Application of the CSM–CROPGRO–Peanut Model in Assisting with the Performance Evaluation of Peanut Lines at the Early Stage of Yield Testing.

J. ANOTHAI*, A. PATANOTHAI, K. PANNANGPETCH, S. JOGLOY, Department of Plant Science and Agricultural Resources, Faculty of Agriculture, Khon Kaen University, Khon Kaen 40002, Thailand; K.J. BOOTE, Agronomy Department, University of Florida, Gainesville, FL 32611-0500; and G. HOOKENBOOM, Department of Biological and Agricultural Engineering, The University of Georgia Griffin, GA 30223-1797.

The success in deriving the cultivar coefficients from a reduced set of field data allows the use of crop models in assisting with performance evaluation of crop breeding lines at the early testing stage. At this stage, the lines are normally tested in only a few environments, and selection decisions are based on these limited tests. The model can provide simulated yield of the tested peanut genotypes for a wide range of environments and in multiple years. These simulated yield data can help plant breeders make decisions on line selection more accurately and effectively. However, the actual practice of this application so far has not been evaluated with real data. The objective of this study was to evaluate the application of the Cropping System Model (CSM)–CROPGRO–Peanut in assisting with performance evaluation of peanut breeding lines at the early testing stage. Two sets of peanut lines in the preliminary yield trial (PYT) stage, referred to as Set I and Set II, were yield tested at Khon Kaen University for three environments during 2004–2005. Separate experiments for these lines were also simultaneously conducted for two seasons to obtain reduced data sets for determining the cultivar coefficients that are needed for the CSM–CROPGRO–Peanut model. The model was then used to simulate pod yield of the test lines for the same three environments in which they were actually tested in the PYTs. In addition, the model was used to simulate pod yield for 130 locations that covered all major peanut production areas in Thailand for 30 years for a total of 3,900 unique environments in order to extend the range of the environments of the PYTs. Three selection scenarios were employed based on genotypic ranking by observed yield from the PYTs, by simulated yield for 3,900 environments, and by both observed and simulated yields. The results showed that model simulation picked up more genotype x environment (G x E) interaction in extending the range of the test environments from 3 to 3,900. Among the top 50% highest yielding lines in Sets I and II, actual PYTs and model simulations were found to identify the same four out of nine lines in Set I and nine out of 12 lines in Set II. The results from the model simulations also indicated that some lines with high yield potential could have been eliminated in the early stage of yield evaluation if selection was based on only observed yield from the PYT. Likewise, some lines with high observed yield could have also been eliminated if selection was based on only simulated yield. It was concluded that using both simulated yield based on the CSM-CROPGRO-Peanut model and observed yield from actual PYT as the basis for selection will ensure that these lines will not be eliminated, and will make line selection at the early evaluation stage more effective.