

Applications of Crop Simulation Model in Peanut Breeding

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Abstract

The ability of crop simulation models to simulate growth and yield of crop cultivars in different environments make them an attractive tool for crop improvement. Potential breeding applications of these models include assisting multi-environment evaluation of crop breeding lines, understanding the nature of genotype by environment (G x E) interactions and identification of desirable traits leading to plant-type design. All these applications have been investigated at Khon Kaen University for peanut breeding using the CSM-CROPGRO-Peanut model.

Model application in assisting multi-environment evaluation of peanut breeding lines was first evaluated with 12 large-seeded advanced breeding lines tested in 12 environments. The results showed that the model could predict yield performance and stability of these lines quite well. A subsequent study with 13 diverse peanut lines tested at 11 environments also confirmed these results. We have also used the CSM-CROPGRO-Peanut model in investigating the dynamic of genotype x year (G x Y) and genotype x location (G x L) interactions, assessing crop traits and environmental factors causing G x E interaction, identifying effective test locations for a more efficient evaluation of peanut breeding lines, and designing the peanut ideotype for a target environment. We have also found ways to overcome the problem of extensive data collection for the determination of cultivar coefficients of new breeding lines which is a major limitation for breeding application of the model. Results of these are highlighted in the paper.

Media summary

Crop simulation models could be a valuable tool for various applications in crop breeding.

Key words

Crop model, varietal evaluation, G x E interaction, plant-type design, peanut breeding

Introduction

Physiologically-based crop simulation models have been developed as a multipurpose tool for application in agricultural research (Hoogenboom et al., 1999; Jones et al., 2003). These models can simulate yield of crop cultivars under various management and environmental conditions, making them an attractive tool for crop improvement. Potential contributions of crop models to crop improvement process include assisting with multi-location evaluation of crop breeding lines, understanding the nature of genotype by environment (G x E) interactions, identification and evaluation of desirable traits leading to the design of a crop ideotype for a specific environment (Aggarwal et al., 1995; White, 1998; Boote et al., 2001). All of these model applications have been investigated at Khon Kaen University (KKU) in Thailand for peanut breeding using the Cropping System Model (CSM)-CROPGRO-Peanut model. This paper summarizes the studies that have been done or are underway.

Assisting multi-environment evaluation of crop breeding lines

The first study examining the possibility of using the CSM-CROPGRO-Peanut model to evaluate yield performance and stability of peanut lines was conducted with 12 advanced peanut lines under testing at the regional yield trial stage across 10 environments in Thailand (Banterng et al., 2006). The results showed that the model predicted the relative mean pod yield over 10 environments of the tested peanut lines reasonably well; five out of the six highest yielding lines (top 50 %) were identified by both experimentation and simulation. The model also gave estimates of the regression coefficient of entry mean yield against site mean yield that were in good agreement with those obtained from actual testing. Some discrepancies were observed, but these were seen as providing additional information for the responses of the test genotypes to environmental factors that were not accounted for by the model. These findings were confirmed by a follow up study conducted with 17 diverse peanut lines that were tested across 11 environments (Suriharn, 2008). It was concluded that the CSM-CROPGRO-Peanut model could be used in assisting with yield performance and stability evaluation of peanut breeding lines.

A major limitation to this model application is the estimation of the cultivar coefficients (GCs) of new breeding lines as it requires elaborated data collection from field experiments conducted under non-stress condition over multiple environments (Hoogenboom et al., 1999). To reduce the data to be collected, we first established that two seasons of such data collection were sufficient (Banterng et al., 2004; Suriharn et al., 2006). However, the methodology was still too intensive to be applicable to breeding lines at the early testing stages. Another study was then conducted to reduce the intensity of the data collection (Anothai et al., 2008a). The results indicated that it is possible to reduce the data collection to determining only 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). The GCs derived from the reduced data set gave good prediction of yield performance of two sets of peanut lines in the regional and standard yield trials conducted at 10 and 8 environments, respectively (Anothai et al., 2008b). We were also successful in deriving the GCs of peanut lines from performance trial data using the Genotype Coefficient Calculator (GENCALC) program (Anothai et al., 2008c).

