# GENETICAL STUDIES ON DROUGHT TOLERANCE IN MAIZE

By

#### EBRAHIM HASSAN MOHAMED HAFEZ

B.Sc. Agri. Sci. (International Agriculture), Fac. of Agric., Cairo Univ., 2005

#### **THESIS**

Submitted in Partial Fulfillment of the Requirements for the Degree of

### MASTER OF SCIENCE

In

Agricultural Sciences (Agronomy)

Department of Agronomy
Faculty of Agriculture
Cairo University
EGYPT

2016

#### APPROVAL SHEET

# GENETICAL STUDIES ON DROUGHT TOLERANCE IN MAIZE

M.Sc. Thesis In Agric. Sci. (Agronomy)

By

### EBRAHIM HASSAN MOHAMED HAFEZ

B.Sc. Agri. Sci. (International Agriculture), Fac. of Agric., Cairo Univ., 2005

### APPROVAL COMMITTEE

Dr. MOHAMED S. M. SOLIMAN Head Research of Agronomy, Field Crops Res. Inst., ARC
Dr. MAZHAR M. FAWZY ABDALLA
Professor of Agronomy, Fac. Agric., Cairo University
Dr. ABDALLA M. ALI ABDALLAA
Professor of Agronomy, Fac. Agric., Cairo University
Dr. AHMED MEDHAT M. AL-NAGGAR
Professor of Agronomy, Fac. Agric., Cairo University

Date: 13/12/2016

#### SUPERVISION SHEET

## GENETICAL STUDIES ON DROUGHT TOLERANCE IN MAIZE

M.Sc. Thesis In Agric. Sci. (Agronomy)

By

#### EBRAHIM HASSAN MOHAMED HAFEZ

B.Sc. Agri. Sci. (International Agriculture), Fac. of Agric., Cairo Univ., 2005

#### SUPERVISION COMMITTEE

Dr. AHMED MEDHAT MOHAMED AL-NAGGAR Professor of Agronomy, Fac. Agric., Cairo University

DR. ABDALLA MOHAMED ALI
Professor of Agronomy, Fac. Agric., Cairo University

DR. AHMED MOHAMED ABDELHAMID GOHAR Research Manager, Dura Seeds, Beba, Sids, Egypt

Name of Candidate: Ebrahim Hassan Mohamed Hafez

Degree: M.Sc.

Title of Thesis: Genetical studies on drought tolerance in maize.

**Supervisors:** Dr. Ahmed Medhat Mohamed Al-Naggar

Dr. AbdAlla Mohamed Ali Abdalla

Dr. Ahmed Mohamed Abdelhamed Gohar

**Department: Agronomy** 

#### **ABSTACT**

Two hundred fifty four test-cross hybrids of maize (Zea mays L.) were produced in 2011 season between 254 doubled haploid (DH) lines developed via the in vivo (inducer) technique and an inbred line tester. A field experiment was conducted in 2012 season to screen 256 genotypes; namely 254 top crosses and two check cultivars) for drought tolerance at flowering (WSF) and grain filling (WSG). The objectives were to identify tolerant maize DH lines x tester crosses under WSF and/or WSG, (ii) to describe the effects of WSF and WSG on different traits of maize and (iii) to study the response of heritability and genetic advance from selection to the two types of drought. A split plot design in lattice arrangement (16 x 16) was used; main plots were allotted to three irrigation regimes (well-watering; WW, water stress at flowering; WSF, and water stress at grain filling; WSG) and sub-plots to 256 genotypes. In general, WSF and WSG caused a significant reduction of 38.92 and 39.47% in grain yield/plant (GYPP), 39.09 and 41.19% in grain yield/fed (GYPF), 21.79 and 20.93% in number of ears/plant (EPP), 11.11 and 7.78% in plant height (PH), 5.88 and 8.82 % in ear height (EH), respectively, but caused a significant increase in anthesis-silking interval (ASI), barren stalks (BS), leaf rolling (LR), days to anthesis (DTA) and days to silking (DTS). The best top crosses in drought tolerance, mean performance and breeding value under WSF and WSG were identified, so their corresponding DH lines were recommended for further exploitation in the breeding program aiming at developing drought tolerant maize hybrids. The magnitude of heritability (h<sup>2</sup><sub>b</sub>) and expected genetic advance (GA) from direct selection was higher under WSF and WSG than under WW for DTA, DTS, PH, BS, and EPP. However, the h<sup>2</sup><sub>b</sub> and expected GA from selection was higher under WW than under WSF and WSG for ASI, EH, GYPP and GYPF. Thus it was recommended that selection for grain yield would be better practiced under well-watered environment to obtain higher values of genetic advance.

