Kafrelsheikh University
Faculty of Agriculture
Genetics Department

Genetical and Molecular Studies on Some Wheat Genotypes for Rusts Resistance

BY

Mahmoud Abd El-Lateef Hussein Abd El-Lateef

B.Sc. Agric. (Genetics) Fac. Agric., Kafrelsheikh University, (2010).
M.Sc. Agric. (Genetics) Fac. Agric., Kafrelsheikh University, (2014).

THESIS

Submitted in Partial Fulfillment of
The Requirements for degree
of
Doctor of Philosophy

in

Agricultural Sciences (Genetics)

2021

Kafrelsheikh University
Faculty of Agriculture
Genetics Department

Genetical and Molecular Studies on Some Wheat Genotypes for Rusts Resistance

BY

Mahmoud Abd El-Lateef Hussein Abd El-Lateef

B.Sc. Agric. (Genetics) Fac. Agric., Kafrelsheikh University, (2010).

M.Sc. Agric. (Genetics) Fac. Agric., Kafrelsheikh University, (2014).

Supervision committee:

Prof. Dr. Ali Ahmed Abo Shosha

Prof. of Genetics , Fac. of Agric. Kafrelsheikh University

Prof. Dr. Ismael Abd El-Hafez Khatab

Prof. of Genetics, Fac. of Agric. Kafrelsheikh University

Prof. Dr. Assad Ahmed Hamada

Research Prof., Wheat Dept., Crops Res. Inst., A.R.C.

2021

ACKNOWLEDGEMENT

In the name of ALLAH, the most Merciful and the most grace. I am deeply thankful and grateful to ALLAH, who gave me the help, knowledge and ability to start, continue and complete this study.

Special thanks and gratitude are given to ***Professor Dr. Ali A. Abu Shousha,*** *Professor of Genetics , Faculty of Agriculture, Kafrelsheikh University for supervision, suggesting the research problem, assistance, helpful criticism and extraordinary effort during the achievement of this investigation.*

Sincere thanks and deepest grateful appreciation are extended to ***Professor Dr. Ismael A. Khatab****, Professor of Genetics Dep., Faculty of Agriculture, Kafrelsheikh University for his supervision, suggesting the research problem, valuable advice and many helpful suggestions, time constructive criticism throughout the progress of this study and helping in writing thesis.*

The author wishes to express his gratitude and appreciation to ***Professor Dr. Assad A. Hamada,*** *Wheat Research Department, Field Crop Res. Institute (FCRI), Agricultural Research Center (ARC), for suggesting the research problem, valuable guidance.*

Sincere thanks are also due to all the staff members at the department of Genetics, Faculty of Agriculture, Kafrelsheikh University, for their support, cooperation and encouragement.

I am deeply grateful to ***Professor Dr. Tag El-Din M shehab El-Din,*** *Wheat Research Department, Field Crops Res. Institute (FCRI), Agricultural Research Center (ARC), for his encouragement, valuable advices, actual guidance and revising the manuscript.*

Sincere thanks and gratitude are extended to the soul of my father ***Prof. Dr. Abd El-lateef H. Abd El-lateef,*** *for everything in my life.*

Hearty thanks are also given to my mother, brother and sisters for their valuable support, patience and continuos encouragement during the course of this study.

LIST OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

INTRODUCTION

1.INTRODUCTION

Wheat (Triticum aestivum L.) is the world's most widely grown cereal crop. It is considered to be the main winter cereal crop in Egypt and the national output of wheat is insufficient to meet local consumption due to higher population increases, especially in recent years. National production of wheat is estimated at approximately eight million tonnes produced from three million Faddans (1 Faddan= 0.42 ha), while annual consumption of wheat fluctuates from 12 to 14 million tonnes. In the other words, the gap between production and consumption lies between six to eight million tons annually.

moreover, crop production is greatly reduced by biotic and abiotic stresses. Around 14 percent of world crop production is diminished by diseases. Wheat is prone to many pathogens caused by Puccinia P. striiformis f.sp., including strip and stem rusts. *Puccinia graminis* f.sp. and *tritici* (Pst) They are the most severe wheat diseases that cause significant yield losses (Ellis et al., 2014).

The big foliar disease of wheat is yellow (stripe) rust, resulting in loss of yield all over the world Kolmer, (1966). In Egypt, stripe rust caused significant losses in the production of most Egyptian wheat cultivars El-Daoudi *et al* . (1996). It was confirmed that the disease prevailed at higher altitudes, cool and temperate regions wherever wheat is grown (Johnson, 1992; McIntosh et al., 1996 and Boyed, 2005). In most places around the globe, the causative agent (Pst) plasticity and adaptability to changing climatic conditions made it fit. Such characteristics include mutation, migration, somatic and sexual hybridization of wheat rusts (Stubbs, 1985; Kolmer, 2005 and Jin and Carson., 2010). Also, the disease attacks from early in the growing season, plants are usually stunted and weakened, causing

severe yield losses up to 70%. The disease reduced yield, quality and size of the harvested grains.

In addition, the recent discovery of the broadly virulent Ug99 race in Uganda in 1998 challenged the misconception that stem rust was a conquered disease Singh *et al.* (2006 and 2008). Up to 90 percent of the world's wheat cultivars are now known to be vulnerable to stem rust Singh *et al.* (2006 and 2011), and the disease threatens 120 million tonnes or 20 percent of the world's wheat in the Middle East, North and Central Africa, and Asia, with a population of more than one billion people Dixon *et al.* (2009).

In light of the Egyptian government's tendency to establish new farms in Africa to grow wheat, stem rust is one of the most important obstacles it faces, especially in countries located in central Africa such as Uganda, Congo and Tanzania. Where stem rust leads to a significant decrease in yield, which may reach 100% under favorable conditions Olivera et al. (2015). Therefore, it has become imperative to work on producing high-yielding and resistant to stem and yellow rusts varieties to grow them in these environments.

So, understanding the genetical behavior of wheat resistance to these diseases are essential for deciding the breeding method that maximizes the genetical improvement of these characters (Shehab El-Din et al., 1991a). Wheat resistance to rusts has been documented to be a simple inherited character since Biffin (1905), governed by one, two or a few number of major gene pairs Bai et al. (1997) and Shahin and Ragab (2015). Meanwhile, several investigators indicated that resistance is a quantitative character controlled by many genes as well as the prevailing environmental conditions, Shehab El-Din et al. (1991a), Yadav and Naringhani (2000) and Sharshar (2015). Furthermore, resistance was dominant over susceptibility in most cases, Shehab El-Din and Abd El-Latif (1996), Bai et

al. (1997) and Patil et al. (2000), and vice versa was true in others, El-Fadly et al. (1991) and Ganeva et al. (2001). On the other hand, some cases best fit a simple additive genetical model with no dominance or epistatic interactions, while dominance and / or epistasis were more pronounced and had important roles, Said (2003), Ragab (2005) and Sharshar (2015).

The production of molecular markers for common yellow and stem genes enables the rust identification of these genes independently of the phenotype. Molecular markers can be used in marker-assisted selection for an efficient combination of genes in the pyramiding strategy to create a more durable resistance (Feuillet *et al*., 1995). Simple sequence repeats (SSR) are useful tools for molecular genetic analysis as they are more abundant and display higher levels of polymorphisms in many plant species (Hitta *et al*., 1995 and Plaschke *et al*., 1995). SSR markers i.e. Yr5, Yr10, Yr15, Yr24, YrH52, Sr2, Sr26, Sr36 and Sr22 have been reported for several stripe and stem rusts resistance genes (Peng *et al*., 1999; Sun *et al*., 2002; Wang *et al*., 2002; Zakari *et al*., 2003; Olson *et al.,* 2010; Tsilo *et al*., 2008). In marker-assisted selection and for pyramiding resistance genes, as well as for understanding the relationships between different genes, such markers have been used.