Studies on G x E interactions

Determination of mega-environment in Thailand for targeting peanut breeding

The growing interest to breed crop cultivars for specific adaptation to local environments requires that all production areas of the crop should be sub-divided into mega-environments to be the targets for crop breeding. A mega-environment is a group of growing areas that are similar and consistent in genotypic responses across years. It is generally identified through the analysis of METs of crop breeding lines. The process involves analyzing the environmental responses of the test genotypes and then grouping the test environments on the basis of their similarity in genotypic responses. We have used the CSM-CROPGRO-Peanut model in examining whether peanut production areas in Thailand are sufficiently diverse to justify a sub-division into mega-environments. The model was used to simulate pod yields of 17 peanut lines in 57 environments in the early rainy season, 26 environments in the mid rainy season and 47 environments in the dry seasons, totaling 130 environments in each year, for 30 years. Data for each year were used to sub-divide peanut production areas in Thailand into sub-regions based on the G x E interactions, using a cluster analysis (Collaku et al., 2002) and a GGE biplot (Yan et al., 2000). Both cluster analysis and GGE biplot showed inconsistent results of environmental grouping and non-repeatable relative performances of peanut genotypes across years, indicating that Thailand should be considered as one mega-environment for peanut breeding.

Determination of effective test sites for breeding lines evaluation

Choosing test sites is another important breeding decision, as it would affect the efficiency of breeding lines evaluation. We have examined this for the evaluation of peanut lines in Thailand using the CSM-CROPGRO-Peanut model. Simulated pod yields of 17 peanut lines for 57 environments in the early rainy season, 26 environments in the mid rainy season and 47 environments in the dry seasons over 30 years were used for environmental grouping by cluster analysis. Five strategies for selecting test sites based on geographical distribution and on the results of environmental grouping were compared. Preliminary results indicated that the most efficient test sites were those selected based on environmental grouping.

Crop characters and environmental factors causing G x E interactions

As G x E interactions are important for crop breeding, better understanding of the nature of G x E interactions is needed to be able to use them effectively through appropriate breeding methodologies. Currently, crop characters and environmental factors that give rise to G x E interactions are not well understood. Work is now underway to examine these questions using a crop simulation model. The full data set of simulated pod yields of 17 peanut lines at 112 locations for 3 seasons and 30 years was reduced in such a way that most of the G x E interactions was retained. The reduced data set consisted of 30 locations in 10 years, from which the patterns of genotypic responses to environments were determined. Work is underway to examine the crop characters and the environmental factors causing differential responses to environments in pod yield between the peanut lines by sensitivity analyses using the CSM-CROPGRO-Peanut model.

Dynamic of G x Y and G x L interactions

Allocation of resources for testing of breeding lines is an important decision for breeders. Generally, effective allocation of resources for testing of genotypes across locations and years is based on the relative importance of G x L, G x Y, and G x L x Y interactions. As actual METs data are limited in the number of test locations and years, for a given target region, it is normally 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 years. A study was conducted to investigate the dynamic patterns of G x Y and G x L interactions for pod yield of peanut using the CSM-CROPGRO-Peanut model (Phakamas et al., 2008). It involved analyses of simulated pod yield of 17 diverse peanut lines at 112 locations covering all peanut production areas in Thailand over 3 seasons (early-rainy, mid-rainy and dry seasons) and 30 years (1972-2002). The results showed that increasing number of years in the analyses resulted in an increase in the magnitude of the G x Y and G x L x Y interactions, but a decline in the G x L contribution. Both the G x L and G x L x Y interactions became stable when 6 or more years were included. Several cross over in the performance ranking of the test peanut lines in two contrasting years were also observed for the mid-rainy season. These results raise a question on the effectiveness of the strategy for using locations to replace years in varietal testing that is normally employed by breeders. The study also demonstrated that the practical limit of multi-year evaluation of crop breeding lines could be overcome by the use of a crop simulation model.

Designing a peanut ideotype for a target environment

The concept of plant ideotype, though has long been proposed, has never been used directly because of the difficulty in evaluating the effect of the desirable trait or combinations of traits. Crop simulation models can help overcome this difficulty. 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. We have used this approach in designing a peanut ideotype for the growing environments of Khon Kaen province in Thailand using the CSM-CROPGRO-Peanut model (Suriharn, 2006). More than 70 % improvement in yield performance over the current peanut cultivar KK 5 was achieved for the designed ideotype. 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.

Conclusion

Our studies clearly indicate that crop simulation models could be a useful tool for crop improvement. Further investigations will certainly open up a broader range of breeding applications of crop simulation models.

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