**Key words:** Maize, drought tolerance index, doubled haploids, heritability, genetic advance, general combining ability, top cross analysis

# **DEDICATION**

I dedicate this work to my PARENTS who have made me the man I am now, also to my PARENTS in law who brought my beloved wife to life, to my lovely WIFE who was always been a great support, and to the light of my life my daughter JANA.

# ACKNOWLEDGEMENT

### الحمد لله وكفي

I wish to express my deepest gratitude and appreciation to **Dr. Ahmed Medhat Al-Naggar,** Professor of plant breeding, Fac. Agric., Cairo Univ. for being a great support and amazing role model for me and I believe that this work wouldn't be finished in this shape without his patience and motivations.

Sincere thanks and grateful appreciation are extended to **Dr. Abdallah Mohamed Ali,** Associate Professor of Agronomy, Faculty of Agriculture, Cairo Univ. and the member of supervision committee for being great motivation to end this Master degree.

Sincere thanks and grateful appreciation are extended to **Dr. Ahmed Gohar** for his support and help during 6 years of hard work.

Many thanks to **Dr. Abd el Samad M. Yonis** for his valuable help and efforts offered during the statistical analysis of this study and.

I like to express my deepest thanks to **DuPont Pioneer family** my second home and the place that helped me to develop and grow knowledge and skills.

### Special thanks to:

**Dr. Anand Pandravada,** South Asia Research Director- DuPont Pioneer, for accepting the use of Pioneer India team germplasm and for his scientific guidance.

**Dr. Peter Freymark**, Africa Research coordinator- DuPont Pioneer, for his technical and scientific guidance though my work and for being a spiritual motivator.

# **CONTENTS**

INTRODUCTION	
REVIEW OF LITERATURE	
1. Definitions of drought	
2. Effect of drought stress on maize	
3. Drought adaptive traits	
4. Combining ability	
5. Heritability	
MATERIALS AND METHODS	
RESULTS AND DISCUSSION	
1. Analysis of variances	
2. Effect of drought stress	
3. Effect of genotypic	
4. Yield superiority of DHL x tester crosses	
5. Drought tolerance index	
6. Superiority of drought tolerant (T) to sensitive (S)	
genotypes	
7. Grouping genotypes based on water efficiency and	
responsiveness	
8. Grouping genotypes based on drought tolerance and	
grain yield	
9. Trait interrelationships	
10. Breeding value (GCA effects) of the DH lines	
11. Genotypic and phenotypic coefficient of variation.	
12. Heritability and genetic advance	
CONCLUSIONS	
SUMMARY	
REFERENCES	
ARABIC SUMMARY	

# LIST OF TABLES

No	Title	Page
1	Pedigree and drought tolerance for all the genotypes used in the current study	33
2	Soil and water analysis for the experimental site	38
3	Meteorological data during planting season of the experiment in Sandanhoor, Kalyobia, Egypt	39
4	Analysis of variance and expected mean squares (EMS) of separate and across the three treatments	42
5	Analysis of variance of split plot design for all studied traits of 254 DH lines and two check cultivars of maize in 2015 season	46
6	Mean squares for studied traits of DHL × tester crosses under well-watering WW), Water stress at flowering (WSF) and water stress at grain filling (WSG) in 2015 season	47
7	Basic statistics of ten agronomic traits of test crosses under well-watering (WW), water stress at flowering (WSF) and water stress at grain filling (WSG) in 2015 season	49
8	Means $(\bar{x})$ of the best 25 and the worst 10 test crosses and two check cultivars under well-watering (WW), water stress at flowering (WSF) and water stress at grain filling (WSG) in 2015 season	54