The objectives of this research were to study:-

1. Studying the nature of inheritance of stripe and stem rusts disease resistance caused by *Puccinia striiformis* and *Puccinia gramenis f.sp. tritici*, respectively.
2. Studying the natural inheritance of some agronomic traits including grain yield and its components.
3. Detection of SSR markers associated with strip and/or stem rusts resistance in studied breed wheat crosses.

REVIEW OF LITERATURE

2.REVIEW OF LITERATURE

Rusts have caused significant and severe losses on susceptible wheat cultivars worldwide (Wellings, 2011). Stripe rust (*Puccinia striiformis*) and stem rust (Puccinia graminis), are the most destructive foliar diseases of wheat in Egypt and worldwide. Historically and presently, stripe and stem

Breeding programs for resistance to diseases are more advantageous than using pesticides or any other disease control mean; recently, developing new resistant lines became the main objective of many wheat breeding programs. Knowledge of the inheritance of wheat reaction to stem and stripe rusts is essential before deciding on the breeding method to be employed for maximum genetic improvement of this trait.

In this investigation, the review of literature divided into the following topics:

2.1.Nature of inheritance of some agronomic traits in wheat.

2.2. Nature of inheritance of stripe and stem rust diseases in wheat.

2.3.Molecular breeding for wheat stripe and stem rusts resistance.

2.1. Nature of inheritance of some agronomic traits in wheat.

Ghimiray and Sarkar (2000) estimated the mean phenotypic and genotypic coefficients of variation, heritability in a broad sense and expected genetic advance for seven quantitative characters in wheat. The results indicated that phenotypic coefficient of variation was in general higher than the genotypic coefficient of variation for all the characters except plant height. High heritability coupled with high genetic advance was recorded for number of spikes/plant and number of kernels/spike. This association indicated the importance of additive

gene effects in the inheritance of these characters.

Yadav and Narsinghani (2000) studied the twelve genotypes of bread *(Triticum aestivum L.)* and *(Triticum durum)* wheat, they estimated heterosis for days to heading, plant height, number of tillers/plant, number of grains/spike, 1000 grain weight and grain yield/plant. They mentioned that some crosses exhibited significant negative of heterosis heading date, 1000 grain weight, and grain yield/plant. Significant positive heterosis was observed for number of tillers / plant, 1000 grain weight, and grain yield / plant.

Ashoush *et al*. (2001) estimated heterosis for some agronomic characters. For plant height, eleven and eight hybrids exhibited significant positive heterotic effects relative to mid-parent and the better parent, respectively. Meanwhile, for number of spikes per plant, eleven and eight crosses exhibited a significant positive heterotic effect to mid and the better parent, respectively. For number of kernels per spike, nine and five crosses were significantly exceeded the mid-parent and the better parent. For 1000-kernel weight, five and one crosses showed significant positive heterotic effect relative to mid-parent and the better parent, respectively. For grain yield per plant, seven and three hybrids had significant positive heterotic effect relative to mid-parent and the better parent, respectively.

Chowdhry *et al.* (2001) studied heterosis and inbreeding depression in crosses of (*Triticum aestivum*). They noticed the presence of significant genotypic differences among the studied characters. They also indicated that additive types of gene action were present in most studied traits. Furthermore, inbreeding depression was found with varying degrees almost in all the crosses for yield and yield components.

Talbert *et al*. (**2001**) determined the genetic variation for days to heading, days to maturity and grain yield/plant in a set of spring wheat crosses. The results

were significant for crosses for all studied traits. Heritability values exceeded 0.70 in all crosses for days to heading. Also, its ranged from 0.35 to 0.81 and 0.22 to 0.78 for days to maturity and grain yield/plant, respectively.

Chowdhry *et al*. (2002) studied the analysis of variance for five wheat genotypes in a diallel fashion to achieve the genetic control of some polygenic traits revealed that the differences among genotypes for all studied traits were highly significant. Also, plant height, number of grains/spike, 1000-kernel/weight and grain yield/plant were controlled by the over-dominance type of gene action.

Esmail and Kattab (2002) considered the genetic behavior of yield and its components in three bread wheat crosses. They obtained significant useful positive heterosis for grain yield/plant in the first cross (29.34 %) and second cross (9.48 %) and 100-grain weight in the third cross (17.85 %). Highly significant negative inbreeding depression values were obtained for spikes/plant and grain yield/plant in the three wheat crosses. Additive, dominance and epistatic gene effects were playing an important role in the inheritance of plant height, spikes/plant, spike length, 100-grain weight and grain yield/plant in the three wheat crosses. Additive × additive gene interaction contribute the major portion of the gene pool.

Salgotra *et al.* (2002) determine heterosis over better parent in the F_1 hybrid which comes from hybridization between 13 winter wheat varieties and four diverse testers of spring wheat for grain yield and seven other traits . They found that the estimates of heterosis for days to maturity, tillers/plant, and number of kernels/spike were presented in 15 crosses. Also, for grain yield in 19 crosses.

Abdel-Hafez *et al.* (2003) demonstrated that additive gene action played the major role in the inheritance of days to heading, days to maturity and grain filling period. Also, the three types of epistatic gene effects were observed for all studied characters with predominant for additive × additive gene effects. They added that

heritability values in a broad sense were high and intermediate in the narrow sense. The expected genetic gain from selection was low to moderate for earliness characters.

Said (2003) studied the inheritance of some agronomic traits. The results indicate that, high values of heritability in a broad sense for days to heading, days to maturity, plant height, number of kernels/spike and 100-kernel weight and grain yield, while moderate values were obtained for a number of spikes/plant. Heritability in narrow sense was high for days to heading, plant height, number of kernels/spike and 100-kernel weight, while moderate values were obtained for days to maturity. Meanwhile, low values were obtained for number of spikes/plant and grain yield/plant.

Chandra *et al.* (2004) conducted an investigation to measure variability, heritability and the expected of genetic advance of nine characters on fifty F_5 bulk lines of five bread wheat crosses. Very high heritability and moderate to high genetic advance were observed for spikes/plant and plant height in three crosses and number of grains/spike and grain yield plant in all crosses. The heritability estimates for 100-grain weight was moderate to high with low to very low values of the expected genetic advance from the selection.

Farooq and Khaliq (2004) estimated heterosis over mid and better parents in twenty crosses of bread wheat for yield and its components. They reported that 1000-kernel weight showed maximum heterosis over mid-parent followed by number of kernels/spike, plant height, grain yield/plant and number of spikes/plant. The maximum heterobeltiosis estimates were recorded for 1000-kernel weight, plant height, number of kernels/spike, grain yield/ plant and number of spikes/plant.

Fida *et al*. (2004) evaluated heterosis in an F_1 generation by crossing eight bread wheat (*Triticum aestivum L*.) cultivars in a diallel fashion. They studied some agronomic traits such as plant height, number of spike per plant, number of kernels/spike, 100-kernels weight and grain yield/plant under leaf rust conditions. They found highly significant differences among genotypes for all the studied traits. Significant positive heterosis and heterobeltiosis were observed for grain yield/plant in all crosses. of total crosses, 68% and 32% had positively significant heterosis over mid and better parents estimates for plant height, respectively, while 44% and 35% crosses gave significant positive values in number of spikes/ plant.

Abd El-Aty *et al.* (2005) determined the types of gene effects and to create new genetic combinations, using the six populations of four wheat crosses. The F_1 mean values exceeded the mid-parent for all studied traits in the four crosses, except for days to heading which was earlier than the mid-parent, indicating partial dominance. The F_2 mean values were approximately equal to the mid-parent values and less than the F_1 mean values, indicating that inbreeding depression has occurred. BC_1 and BC_2 mean values varied according to the trait itself. They added that the additive effect was more important and greater than the dominance effect for most traits. Among the epistatic components, the dominance × dominance was greater in magnitudes than additive × additive and additive × dominance in most studied traits. Heritability estimates in narrow sense were low to moderate for all the studied characters in all crosses. The predicted genetic advance was low in all the studied traits except for spike weight which was moderate.

