CHAPTER I
INTRODUCTION

Peanut (*Arachis hypogaea* L.) is largely grown under rain-fed conditions in the semi-arid tropics, where drought is a major production constraint because of erratic and insufficient rainfall (Nageswara Rao et al., 1989; Reddy et al., 2003). Peanut genotypes respond differently to water stress for productivity depending on growth stages. Drought stress especially during pod and seed formation stages can reduce pod yield up to 56-85% (Nageswara Rao et al., 1989). However, water stress during the vegetative or early flowering stages is not detrimental and sometimes actually increases yield (Nageswara Rao et al., 1985; Nautiyal et al., 1999; Puangbut et al., 2009). Moreover, drought also increases the likely of aflatoxin contamination and can result in deterioration of peanut quality (Holbrook and Stalker, 2003; Arunyanark et al., 2009; Girdthai et al., 2010). Improving water access and management is difficult as water is an inadequate resource, and, hence, breeding for drought resistance has been an important strategy in alleviating the problem.

The identification of drought resistance germplasm is an important stage of breeding for drought resistance. Yield has been a primary target trait of drought resistance breeding in peanut, but selection for yield has slow progress because of the complex nature of the trait that causes high genotype by environment interactions (Branch and Hildebrand, 1989; Jackson et al., 1996; Araus et al., 2002). Therefore, alternative selection strategies in order to breed for drought resistance are worth exploring. Water use efficiency (WUE) is one of such traits that can contribute to productivity when water resources are limited (Wright et al., 1994). WUE is used to express the amount of total biomass produced per unit of water use in evapotranspiration (Teare et al., 1982). The trait is used to compare peanut genotypes with similar water use and different in biomass production. However, the selection through this process is difficult or even unsuccessful due to genotypes and environmental variations (Arunyanark et al., 2008). This hinders the progress in breeding for drought resistance. The identification and use of surrogate traits for

WUE that are simple and have low environmental variations under drought conditions would be more effective and efficient.

The relationships among WUE related physiological traits have been demonstrated in peanut such as positive relationship between SPAD chlorophyll meter reading (SCMR) and WUE and negative relationship between specific leaf area (SLA) and WUE. Chlorophyll content can be measured simply and rapidly by handheld portable SPAD chlorophyll meter and the association between chlorophyll content and SPAD reading is high and positive (Samdur et al., 2000; Arunyanark et al., 2008). Thus, SLA is another trait potentially useful for breeding program for drought resistance (Wright et al., 1994). Furthermore, the interest has been paid on finding genotypes with ability to maintain low canopy temperature under field conditions. Peanut canopy temperatures are correlated with visual drought stress rating and yield (Rucker et al., 1994). The investigation in a large number of peanut genotypes and different levels of soil moisture gradients will provide useful information for explaining the relationships between surrogate traits and WUE in order to breed for drought resistance.

Drought resistance may be enhanced by improving the ability of the crop to extract water from the soil (Wright and Nageswara Rao, 1994). Deep rooting, root length density (RLD) and root distribution have been identified as drought adaptive traits (Passioura, 1983; Turner, 1986; Dardanelli et al., 1997; Matsui and Singh, 2003; Taiz and Zeiger, 2006). The peanut genotypes having the higher RLD at lower soil depth enhanced drought tolerance and such response can help peanut genotypes to obtain high pod yield and harvest index, indicating that the genotypes which were classified as drought responsive as they increased RLD in deeper soil layer (Songsri et al., 2008a). Therefore, root responses to drought play an important role for yield maintenance in peanut especially under pre-flowering drought. Unfortunately, information on the responses of root characteristics of diverse peanut genotypes to pre-flowering drought under field conditions is still lacking. A better understanding on root responses should provide insight into the mechanisms underlying the adaptation of peanut under early drought environment. Peanut root distribution patterns are also not well understood and have not been studied extensively. Especially, there is a lack of information on classification of root distribution patterns

for many peanut genotypes under mid-season drought, which could be useful for peanut drought resistant breeding programs. Nevertheless, root collecting is difficult, time consuming and labor intensive. Thus, the problem has to be resolved.

Crop simulation models have increasingly been used to support agricultural research, field agronomic advice, and even decision support for agricultural policy formulation. The CSM-CROPGRO-Peanut model is one of the crop simulation models that encompass the Decision Support System for Agrotechnology Transfer (DSSAT) (Tsuji et al., 1994; Jones et al., 2003; Hoogenboom et al., 2004; Banterng et al., 2006; Suriharn et al., 2008; Phakamas et al., 2008). Simulation model is very useful to assist breeding for drought resistance program, and it is benefit for the future research on the traits with difficulty to measure such as rooting traits. However, the simulation can be effective and efficient, if accurate inputs can be obtained. The model requires input data including environmental conditions, management practices, and characteristics of cultivar-specific genetic coefficients (Boote et al., 1998). The cultivar coefficients are crop values that define the development, vegetative and reproductive growth of individual genotypes (Hunt et al., 1993; Boote et al., 2003). Before the application of the CSM-CROPGRO Peanut model, it is necessary to first determine the cultivar coefficients if the cultivars are new breeding lines or local cultivars that have not been used previously with the model. Hence, finding the tool to calibrate accurately the fit values of cultivar coefficients is needed.

GENALC and GLUE programs have been used for evaluation of cultivar coefficients in the DSSAT. Although the GENCALC performed well in previous evaluation Anothai et al. (2008b), they also suggested further evaluation of the sequence of optimization in GENCALC to calculate the new cultivar coefficients. Thus, the capability of the program depends on heuristic rules. GLUE can be used for estimating cultivar coefficients without intervention by user, making it simple to implement for addition a new cultivar to DSSAT. But, the capability of the GLUE in estimation genotype coefficients needs to be firstly established.

The aims of this research were (i) to investigate the effect of drought stress on total dry matter (TDM), pod yield, WUE, harvest index (HI), SCMR, SLA and canopy temperature, (ii) to identify drought resistant peanut genotypes from a collection of peanut germplasm, (iii) to establish the relationships among drought

resistance traits, iv) to investigate the responses of root dry weight and root length density of peanut genotypes to pre-flowering drought stress and their relationships with pod yield, v) to classify the root distribution pattern of peanut genotypes under mid-season drought, and to determine of the relationships between RLD in different soil depths and yield under these conditions, and vi) to compare the capability of GLUE with GENCALC and manual calibration in estimating cultivar coefficients of peanut lines for use with the CSM-CROPGRO-Peanut model.