

## ABSTRACT

**Mahmoud Shawky Abd El-Latif: Inheritance of Agronomic Traits and Genetic Markers for Drought Tolerance in Maize. Unpublished Ph. D. Thesis, Department of Agronomy, Faculty of Agriculture, Ain Shams University, 2014.**

This investigation was conducted at Giza Agricultural Research Station of the Agricultural Research Center (ARC) in the seasons from 2011 to 2013, to estimate some genetic parameters for grain yield and yield related traits, using the six populations *i.e.* P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> of the two maize crosses (*Zea mays*, L.) *viz.* Gz-602 × Gz-628 (Cross I) and Sd-7 × Sd-63 (Cross II) under drought stress condition (preventing the 4<sup>th</sup> and 5<sup>th</sup> irrigations during flowering stage) and to study the relationship between the ISSR-PCR and field results in an attempt to develop molecular markers for drought tolerance.

Results of analysis of variance indicated significant differences among the studied generations of each cross for all studied traits. The genetic variances within F<sub>2</sub> population were also found to be significant for all traits studied in the two crosses, therefore needed genetically parameters were estimated.

The scaling test values of A, B, C and D were significant for different traits studied, suggesting the presence of non-allelic interaction. F<sub>2</sub> deviation (E1) and backcross deviation (E2) were significant, with few exceptions, retiring the contribution of epistatic gene action in the inheritance of the studied traits.

The six parameters model showed that the dominance gene effect (d), followed by the additive gene effect (a) and the additive × dominance (ad) type of epistatic gene action contributed with the large part of genetic component controlling the inheritance of the studied traits compared to the dominance × dominance (dd) additive × additive (aa) and type of epistatic gene effects.

Moderate to high heritability estimates in broad sense were detected in most of the traits studied with values ranged from 51.58% for chlorophyll content in cross II to 95.12% for ear height in cross II. Low to moderate heritability estimates in the narrow sense were detected in most of the studied traits with values ranging from 14.56% for plant height in cross I to 63.39% for leaf proline content in cross II.

The expected genetic advance of the  $F_2$  mean ( $\Delta g\%$ ) for the studied characters were found to be moderate to high with values which ranged from 2.24% for silking date in cross I to 17.89% for number of rows per ear in cross II

Concerning biochemical results, the primers 14-A, 44-B, HB-08, HB-13 and HB-15 showed close relationship for drought tolerance segregates in the  $F_2$  generation and thus it could be used as markers assistant selection for drought. Therefore, the ISSR-PCR analysis could be considered as reliable molecular markers associated with drought tolerance in maize that can be utilized during breeding programs *via* marker-assisted selection.

**Key Words:** Maize (*Zea mays*, L.), Drought tolerance, Heterosis, Inbreeding depression, Potence ratio, Gene action, Heritability, Genetic advance, Correlation, Path coefficient and ISSR-PCR.

## CONTENTS

	<b>Page</b>
<b>LIST OF TABLES</b>	<b>III</b>
<b>LIST OF FIGURES</b>	<b>V</b>
<b>INTRODUCTION</b>	<b>1</b>
<b>REVIEW OF LITERATURE</b>	<b>3</b>
1. Drought tolerance.	<b>3</b>
2. Heterosis, inbreeding depression and potence ratio.	<b>4</b>
3. Genetic components of variance.	<b>7</b>
4. Phenotypic and genotypic coefficients of variability (PCV and GCV), heritability and genetic advance.	<b>12</b>
5. Correlation and path coefficient analysis.	<b>19</b>
6. Molecular markers.	<b>23</b>
<b>MATERIALS AND METHODS</b>	<b>26</b>
<b>A. Field experimental work</b>	<b>26</b>
I. Genetic materials.	<b>26</b>
II. Experimental work.	<b>26</b>
III. Statistical and genetical analysis.	<b>29</b>
1. Analysis of variance.	<b>29</b>
2. Phenotypic and genotypic coefficient of variability.	<b>30</b>
3. Genetic parameters estimated.	<b>30</b>
<b>B. Biochemical genetic work.</b>	<b>40</b>
<b>RESULTS AND DISCUSSION</b>	<b>45</b>
1. Analysis of variance.	<b>45</b>
2. Mean performance.	<b>48</b>
3. Heterosis, inbreeding depression and potence ratio.	<b>58</b>
4. Scaling test, F <sub>2</sub> -deviation (E1), backcross-deviation (E2) and types of gene action.	<b>66</b>

	<b>Page</b>
5. Heritability estimates and expected genetic advance from selection.	<b>75</b>
6. Correlation and path coefficient analysis studies	<b>83</b>
7. Molecular markers.	<b>90</b>
<b>SUMMARY</b>	<b>96</b>
<b>REFERENCES</b>	<b>104</b>
<b>ARABIC SUMMARY</b>	