Jan *et al*. (2005) estimated the magnitudes of heterosis relative to mid- and the better-parent for days to heading, plant height and days to maturity in 8 × 8 full diallel set of bread wheat (*Triticum aestivum L*.). They found that out of the 56 F_1 hybrids, 18 and 16 hybrids expressed significant heterosis relative to mid - and

better parent for days to heading and 8 and 3 hybrids for days to maturity. Maximum limits of heterotic effects relative to better parent for plant height, days to heading and days to maturity were, 3.27%, 2.60%, and 1.82%, respectively.

Abd El-Nour (2006) used seven populations to study gene action, heritability and predicted genetic gain from selection in three bread wheat crosses derived from four diverse bread wheat genotypes.The data obtained showed significant and positive heterosis effects for grain yield/plant in all crosses and for plant height, No. of spikes/plant and 100-kernel weight in two crosses. Inbreeding depression was significant for most studied characters. Overdominance towards higher parents was found for grain yield/plant and for most studied characters in a cross. Moreover, high to moderate values of heritability estimates were found to be associated with moderate to low genetic advance as a percentage of F_2 and F_3 means in most studied characters. The results showed that the additive gene effect in the six parameter model and in five parameter model was found to be significant for most studied characters in all crosses. Both dominance and epistasis were found to be significant for most studied characters under investigation.

Abd-El-Nour and Mosherf (2006) estimated genetic variance, gene action, heritability and comparison between actual and expected genetic gain of three bread wheat crosses derived from five parental bread wheat genotypes using five populations of each cross. Significant and negative heterotic effects for No. of kernels/spike in all studied crosses. However, over-dominance towards the high parent was detected for most studied characters. The inbreeding depression estimates were found to be significant for most studied characters in all crosses. F_2 and F_3 deviations estimates were significant for most studied characters in all crosses. The additive and additive × dominance gene effects were significant for most studied characters in all crosses. They reported that high to medium values of

heritability estimates were found to be associated with high to moderate expected and actually gained from selection in most characters.

El-Sayed and El-Shaarawy (2006) indicated that significant differences among the studied generations for all studied characters. The results indicated the presence of a non-allelic interaction for the significant values in most studied characters in all crosses. Additive, dominance, additive × additive, additive × dominance, and dominance × dominance gene effects were significant for most studied characters in all crosses with predominant for epistasis components. Significant positive or negative heterosis values based on better parent values were obtained for most studied characters in all crosses. All crosses showed significant inbreeding depression for all characters in one cross. High heritability estimates in a broad sense were observed for all studied characters for all crosses. Narrow sense heritability ranged from low to moderate for most studied characters.

Ahmadi *et al*. (2007) reported that most of the genetic parameters including mean (m), additive (d), dominant (h), additive × additive (i), additive × dominant (j) and dominant × dominant (l) effects were significant. However, all gene effects were not significant in all traits. The dominant gene effect was the most contributory factor to the inheritance of the majority of traits. For the majority of the traits, additive gene effect was significant, but its magnitude was less than dominant gene effect. Also the dominant × dominant (l) epistasis was more important than additive× additive (i) epistasis. The degree of dominance in most of the traits indicated the predominance of dominant gene effects.

Hammad and Abd El-Aty (2007) found that additive and non-additive genetic variances were significant or highly significant for all studied characters including days to heading and days to maturity. Mean degree of dominance

indicated the presence of partial dominance for all studied characters. Heritability estimates in narrow sense were high for days to heading and days to maturity.

Hendawy and Seleem (2007) gained significant and desirable heterosis in a positive direction for number of kernels/spike and 100-kernel weight. Highly significant negative inbreeding depression was obtained for number of spikes/plant, spike length, number of kernels/spike and grain yield/plant. Overdominance towards the higher parent was detected for; number of spikes/ plant, spike length, and number of kernels/ spike . Heritability estimates in a broad sense were high to moderate in most cases. The narrow sense heritability estimates were low and moderate in most cases.

Shehab El Deen (2008) studied heterosis for earliness, agronomic and yield traits in some bread wheat genotypes and their diallel F_1 crosses under different irrigation regimes (normal and stress). Mean squares due to genotypes were highly significant for all studied traits. Mean squares due to parents vs. crosses (heterosis) were highly significant for number of spikes per plant, number of kernels per spike and grain yield per plant under both water stress and non-stress water conditions, 100KW under non-stress conditions only. Highly significant estimates of general combining ability and specific combing ability mean squares for all studied traits were detected. Average degrees of dominance was less than unity for number of kernels per spike under water stress and non-stress and number of spikes per plant and 100-kernel weight under non-stress, indicating that partial dominance played the most important role in the inheritance of these traits.

Aboshosha and Hammad (2009) found that values of A, B, and C scaling tests for days to heading and maturity in the two crosses were significant. The dominance effect was more important and greater than additive effect for days to heading and maturity for the two crosses. Heritability in the broad and narrow

sense indicated the importance of non-additive variance components in the inheritance of days to heading and maturity. The expected genetic advance estimates in the F_2 were low for both days to heading and maturity.

Khattab (2009) used the six populations (P_1, P_2, F_1, F_2, BC_1 & BC_2) to study the genetic behavior of some traits of bread wheat using. The results revealed that the genetic variances within the F_2 population were found to be significant for plant height, number of spikes per plant and grain yield per plant in the three crosses. F_2 mean performance was found to deviate significantly from the average of the F_1 and mid-parent value for plant height, number of spikes and grain yield/plant in the three crosses except grain yield/plant in the second cross. The additive gene effects (a) were found to be highly significant for number of spikes/plant in the three crosses under investigation. Dominance gene effects (d) were found to be highly significant for plant height in the three crosses under investigation. Additive × additive (aa) epistatic type of gene effects was found to be significant only for number of spikelets/spike in the three crosses under study.

Laghari *et al.* (2010) estimated heritability in the F_5 segregating generation of a cross between HT5 and HT 37 of bread wheat. The genetic parameters calculated were genetic variance, environmental variance and heritability percentage in a broad sense, genetic advance and heritability coefficient. The highest heritability was observed for number of grains per spike (54.5%) and main spike yield (69.5%) associated with high genetic advance (2.8, 22.8 and 1.5 respectively). Moderate to high heritability were recorded for peduncle length (48.75%) and number of grains per spikelet (47.2%) which associated with high genetic advance (2.3 and 0.68 respectively). plant height had shown acceptable heritability values. The present finding suggests that most of the yield associated traits have been successfully transmitted. The information generated will be helpful

for better understanding and selection of suitable, desirable material especially in advance generations.

Abd EL-Nour (2011) used six populations (P1, P2, F_1, F_2, BC1 and BC2) of three bread wheat crosses, to estimate genetic parameters for grain yield/plant and certain related characters under two nitrogen fertilizer levels. Results revealed that heterosis values were positive and significant relative to better-parent in the three crosses under the two nitrogen levels for most of the studied characters. Meanwhile, heterosis values were negative and significant for number of kernels/spike in the first and the third cross.

Aykuttonk *et al*. (2011) estimated gene effects for plant height and fertile tiller number, using six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) 0ff in order to improve some agronomical traits, Genetic analyses were performed using the joint scaling test based on three and six parameter models. In addition to additive and dominance gene effects, epistatic effects were significant for all measured traits due to different origins of the parents used in the study. It was suggested that selection for all agronomical traits should be effective in advanced segregating generations due to epistatic gene effects.