9	List of test crosses showing the 12 highest and 12 lowest top crosses and ranges for studied traits under well-watering (WW), water stress at flowering (WSF) and water stress at grain filling (WSG) conditions	61
10	Superiority (%) of the best 25 DHL × tester crosses over the best check cultivar in grain yield/fed under well-watering (WW), water stress at flowering (WSF) and water stress at grain filling in 2015 season	63
11	Drought tolerance categories of 254 top crosses and 2 check cultivars based on drought tolerance under water treatments.	65
12	Superiority (%) of the five most tolerant (T) over the five most sensitive (S) top crosses for studied traits under water stress at flowering (WSF) and water stress at grain filling (WSG) conditions	68
13	Genetic correlation coefficients between GYPF, GYPP or DTI and other studied traits across 245 top crosses under WW, WSF and WSG environments	77
14	Breeding values (GCA effects) of the best 25 and the worst 10 doubled haploid lines of maize under well-watering (WW), water stress at flowering (WSF) and water stress at grain filling (WSG) conditions in 2015 season	79
15	Genotypic (GCV%) and phenotypic (PCV%) coefficient of variation for studied traits of maize DHL's x tester crosses under well-watered (WW), water stress at flowering (WSF) and water stress at grain filling (WSG) conditions	85
16	Heritability in the broad sense $(h^2_b)$ and genetic advance (GA) from selection for studied traits of maize DHL's x tester crosses evaluated under well-watered (WW), water stress at flowering (WSF) and water stress at grain filling (WSG) conditions.	89

# LIST OF FIGURES

No.	Title	Page
1	Means of DTA, DTS, ASI, PH, EH, LR, BS, EPP, GYPP and GYPF traits under well-watering (WW), water stress at flowering (WSF) and at grain filling (WSG) (the bar above each column denotes the standard error)	51
2	Relationships between GYPF of top crosses under well-watering (WW) and water stress at flowering (WSF)	70
3	Relationships between GYPF of top crosses under well-watering (WW) and water stress at grain filling (WSG)	71
4	Relationships between drought tolerance index and means of GYPF of top crosses water stress at flowering (WSF)	73
5	Relationships between drought tolerance index and means of GYPF of top crosses water stress at grain filling (WSG)	73
6	Genotypic coefficient of variation(GCV%) for studied traits of maize top crosses under WW, WSF and WSG conditions	87
7	Phenotypic coefficient of variation (PCV%) for studied traits of maize top crosses under WW, WSF and WSG conditions.	88
8	Broad sense heritability (h² <sub>b</sub> ) for studied traits of maize top crosses under WW, WSF and WSG conditions	92
9	Genetic advance (GA) from selection for studied traits of maize top crosses under WW, WSF and WSG conditions	93

#### INTRODUCTION

Maize (*Zea mays* L.) is one of the most important cereal crops in the world as well as in Egypt. According to FAOSTAT (2016), Egypt grew in 2014, 750,000 hectares (ca 1.78 million feddan) and produced 5.8 million tons of grains, with an average yield of 7.73 tons ha<sup>-1</sup> ( ca 23.21 ardabs/feddan). According to the same report, Egypt ranks the fifth in the world with respect of average productivity after USA, France, Germany and Italy. However, the local production of maize is not sufficient to satisfy the local consumption. So Egypt imports every year about six million tons of maize grains. The problem in the future is that there will be no available maize grain in the producing countries for export, because they will use it in the manufacture of ethanol; a new alternate energy source.

To reach self-sufficiency of maize production in Egypt, efforts are devoted to extend the acreage of maize; in the desert and to improve the maize productivity from unit area. Growing maize in sandy soils of low water-holding capacity would expose maize plants to drought stress, which could result in obtaining low grain yields under such conditions. Moreover, the expected future shortage in irrigation water necessitates that maize breeders should pay great attention to develop drought tolerant maize cultivars that could give high grain yield under both water-stress and non- stress conditions. Maize is particularly susceptible to drought at the flowering stage (Chapman *et al.*, 1996). Loss in grain yield is particularly severe when drought stress occurs at

this stage (Claassen and Shaw, 1970; Grant et al., 1989 and El-Sayed, 1998).

During the last few decades, considerable efforts have been devoted to improve yield performance of maize under drought stress conditions through breeding, and to understand the mechanisms involved in drought tolerance (Edmeades *et al.*, 1992). In that context, CIMMYT developed some tropical maize drought tolerant populations while maintaining their yield potential under favorable conditions (Bolanos and Edmeades, 1996). Developing such populations requires adoption of proper techniques of identifying and selecting tolerant genotypes to soil water stress. This also requires identifying traits most suitable for selecting drought tolerant maize.

Several investigators studied the correlations between yield and other plant attributes under soil moisture stress in order to practice rapid and accurate indirect selection for drought tolerance. A strong negative association was reported between grain yield and each of anthesis—silking interval (Bolanos and Edmeades, 1993b) and barren stalks (Edmeades *et al.*, 1993). Likewise, a strong positive association was found between grain yield and both number of ears/plant (Guei and Wassom, 1992; Terrazas *et al.*, 1995 and Ribaut *et al.*, 1997) and number of kernels/row (Weerathaworn *et al.*, 1992 and Ribaut *et al.*, 1997). These investigators suggested that such traits could be used as indicators of drought tolerance in maize.

