91: 845-851.

Gauch, H.G., 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 46: 1488-1500.

Hartkamp, A.D., Beurs, K.De., Stein, A., White, J.W., 1999. Interpolation techniques for climate variables. NRG-GIS Series 99-01. CIMMYT, Mexico, D.F.

Hoogenboom, G., Wilkens, P.W., Tsuji, G.Y. (Eds.), 1999. DSSAT Version 3, Vol. 4. University of Hawaii, Honolulu, Hawaii.

Hoogenboom, G., Jones, J.W., Wilkens, P.W., Porter, C.H., Batchelor, W.D., Hunt, L.A., Boote, K.J., Singh, Uryasev, O., Bowen, W.T., Gijsman, A.J., Du Toit, A.S., White, J.W., Tsuji, G.Y., 2004. Decision Support System for Agrotechnology Transfer Version 4.0. [CD-ROM]. University of Hawaii, Honolulu, Hawaii.

Jintrawet, A., Promrit, S., Sringam, P., 2002. Calculating solar irradiance from recorded daily sunshine duration or air temperature. Agric. J. 18: 189-206.

Jones, J.W., Tsuji, G.Y., Hoogenboom, G., Hunt, L.A., Thornton, P.K., Wilkens, P.W., Imamura, D.T., Bowen, W.T., Singh, U., 1998. Decision support system for agrotechnology transfer, DSSAT v3. In: Tsuji, G.Y., Hoogenboom, G., and Thornton, P.K. (Eds.), Understanding Options for Agricultural Production. Kluwer Academic Publishers, Dordrecht, Pp: 157-177.

Jones, J.W., Hoogenboom, G., Porter, C.H., Boote, K.J., Batchelor, W.D., Hunt, L.A., Wilkens, P.W., Singh, U., Gijsman, A.J., Ritchie, J.T., 2003. The DSSAT cropping system model. Europ. J. Agron. 18: 235-265.

Kang, M.S., 1990. Understanding and utilization of genotype-by-environment interaction in plant breeding. In: Kang, M.S. (Ed.), Genotype-by-Environment Interaction and Plant Breeding. Louisiana State University, Baton Rouge, Louisiana, Pp: 52-68.

Kang, M.S., 1998. Using genotype-by-environment interaction for crop cultivar development. Adv. Agron. 62: 199-252.

Lin, C.S., Binns, M.R., Lefkovitc, L.P., 1986. Stability analysis: where do we stand? Crop Sci. 26: 894-900.

Lin, C.S., Binns, M.R. 1988. A methods for analyzing cultivar x location x year experiments: a new stability parameter. Theor. Appl. Genet. 76: 425-430.

Mavromatis, T., Boote, K.J., Jones, J.W., Irmak, A., Shinde, D., Hoogenboom, G., 2001. Developing genetic coefficients for crop simulation models with data from crop performance trials. Crop Sci. 41: 40-51.

Mavromatis, T., Boote, K.J., Jones, J.W., Wilkerson, G.G., Hoogenboom, G., 2002. Repeatability of model genetic coefficients derived from soybean performance trials across different states. Crop Sci., 42: 76-89.

Nachit, M.M., Nachit, G., Ketata, H., Gauch, H.G., Zobel, R.W., 1992. Use of AMMI and linear regression models to analyze genotype-environment interaction in durum wheat. Theor. Appl. Gen. 83: 597-601.

Phakamas, N., Patanothai, A., Pannangpetch, K., Jogloy, S., Hoogenboom, G., 2008. Dynamic patterns of components of genotype x environment interaction for pod yield of peanut over multiple years: A simulation approach. Field Crops Res. 106: 9-21.

Piper, E.L., Boote, K.J., Jones, J.W., 1998. Evaluation and improvement of crop models using regional cultivar trial data. Appl. Eng. Agric. 14: 435-446.

Putto, W., Patanothai, A., Jogloy, S., Hoogenboom, G., 2008. Determination of mega-environments for peanut breeding using the CSM-CROPGRO-Peanut model. Crop Sci. 48: 973-982.

Suriharn, B., Patanothai, A., Pannangpetch, K., Jogloy, S., Hoogenboom, G., 2007. Dertermination of cultivar coefficients of peanut lines for breeding applications of the CSM-CROPGRO-Peanut model. Crop Sci. 47: 605-619.

Thornton, P.K., Hoogenboom, G., 1994. A computer program to analyze single-season crop model outputs. Agron. J. 86: 860-868.

Tsuji, G.Y., Jones, J.W., Balas, S. (Eds.), 1994. DSSAT Version 3. University of Hawaii, Honolulu, Hawaii.

White, J.W., 1998. Modeling and crop improvement, In: Tsuji, G.Y., Hoogenboom, G., Thornton, P.K. (Eds.), Understanding Options for Agricultural Production. Kluwer Academic Publishers, Dordrecht, the Netherlands, Pp: 179-188.

Yan, W., Hunt, L.A., 2001. Interpretation of genotype x environment interaction for winter wheat yield in Ontario. Crop Sci. 41: 19-25.

Yan, W., Kang, M.S., Ma, B., Woods, S., Cornelius, P.L., 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci. 47: 643-653.

Zobel, R.W., Wright, M.J., Gauch, H.G., 1988. Statistical analysis of a yield trial. Agron. J. 80: 388-393.