Koumber and El-Gammaal (2012) used five populations for three crosses. Highly significant heterotic values in the positive direction were found for all characters except for plant height and 1000-grain yield in the first cross, and plant height, No. of grains/spike and No. of spikes/plant in the third cross. Overdominance for all characters except plant height and 1000-grain weight in the first cross, and No.of grains /spike in the third cross was detected. Inbreeding depression was obtained in two out of three crosses for No. of grains/spike, No. of spikes/plant, 1000-grain weight and grain yield/plant and in one out of the three crosses for plant height. The important roles of both additive and non-additive gene

action were found in certain studied traits. High to medium values of heritability estimates were found to be associated with high and moderate expected and actual gain in most traits. These obtained results indicated that these traits could be used in the early generations, but would be more effective if postponed to late generations.

Zaazaa, *et al*. (2012) found that the mean value of F_1 population was higher than the respective parents (P1 and P2), F_2, BC1 and BC2 populations for most studied traits in the three crosses. Heterosis in F_1 crosses over their respective mid and better parents for grain yield. Significant positive values of inbreeding depression were detected for all studied traits in the three crosses as well as 100-grain weight in the first and the second crosses. The highest values of phenotypic and genotypic coefficient of variations were obtained for number of spikes/plant, grain weight/spike, and grain yield/ plant. Additive × dominance gene effects were of minor importance in general for most of the studied traits. They concluded that selection for grain yield and its components should be delayed to later generations in breeding programs.

Hassan *et al*. (2013) used forty crosses with the parental lines to study some quantitive traits in bread wheat. Additive (A) and dominance (D) genetic variances were significant in all the studied traits. The predominance of an additive component indicates that the additive gene effect was more effective than non-additive in the inheritance of these characters. However, the dominance was higher than additive for plant height, number of spikes/plants, spike length, number of kernels/plant and grain yield/plant (g). On the other hand, significant of additive and dominance components indicated that both additive and dominance gene effects were important in the inheritance of these traits. Also, selecting desirable characters may be practiced in the early generations, but it would be effective in

the late ones. Heritability both in broad and narrow senses was found to be high in majority cases indicated higher importance of genetic effects in control of traits. But in some cases these values were moderate or low.

Mohamed (2013) estimated genetic variance, gene action, heterosis, inbreeding depression, heritability and genetic advance for grain yield and its components and some agronomical characters. Six populations for three crosses were used in this study .Analysis of variance showed significant differences among the studied. generation means for all studied traits. Additive type of gene effect was significant either positive or negative for no .of spikes / plant, 100-kernel weight and grain yield /plant in the first and second crosses. Dominance gene effects were significantly positive for most the studied traits. Additive × additive and additive × dominance type of gene actions were significantly positive or negative for most the studied traits in the three crosses. Heritability for days to heading in narrow sense was high and nearly equal to its corresponding in a broad sense. High estimates for heritability in a broad sense were accompanied by the moderate value of narrow sense for no. of kernels /spike, 100 –kernel weight and grain yield plant in the three crosses.

Sial *et al*. (2013) studied heritability in 30 F_2 segregating population through cross combinations of six different parental lines/varieties of bread wheat. The highest mean number of grains per spike and main spike yield were recorded in 23 progenies. Eighteen progenies showed the highest heritability (81.2 to 94.3%) broad sense (h^2) coupled with higher genetic advance (1.69-30.58%) for number of grains per spike; indicating more effective selection which could be possible from segregating progenies for this particular trait. Twenty-six progenies showed the highest heritability (59.4 to 97.1%) for main spike grain yield character. The results depicted that most of the segregating progenies showed

genetic improvement in both quantitative traits in terms of more heritability (h^2 b.s.) and genetic advance.

Khan *et al*. (2014) reported that major genes heritability was higher than that of the polygene in the segregating populations of all the crosses with highest environmental influence. Additively controlled nature of the trait predicts that selection of desirable recombinants for higher grain yield per plant may be delayed up to advance generations until favorable genes are accumulated in homozygous condition.

Sharshar (2015) indicated that dominance gene effects were larger in magnitude than the additive gene effects for days to heading, days to maturity, plant height, and number of spikes/plant, number of kernels /spike, 100 kernels weight and grain yield / plant. The estimates of heritability in a broad sense were high in most studied crosses. Narrow sense heritability estimates were low to relatively high for all the studied crosses.

Ljubicic *et al*. (2016) mentioned that the results of the analyses of components of genetic variation indicated over-dominance in the inheritance of yield and its components examined traits suggested that selection in later segregating generations may lead to fairly good improvement in these characters.

Sharshar and Esmail. Samar (2019) determined type of gene action and some genetic parameters in three wheat crosses derived from four parental wheat genotypes. Genetic material included six populations (P1, P2, F_1, F_2, BC1 and BC2) for each cross. The studied characters were plant height, number of spikes/plant, number of kernels /spike, 100 - kernel weight and grain yield / plant. Results in general indicated that negative heterotic effects relative to the mid-parent and better-parent were found for most of the agronomic traits and most crosses. Non-allelic interaction was found for all studied traits in all the crosses under study.

Dominance gene effects were larger in magnitude than the additive gene affects for most studied traits. The estimates of heritability in broad sense were high in most studied crosses. Narrow sense heritability estimates were low to relatively high for all the studied crosses.

2.2. Nature of inheritance of stripe and stem rust diseases in wheat.

Wheat rusts resistance has been recognized to be governed by one or a few gene pairs **(Biffin 1905)**. Latter, in **1963, Vander Plank** had classified disease resistance into two categories: (vertical and horizontal), vertical resistance was characterized by discrete classes of infection types and simply inherited differences in phenotype, whereas horizontal resistance was characterized by small, but important differences in pathogen development with different host plants. These latter differences were believed by **Vander plank (1963)** to be quantitatively inherited and not influenced by the pathogen genotype.

Through series of genetic studies on flax rust, **Flor (1955a, 1955b, 1956 and 1971)** proposed and defined his “gene-for-gene hypothesis” as "for each gene conditioning rust reaction in the host, there is a specific gene conditioning pathogenicity in the parasite". **Loegering (1984)** suggested that the parasite and its host together form a new organism which is neither parasite nor host, and used the term "aegricorpus" to describe the new organism.

The following review will deal with some of the world literature beside summary of the available local investigations carried out in Egypt in this respect. In a study of genetic control of disease expression in the wheat stripe and stem rusts.

Shehab El-Din *et al*. (1991a) studied the inheritance of wheat resistance to stem rust at the adult stage in two bread wheat cultivars Sakha 8 and Mabrouk. They found that heritability in broad sense were high and ranged between (0.75%,

0.84%), and (0.58%, 0.70%) in narrow sense. Dominance of resistance over susceptibility , complete dominance in the F_1 and partial dominance in the F_2 were detected .

Shehab El-Din *et al*. (1991b) investigated two crosses to study the inheritance of resistance to stem rust in Sakha 61 cultivar. Results indicated that Sakha 61 resistance depends on both host-and pathogen as well as environmental conditions. Heritability values in broad and narrow senses were high in the first cross and intermediate in the second one. The expected genetic advance estimates were high for both crosses .The additive, dominance and the epistasis (additive × dominance) were the importance of effects in the gene expression of the first cross, while for the second one, the main portion of the genetic effects were due to the epistasis of additive × dominance and dominance × dominance.

Xianming and Roland (1993) studied the inheritance of yellow rust resistance in the wheat cultivar Carstens v. They found that, Carstens v has three genes for resistance to North American race CDL-21, two genes for resistance to races CDL 17, CDL-20 and CDL-29 and one gene for resistance to race CDL-27. The three genes were either dominant or recessive depending upon the race used in the test and the cultivar used in the cross.

Chen and Line (1995) estimated the number of genes and heritability of resistance to yellow rust in two wheat cultivars. They revealed that the estimated broad and narrow sense heritabilities of the high-temp, adult-plant. The obtained values of broad sense heritability was 95.8 % for Druchamp and 95.3% for Stephens. While, narrow sense heritability was 86.1 - 89.1 % for Druchamp and 95.4% for Stephens.