Breeding for tolerance to drought is difficult because the genetic mechanism that controls the expression of such tolerance in crop plants is poorly understood and because of the polygenic nature of such a complicated character (Rossiele and Hambling, 1981; Kebede *et al.*, 2001). Selection for increased drought tolerance was associated with a significant reduction in anthesis-silking interval (ASI) and barrenness, and an increase in ears plant<sup>-1</sup>, stay green and harvest index (Banziger *et al.*, 2002; Magorokosho *et al.*, 2003; Shaboon, 2004; Monneveux *et al.*, 2006 and Al-Naggar *et al.*, 2000, 2008, 2009, 2011;).

Maize breeders are always looking for new methods to enrich breeding material of better tolerance to drought stress. Using modern biotechnological techniques in plant breeding could contribute to a great extent in the induction of novel genetic variation, which are not existed in the gene pool, such as somaclonal and gametoclonal variation (Khan et al., 2001). The in vivo (inducer) technique helps in developing doubled haploids, in a short time from maize crosses that show new genetic variation amenable for efficient selection for drought tolerant genotypes (Michell et al., 1992). Recently, doubled haploid (DH) lines are routinely applied in many commercial hybrid maize breeding programs. Major advantages of DH lines compared to selfed lines include (i) maximum genetic variance between lines for per se and testcross performance from the first generation, (ii) reduced breeding cycle length, (iii) perfect fulfillment of DUS (distinctness, uniformity, stability) criteria for variety protection, (iv) reduced expenses for selfing and maintenance breeding, (v) simplified logistics, and (vi) increased efficiency in marker-assisted selection, gene introgression, and stacking genes in lines (Geiger and Gordillo, 2009).

To our knowledge, all present commercial DH-line breeding programs are based on *in vivo* induction of maternal haploids (Seitz, 2005; Barret et al., 2008; Rotarenko *et al.*, 2009). Other techniques have proven to be less effective or too genotype specific.

DH lines display maximum genetic differentiation for *per se* and testcross performance from the first generation and allow the breeder to drastically reduce the 'time to market'. As a consequence, most internationally leading seed companies have converted their line development (LD) programs to the DH technology during the last years or have initiated this process (Geiger and Gordillo, 2009). The technology has also found its way into research but much slower than in breeding because experienced staff and appropriate experimental facilities are needed to apply it successfully.

Because of the genetic, methodological, and logistic advantages, further progress in maize breeding is expected to increase considerably with the development of DH lines. Yet, the success of employing DH lines depends on a robust and efficient haploid induction technology as well as on breeding strategies that make optimum use of the breeder's genetic, technical, and monetary resources (Gordillo and Geiger, 2008 a,b).

Top cross analysis is the simplest method of elimination of a considerable number of undesirable lines and identifying those lines of high breeding value, *i.e.* of high general combining ability (GCA) effects in the beginning of a breeding programme (Sharma 1998). The

topcross method deals with a series of single crosses developed between a single tester and a number of inbred lines to be studied for their genetic constitution. It was first proposed by Jenkins and Brunsen (1932) as a method of testing inbred lines of maize in cross-bred combinations. Later Tysdal and Crandall (1948) renamed it "top-cross".

The inbred-tester crosses are in fact half-sib (HS) families. The inbreds involved in the best crosses might carry adequate fixable genetic variance (variance of breeding value) so as to produce better hybrids with a number of other inbreds (Sharma 1998). Such inbreds possess high breeding value for the trait of interest. Breeding value is the main parameter of initial screening through topcross analysis as it represents the GCA effect of individual test inbred (Sharma 1998). Therefore, operation of additive gene action warranted by GCA effects (breeding value) is a clean indication in the group of test inbreds.

Two hundred fifty four maize doubled haploid (DH) lines developed by DuPontPioneer *via* the *in vivo* (inducer) technique from the crosses between drought tolerant inbreds and good general combiners obtained from Research Department of the Pioneer Hi-Bred Inc. Two hundred fifty four test-cross hybrids were produced as a result of crossing between the 254 DH lines and the inbred line tester PHDMF that shows drought tolerance performance and high general combining ability. These DH line x tester crosses are expected to include test cross(es) that accumulated favorable genes for both high-yielding and drought tolerance.