

<b>Thesis Title</b>	Response and Inheritance of Soybean Genotypes to Saline Soil Conditions		
<b>Author</b>	Miss Praphatsara Patoomrut		
<b>M.S.</b>	Agriculture (Agronomy)		
<b>Examining Committee</b>			
	Assist.Prof.Suthat	Julsrigival	Chairman
	Lecturer Phrek	Gypmantisiri	Member
	Assist.Prof.Dr.Niwat	Hirunbrurana	Member
	Lecturer Dr.Dumnern	Kaladee	Member

### Abstract

Studies of response and inheritance of soybean genotypes to saline soil conditions consisted of two experiments. Experiment 1 was screening for saline tolerance of 31 soybean varieties by growing young soybean seedlings for two weeks under four different salinity levels 0,6,8 and 10 mmhos.cm<sup>-1</sup> of Modified Hoagland's No.2 nutrient solution. The seedling parameters including root distribution, root length and leaf color were employed for examining the salinity response of each soybean genotype.

Results showed that there were salt tolerance traits existed and showed a wide range of variability among the soybean genotypes. It was also found that the tolerance ability of each genotype was decreased with increasing in salinity levels.

The soybean varieties such as EMGOPA 302, XANH TIAN TAI(VIR) and SJ.5 were identified as salt tolerant genotypes.

Experiments 2 was to estimate the inheritance of agronomic traits of salt tolerant soybean varieties. Results obtained from the estimation of both broadsense and narrow sense heritability revealed that at  $2 \text{ mmhos.cm}^{-1}$  salinity level provided higher values of broadsense heritability than at  $6 \text{ mmhos.cm}^{-1}$ . Low values of narrow sense heritability were obtained at both 2 and  $6 \text{ mmhos.cm}^{-1}$  levels. This would indicate that environmental effect connected with nonadditive gene effect importantly attributed to genotypic expression among the traits. Genetic advance under selection ( $G_s$ ) also indicating that yield and yield component characters of salt tolerant soybean genotypes could be transmitted to further generations with a significant gain possible through selection in early generation.

The segregation analysis of  $F_2$  generation of each cross at both two salinity levels revealed that transgressive segregation was predominantly exhibited among the important yield component characters such as number of branches, pods as well as seeds per plant. In addition, such characters also showed positively high association with its seed yield. Path coefficient analysis indicated that seed yield per plant has the highest positive direct effect with the number of seed per plant.