Shehab El-Din and Abd El-latif (1996) indicated the importance of both additive and dominance effects in the expression of wheat resistance to stripe rust. The manifestation of additive and non-additive effects and hence indicated that

selection would be more effective in late generations**.** Heritability in broad sense was high, while in narrow sense it was medium.

Bai *et al*. (1997) determined the genetic diversity for leaf and stem rust diseases resistance in seven *Triticum monococcum* accessions and inheritance of the resistance. They indicated that the seven accessions carried at least one gene in common for leaf rust resistance. They also reported that 13 F_2 populations segregated for two independent dominant genes. Moreover, two of the *T. monococcum* accessions were resistant to stem rust, They proved that, genotypes carry a single gene for resistance.

Charan and Bahadur (1997) studied the inheritance of stem rust resistance in five bread wheat cultivars to four races of *Puccinia graminis* f.sp. *tritici*. They indicated that segregation of seedlings in F_2 and F_3 families for resistance suggested the presence of three dominant and one recessive genes in HD2135, four dominant genes in HD2189, 3 dominant and two complementary recessive genes in HD2286, two dominant and one recessive genes in HD2160 and five dominant genes in Vaishali.

Patil *et al*. (2000) studied the genetic analysis of wheat cultivars HD2278, NI 5643 and HY65 for resistance to race 40 of wheat stem rust. Each cultivar crossed with a susceptible parent, Pusa 4. They reported that resistance against the race 40 in all cultivars was found to be controlled by a single dominant gene.

Ganeva *et al*. (2001) showed that the resistance of the A-3-86-4-5-3-3 line toward stem rust race 77 which was determined by one recessive gene. Moreover, the resistance of the Gladiator 113 and Maris Habbit sib cultivars and of the A-386-4-5-3-3 line was under the control of various dominant genes.

Mahgoub (2001) proved the important role of both additive and dominance effects in the expression of wheat resistance to stripe, stem and leaf rusts. She found that the reaction of each rust was affected by at least two gene pairs.

Moreover, most estimates of heritability in broad and narrow senses were around an intermediate range.

Aglan (2003) studied the inheritance of wheat resistance to stem rust. The results revealed that the additive genetic effects were more important than those dominance genetic effect in the inheritance of stem rust disease in most cases. Moreover, heritability values in broad and narrow senses for stem rust disease were high and ranged from moderate to high.

Said (2003) studied the inheritance of stripe rust disease and their relationship with molecular marker. The results revealed that the estimates of heterosis related to mid parent were highly significant and negative heterosis values for stripe rust. Heritability in broad and narrow sense were high. Additive, dominance and three epistatic effects (aa, ad and dd) played the major role in the inheritance of stripe rust disease.

Menshawy and Youssef (2004) found that additive gene action presented in the most important part in the total genetic variance components for stripe rust traits. However, dominance effects also appeared to be involved in the inheritance of stripe rust disease resistance. The additive gene action was larger in its magnitude than dominance and that was reflected in average degree of dominance $(H_1 / D)^{1/2}$ where it was less than one for both traits, indicated that the degrees of dominance was in the range of partial dominance.

Menshawy and Najeeb (2004) mentioned that broad and narrow sense heritability values were high for stripe rust trait in bread wheat. They suggested that early generations selection could be effective for improving that trait. Also, genetic component were associated with additive gene action. The average degree of dominance was also less than one for rust traits.

Ragab (2005) claimed that the additive, dominance and epistatic effects played an important role in the inheritance of resistance to stripe and stem rust

diseases. the estimates of heritability in broad and narrow senses were very high for two rusts referring the importance role of additive gene effects for these typed rust diseases.

Mahgoub (2006) cleared that broad and narrow sense heritability values were high in broad sense , while narrow sense were medium to high reflected that resistance to the three rusts is a simple inherited character . controlled by one, two or few gene pairs and proved the results obtained from the qualitative analyses.

Amin and Park (2007) evaluated 105 european wheat cultivars for seedling and adult plant resistance (APR) to stem rust using an array of Australian isolates of *Puccinia graminis* f. sp. tritici. Twenty-seven cultivars were susceptible at both seedling and adult plant growth stages Low levels of APR to stem rust were found in the cultivars Artaban, Forno, Mec, Mercia, Pandas and VladaForno, are believed to carry the leaf rust APR gene Lr34, previously reported to be associated with improved resistance to stem rust.

Bahadur and Mathuria (2008) revealed that genetic analysis confirmed three dominant genes for resistance to stem rust in HD2768, two dominant independent genes each for resistance in HD2733 and HD2784, and one dominant gene in HD2781. Analysis of BC1 and BC2 with pathotype 122 (7G11) confirmed the above number of genes. F_2 segregation of intercrosses HD2733 x HD2781 and HD2781 x HD2784 showed different genes for resistance in above cultivars. An adult plant resistant gene (Sr2) was also identified in HD2733, HD2781 and HD2784 based on mottling effect on the seedlings.

Carmen *et al*. (2008) used three recombinant inbred line populations from the crosses RL6071/Thatcher, RL6071/ RL6058 (Thatcher Lr34*)*, and Thatcher/RL6058, to study the genetics of stem rust resistance in Thatcher and TcLr34. Segregation of stem rust response in each population was used to determine the number of genes conferring resistance, as well as the effect of the

leaf rust resistance gene *Lr34* on stem rust resistance. In field plot tests at least three additive resistance genes segregated in the RL6071/RL6058 population, whereas two resistance genes segregated in the RL6071/Thatcher population. The presence of the gene *Lr34* permitted the expression of additional stem rust resistance in Thatcher-derived lines both at the seedling and adult plant stages.

The inheritance of resistance to leaf rust disease was investigated by **Yasen (2008)** using six generations mating design. Wide differences were detected between each parent within each cross and between the crosses themselves for stripe rust disease resistance. The results suggested that additive genetic components were greater in magnitude than dominance effects in the inheritance of resistance to stripe rust disease. Highly significant to negative direction heterotic effects were found for stripe rust toward resistance.

Datta *et al*. (2009) studied the genetic analysis of common wheat cultivar PBW343 confirmed temperature-sensitive leaf rust resistance and adult plant stripe rust resistance. At low temperatures, PBW343 was resistant to P. triticina (Ptr) pathotype (pt.) 121R63-1, and at high temperature it was resistant to Ptr pt. 121R127. The low temperature resistance to pt. 121R63-1 was attributed to interaction between dominant and recessive genes. The dominant gene involved in low-temperature resistance to pt. 121R63-1 also conferred resistance to pt. 45R35. The high-temperature resistance to Ptr pt. 121R127 was governed by a different single partially dominant gene. Agra Local (a commonly used susceptible check) and IWP94 (a leaf rust differential used in India) are also resistant to pt. 121R127 at high temperatures.

Kaur and Bariana(2010) reported the presence of the adult plant stripe rust resistance gene *Yr30* in cv. Pavon. *Yr30* mapped close to the stem rust resistance gene *Sr2* in chromosome arm 3BS.

Priyamvada *et al*. (2011) reported that all resistance genes in the host population, whether they are major or minor genes are considered to interact in a gene-for- gene way with virulence genes either major or minor, in the pathogen population. Populations with a polygenic resistance based on gene-for-gene action have an increased level of resistance.

Youssef and Hamada (2012) reported that seven crossess out of the F_2 plant populations were segregated fitting the expected ratios 7(R) : 9(S) , 1(R) :15(S) , 3(R) :13(S) and 9(R) : 7(S). While the rest of crosses (Yr 18 X Giza 168 and Yr 2 X Sakha 61) showed no segregation and was directed to the side of dominance of resistance.

Nzuve *et al*. (2013) studied five resistant wheat lines which were resistant and used as parents in crosses with stem rust susceptible line CACUKE to develop genetic populations for determining the inheritance of resistance to stem rust. The F_2:F_3 lines of population (s) exhibiting qualitative variation were grouped as homozygous resistant (HR), segregating (Seg) and homozygous susceptible (HS). Heavy disease pressure was present during the cropping seasons with the check CACUKE displaying 90% susceptibility. Chi square analysis revealed that the segregation data in the parent KSL-2 did not deviate significantly from the single gene model (1:2:1) suggesting that the resistance to stem rust is conditioned by a single dominant gene. The Chi square test also revealed that the stem rust resistance in the parents KSL-3, KSL-5, KSL-12 and KSL-19 was conditioned by two genes. The families from the KSL-2 and KSL-3 crosses also segregated for the presence of the pseudo black chaff implying that the Sr2 gene could be presented in the background of these wheat parents. The superior transgressive segregants identified in these crosses will be used in breeding.

Rehman *et al*. (2013) reported that partial resistance varieties were crossed in a top cross/back cross scheme and the segregating populations were advanced

by selected bulk method, which resulted in the development of material having better yield and rust resistance against Brown, Yellow and Black Rust Fungi than the pre-existing varieties (e.g., Inqlab-91, MH-97). Three varieties, Shafaq-06 and Lasani-08 and AARI-11 from these crosses have been approved for general cultivation. Similarly, the material developed and distributed by CIMMYT, Mexico having this type of resistance is being globally adopted.

Bhardwaj (2013) said that a number of genes are known for resistance to wheat rusts. There is a definite interaction between rust and resistance genes. Puccinia-Triticum interaction is very widely researched and a model system guided by gene-for-gene theory. Many of these gene interactions are dependent on light, temperature and growth stage of wheat plants. Complementary, additive and inhibitory gene interactions have been recorded. Evolution and detection of new pathotypes open new horizons and provided material to study evolution in relation to host resistance.

Cheruiyot *et al*. (2014) estimated the kind of gene action in the inheritance of adult plant resistance to stem rust and yield related traits in wheat and to determine heritability of these traits. Six genotypes, four with known reaction to stem rust and two genotypes adapted to Kenyan growing environments were crossed in complete 6×6 diallel fashion. Results revealed that narrow sense heritability estimates were moderate (0.33 for grain yield) to high (0.78 for days to heading). Additionally, partial dominance for stem rust infection was found for, the number of days to heading and the number of productive tillers while over-dominance was observed for grain yield and plant height. Since all the traits were heritable, recurrent selection will be effective.

Hermas and El-Sawi (2015) reported that the ratio (h2/H2) that referred to the number of gene pairs controlling stem rust resistance and yield characters were less than unity in both F_1 and F_2 generations, suggesting that there is at least one

group of genes governed these characters. Heritability estimates in its broad since were considered to be very high (up to 90%) enough to select plants with an adequate level of stem rust resistance and high yield potentiality in the early generations.

Shahin and Ragab (2015) recorded that dominance of yellow rust resistance over susceptibility was noticed in most cases (in four out of five resistant by susceptible crosses). Segregation in the F_2's population showed the presence of two to three gene pairs controlling plant reaction against the [*Pst*].

Sharshar (2015) reported that dominance gene effects were larger in magnitude than the additive gene effects for stem rust resistance. The estimates of heritability in broad sense were high in most studied crosses. Narrow sense heritability estimates were low to relatively high for all the studied crosses.

Zennah *et al.* (2015) stated that in the F_2 populations evaluations that derived from *Kwale* × PCB52 indicated that the resistance is conferred by a single dominant gene. However, all other F_2 populations showed that the resistance was conferred by two genes complementing each other (duplicate recessive epistasis) thus the ratios 9R: 7S. These identified resistant lines could be evaluated for other qualities and passed as potential varieties or used as sources of valuable stem rust resistance.

Zakeri *et al.* (2016) reported that adult plant resistance to stripe rust disease is commonly controlled by combinations of genes with additive effects.

Ullah *et al.* (2016) mixed inheritance analysis using joint segregation analysis (JSA) for stripe rust (*Puccinia striiformis f. sp. tritici*) resistance was carried out in six basic populations (P_1, F_1, P_2, BC_1, BC_2 and F_2) of four wheat crosses. Genes controlling stripe rust resistance were assessed by using area under disease progress curve (AUDPC). The AUDPC was controlled by mixed two

additive-dominant-epistatic major genes plus additive-dominant-epistasis of polygenes in cross Hashim-08 × LU-26 (model E), while in Farid-06 × Shafaq, it was controlled by mixed two major additive-dominant genes plus additive-dominant polygenes (model E-2). In cross Parula × Blue Silver, the AUDPC was managed by additive, dominance and epistasis of two major genes (model B-1), however, it was controlled by mixed one major gene and additive dominant polygenes in cross TD-1 × D-97603 (model D-1). Genetic variation and heritability was higher in major genes than polygene for all the crosses showing that AUDPC was mainly controlled by major genes. The genetic behavior of the AUDPC revealed that stripe rust resistance was controlled by mixed interaction of one to two major genes plus polygenes.

Serpoush *et al.* (2018) studied the heritability of resistance to stripe rust in bread wheat, F_1, F_2, BC1 and BC2 generations, derived from a cross between two wheat cultivars named Morvarid (resistant) and Bolani (susceptible) along with the parents, were evaluated under greenhouse condition. The seedlings were inoculated using the race 198E154A+ urediniospores. Results of the generations mean analysis showed that additive; dominance and epistasis (especially additive × dominance and dominance × dominance) gene actions have a significant role in control of the trait. Furthermore, high broad-sense heritability was observed for this trait. The narrow-sense heritability was in an average range for infection type and was low for latent period. The number of segregating genes was estimated 1 - 2 for infection type and 1 - 3 for latent period.

Sharshar and Esmail. Samar (2019) studied the resistance of stripe and stem rust diseases in three wheat crosses derived from four parental wheat genotypes. Genetic material included six populations (P1 , P2 , F_1 , F_2 , BC1 and BC2) for each cross. Heritability estimates in broad sense were high for stripe and

stem rust diseases for all the studied crosses, indicating that the phenotypic variability was mostly attributed to genetic effects for these diseases in these crosses. On the other hand, heritability estimates in narrow sense were moderate to high for stripe and stem rust diseases for all the studied traits, according to the cross and/or traits itself, reflecting the importance of additive gene action and their effects in resistant for stripe and stem rust diseases except the second cross in stem rust.

2.3.Molecular breeding for wheat stripe and stem rusts resistance.

Ma et al. (2001) investigated the origin and distribution of Yr26 and inheritance of resistance and molecular marker analysis using pedigree, Triticum turgidum L. was the common ancestor of Yr26. PCR-SSR markers were shown to be very effective for the detection of the Yr26 gene in segregating populations and therefore could be applied in wheat breeding .

Sun et al. (2002) reported that, foundation of DNA markers for the Yr5 gene will encourage marker-assisted selection and gene pyramidng in the breeding program. The Yr5 gene was located on the long arm of chromosome 2B, By33, the donor of Yr5, was crossed and backcrossed with the susceptible line 441, and $BC3F_2$ and $BC3F_3$ segregating populations were used for polymorphism by using 11 microsatellite marker, Xgwm501 with 195 bp and160 bp .

Tsilo et al. (2008) reported that, the identification and validation of molecular markers linked to Sr6 that can be used for the detection of this gene in wheat breeding programs. Bulked segregant analysis (BSA) and 418 SSR markers that covered the entire genome of wheat were used to screen seedling stage. Markers , Xwmc453, Xcfd43, Xcfd77, and Xgwm484, were mapped within a chromosome region that covered 9.7 cM from Sr6. The closest markers, Xwmc453 and Xcfd43, were linked to Sr6 with a distance of 1.1 and 1.5 cM, respectively.

The markers Xwmc453 and Xcfd43 amplified Sr6-specific marker alleles that were diagnostic for Sr6 in a diverse set of 46 wheat accessions and breeding lines developed and/or collected from different regions. These markers could be used for MAS of Sr6 and for pyramiding it with Sr resistance genes .

Wang et al. (2008) screening SSR markers closely linked with Yr26. A total of 500 F_2 plants and the $F_{2:3}$ progenies , the stripe rust resistance was controlled by a single dominant gene, Yr26. The closest SSR marker, Xwe173 and Xbarc181, mapped in 1BL and the genetic distances from Yr26 were 1.4 cM and 6.7 cM, respectively. Eight common wheat cultivars and lines were tested for presence of the markers, only five lines with Yr26 carried the flanking markers whereas three lines without Yr26 were not. The results indicated that the SSR markers should be useful in marker-assisted selection for incorporating Yr26 into wheat cultivars .

Babiker et al. (2009) inoculated Ninety-eight F_2 plants with a stem rust isolate of race QTH to identify molecular markers linked to the stem rust resistance gene Sr35 that provides resistance against many devastating races, including QTH and TTKS (or Ug99), in wheat. Using 21 microsatellite primer pairs to dedect polymorphism among parental lines and F_2 population, only two markers (. Xgwm391 and Xcfa2076) retained significance $\alpha = 0.05$. GWM391 revealed a polymorphic band with 200 bp found only in the susceptible bulk. In contrast, Xcfa2076 amplified polymorphic band with 210 bp in the resistant bulk and its parent. Using linkage analysis Xgwm391 was found to be comparatively close to Sr35 with a genetic distance of 12.2 cM. Whereas searching for closer marker continues, wheat breeders could be obviously promoted by using these markers in their selection of Sr35 in their battle against the brutal stem rust race Ug99 .

Akfirat et al. (2010) used bulk segregant analysis (BSA) to identify molecular markers associated with strip rust disease resistance in bread wheat

(Triticum aestivum L.). DNAs isolated from the selected strip rust resistance and susceptible F_2 individuals derived from a cross between strip rust resistant and susceptible wheat genotypes. SSR markers (Xgwm382) located on chromosome group 2 (A, B, D genomes) was existing in the resistant parent and the resistant bulk but absent in the susceptible parent and its susceptible bulk, suggesting that this marker is linked to a strip rust. The existence of Xgwm382 was also tested in 108 additional bread wheat genotypes differing in Yr rust resistance. This analysis showed that 81% of the wheat genotypes was yellow rust resistant and had the Xgwm382 marker, therefore, in wheat breeding programs Xgwm382 could be useful for marker assisted selection of Yr resistances .

Xu et al. (2014) constructed a high density genetic map and to developed markers for YrC591. Stripe rust resistance gene YrC591, existing in wheat cultivar C591, is effective against now important Puccinia striiformis Westend. f. sp. tritici isolates. Using 34 SSR markers which located on 7BL were used to perform bulk segregant analysis. Out of them only 8 SSR markers, cfa2040, wmc273, wmc166, gwm984, barc32 wmc276, barc182 and gwm146 were polymorphic between the parents and contrasting susceptible and resistant DNA pools. In addition, authentication of the SSR markers cfa2040, wmc273 and barc32, was carried out using C591 line as a parent, indicating that they could be an effective in tracing this gene in MAS .

Yadav et al. (2015) used marker assisted backcrossing (MABC) to transfer three stem rust resistant genes Sr25, SrWeb and Sr50 into the popular Indian wheat. The donor was the CIMMYT breeding line PMBWIR4, and each of the objective genes was marked by a simple PCR assay. The improved lines of HUW234 contain the segment of donor parent carrying genes; Sr25, SrWeb and Sr50. The selected lines may also contain certain amount of linkage drag along

with the target genes. SSR markers; gwm319, wmc245, wmc272, wmc332, wmc361 and gwm382 for the gene SrWeb , while ,gwm302, wmc322, gwm344, barc340, gwm146 and wmc232 were used for recombinant selection for the gene Sr25. Six lines were selected which carried minimum segment of donor parent based on selection on carrier chromosome (recombinant selection).

Yao et al. (2017) used F_2 progenies from crosses between a high level of resistance to yellow rust and a set of 20 CS monosomic lines. Using 141 F_2 plants and their F_3 generations with 7B specific simple sequence repeat (SSR) markers, a linkage map consisting of five SSR loci and the resistance gene locus YrLk was constructed. The linkage map covered a genetic distance of 21.6 cM, and the SSR markers Xwmc396 and Xbarc267 were closely linked to YrLk with genetic distances of 3.3 and 4.4 cM, respectively .

Randhawa et al. (2019) demonstrated that, the usefulness of markers linked with rust resistance genes Yr51, Yr57, Sr22, Sr26, and Sr50. MAS was successfully working to select combination of resistance with most plant stages. The MAS approach is even more useful in the situation of genes that show recessive inheritance. In this study, backcrossing of the recessive gene Yr51 was successfully achieved.

Long *et al.* (2019) performed a genome-wide association to identify effective Yrs resistance loci, using bread wheat landraces based on Diversity Arrays Technology and SSR markers. In total, 19 displayed stable, high degrees of resistance to Yr development when exposed to mixed races of Pst at the adult-plant stage in different field conditions assessments.

Rathi *et al.* (2020) screened F_2 population from cross WH711 (susceptible parent) and PBW698 (resistant parent) against stripe rust was done on the basis of field reaction of yellow rust and 12 morphlogical traits. The genotyping of parents

was done by using 80 SSR markers out of which 11 were found polymorphic. These 11 markers were used to screen 250 individuals of F_2 population. Mendelian inheritance was followed by five markers viz. Xgwm631, Cfa2040, Xsps3000, Barc76 and Xgwm 130 which segregated according to expected ratio of 1:2:1 with chisquare values 5.78, 4.23, 2.75, 9.2 and 7.6 respectively. Single marker analysis showed markers Xgwm631, Cfa2040 (Yr2, Yr6), Xsps3000 (Yr10), Xgwm130 (Yr7), Xwmc407 (Lr17), Barc46, Xgwm413 (Yr15), Barc187 (Yr27) and Xgwm273 (YrH52) were linked with yellow rust locus at 0.01% of significance hence these genes may be present in the breeding population. Cfa2040 was found linked with flag leaf area, number of spikelets and Barc181 with spike weight locus. Markers on chromosomes 7A and 1B showed LOD values 6.64 and 6.86 conferring tight linkage with yellow rust locus thus can be used for MAS.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The present study was carried out at the experimental farm of Sakha Agricultural Research Station, Agriculture Research Center, Egypt. Moreover, the molecular study was conducted at Genetic Engineering and Tissue Culture Lab., accredited based on ISO 17025:2005, Genetics Department, Faculty of Agriculture, Kafrelsheikh University. During the three growing seasons from 2014/2015 to 2016/2017 to study the genetical behavior of some agronomical characters and resistance to strip and stem rusts of wheat.

3.1. Field experimental design:-

In 2014/2015 season, six parental wheat genotypes, i.e., Shandaweel 1, Misr 1, Sakha 95, Sakha 94, Line 1 and Line 2 were crossed to produce the following crosses, (Line 1 × Misr 1), (Line 2 × Sakha 95), (Shandweel 1× Misr 1), (Sakha 94 × Misr 1) and (Sakha 94 × Sakha 95).

In the second season 2015/2016, the F_1 plants were self-pollinated to obtain F_2 grains and backcrossed at the same time to both respective parents to obtain the two backcrosses (BC_1 and BC_2), self-pollination was made for the parents to get parent`s selfed grains, in the same time, the five crosses were made again to obtain $F_1$`s grains.

In the third season 2016/2017, the six populations (P_1, P_2, F_1, F_2, BC_1, and BC_2) of each cross were sown in randomized complete blocks design with three replicates. Each replicate consisted of 13 rows (one row for P_1, P_2, and F_1, two rows for each of BC_1 and BC_2 and six rows for F_2). In addition, two border rows were planted with a mixture of high susceptible cultivars for natural infection. Each row was 3 m in length spaced 30 cm apart and grains were spaced 20 cm between plants.

The experiment was surrounded by mixed wheat cultivars which were highly susceptible to strip and stem rusts as a trap nursery and spreader to help in

both natural and artificial inoculations. The artificial inoculation for stem rust was carried out at the third week of March in the early evening (at sunset) using a mixture of fresh urediniospores for the most prevalent pathotypes of stem rust with talcum powder at a rate of 1: 25 (w/w) and dusted at booting stages, using the methods of **Tervet and Cassell (1951)**. Meanwhile, The artificial inoculation for stripe rust was not carried out because Sakha is considered a hot spot for this disease and it is forbidding to do so in the open fields.

Table (1): Name, pedigree and their rusts reaction of the studied parental bread wheat genotypes.

Genotypes	Cross &Pedigree	Reaction to rusts*	
		YR	SR
Shandweel 1	**SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC** CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH	R	S
Misr 1	**OASIS / SKAUZ // 4*BCN /3/ 2*PASTOR** CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S)	S	S
Line 1	**SAKHA8/YECORA ROJO**	S	S
Line 2	**SIDS BXD 12-13 #3**	S	S
Sakha 94	**OPATA/RAYON//KAUZ** CMBW90Y3180-0TOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.	R	R
Sakha 95	**PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1.** CMA01Y00158S-040POY-040M-030ZTM-040SY26M-0Y-0SY-0S.	R	S

(YR)Yellow rust, (SR) Stem rust, (R) Resistant, (MR)Moderate Resistant, (S) Susceptible.

*Based on data from wheat research department, ARC, Egypt.

At harvesting time, the data were obtained from 45 guarded individual plants for each parent and F_1, 75 plants for each backcross and 300 F_2 plants for each cross from three replications.

3.2. Assessment of the agronomic traits:

The characters were recorded as follows:

1. **Days to heading** (**DH days**): Number of days from sowing to the time of

emergence of the first spike.

2. **Days to maturity (DM days)**: Calculated as a number of days from sowing date to 50% maturity.
3. **Plant height** (**PH cm**): Measured by a centimeter (cm) from the soil surface to the tip of the spikes, excluding owns.
4. **Number of spikes per plant** (**S/P**): Determined by counting the number of fertile spikes per plant.
5. **Number of kernels per spike** (**Kern/S**): estimated by counting the number of kernels of the main spike.
6. **100- Kernel weight** (**100 KW. g**): determined by weighing 100 randomly selected kernels.
7. **Grain yield per plant** (**GY**): recorded by weighing the grains of each individual plant.

3.3. Stripe and Stem rusts assessment:

The infection types for the stripe and stem rusts caused by *Puccinia striiformis* and *Puccinia graminis*, respectively, were recorded and estimated as disease severity according to the scale adopted by Stakman et al (1962). In this method, resistance, moderately resistance, medium, moderately susceptible and susceptible field responses were symbolized as R, MR, M, MS, and S, respectively.

The rust reaction frequency distribution was performed for the six populations of the five crosses at early dough stage and right before harvesting for the stripe and stem rusts, respectively under field conditions. For the quantitative analysis, field response was converted into an average coefficient of infection (ACI) using the method of Stubbes et al. (1986) and modified by Shehab El-Din and Abd El-latif (1996). In this method, an average coefficient of infection could be obtained by multiplying infection severity by an assigned

constant values namely, 0.05, 0.1, 0.2, 0.4, 0.6, 0.8 and 1 for 0, 0;, R, MR, M, MS and S infection types, respectively.

Frequency distribution values were computed for parental, F_1, F_2, BC_1 and BC_2 populations for stripe and stem rusts reaction in all crosses in the adult tests, under the field conditions. With respect to the mode of inheritance, goodness of fit for the observed: expected ratio of the phenotypic classes was determined by the Chi-square (χ^2) analysis according to Steel and Torrie (1960).

3.4. Statistical analysis:-

In each cross, the mean ($\bar{X}$) and the variance of mean ($S^2_{\bar{X}}$) were calculated for (P_1, P_2, F_1, BC_1, BC_2, and F_2) generations. The population means and variances of the mean were used to estimate the type of gene action. One tail F ratio was calculated to test the significance of F_2 variance as follows:

$$F = \frac{\text{Variance of } F_2}{\text{Variance of E}}$$

Where,

$V_E = \left[V_{F_1} + V_{P_1} + V_{P_2}\right]/3$ **…….. Allard (1960)**

If the F ratio was significant, the Gamble's procedure (1962) was used to estimate the components of the genetic effect. When the F ratio was not significant, it would be an indication that, the variation within the F_2 generation was due to mainly the environmental effects. The " t " test was used to test the significant difference between the two parents in each cross.

3.4.1. Scaling test

Adequacy of scale must satisfy two conditions namely, additively of gene effects and independence of heritable component from non-heritable ones. The test of the first condition provides information regarding absence or presence of gene interaction. The test of the adequacy of scales is important because in most

cases, the estimation of additive and dominance components of variances were estimated assuming the absence of epistatic gene interactions. Mather (1949) and Hayman (1954) gave four tests for scale effects A, B, C and D. The values of A, B, C and D should be equal to zero within the limit of their standard error. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. The scaling tests A, B, C, and D were applied according to the formulae proposed by Mather (1949) as well as Hayman and Mather (1955) to test the presence of non-allelic interaction as following:

$A = 2\overline{BC}_1 - \bar{P}_1 - \bar{F}_1$

$B = 2\overline{BC}_2 - \bar{P}_2 - \bar{F}_1$

$V_A = 4V_{\overline{BC}_1} + V_{\bar{P}_1} + V_{\bar{F}_1}$

$V_B = 4V_{\overline{BC}_2} + V_{\bar{P}_2} + V_{\bar{F}_1}$

$V_C = 16V_{\bar{F}_2} + 4V_{\bar{F}_1} + V_{\bar{P}_1} + V_{\bar{P}_2}$

$V_D = 4V_{\bar{F}_2} + V_{\overline{BC}_1} + V_{\overline{BC}_2}$

$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$

$D = 2\bar{F}_2 - \overline{BC}_1 - \overline{BC}_2$

$S.E\ (A) = \sqrt{V_A}$

$S.E\ (B) = \sqrt{V_B}$

$S.E\ (C) = \sqrt{V_C}$

$S.E\ (D) = \sqrt{V_D}$

The (t) values are calculated as follows:-

$t\ (A) = A/S.E\ (A)$

$t\ (B) = B/S.E\ (B)$

$t\ (C) = C/S.E\ (C)$

$t\ (A) = D/S.E\ (D)$

The calculated values of (t) were compared with the tabulated value of (t) of 5% and 1% level of significance. In each test, the degree of freedom is sum of the degrees of freedom of various generation involved.

The following genetical parameters were estimated:-

3.4.2. Gene action (types of gene effect)

Data were analyzed by two methods as follows:-

3.4.2.1. Generation mean analysis

The means of the six populations in each cross were used to estimate the six parameters of gene effects, using Gamble's procedure (1962) as follows:

$m = \bar{F}_2$

$a = \overline{BC}_1 - \overline{BC}_2$

$d = -\frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2 + \bar{F}_1 - 4\bar{F}_2 + 2\overline{BC}_1 + 2\overline{BC}_2$

$aa = -4\bar{F}_2 + 2\overline{BC}_1 + 2\overline{BC}_2$

$ad = \frac{1}{2}\bar{P}_1 + \frac{1}{2}\bar{P}_2 + \overline{BC}_1 - \overline{BC}_2$

$dd = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\overline{BC}_1 - 4\overline{BC}_2$

Where, the parameters m, a, d, aa, ad, and dd refer to mean effects, additive, dominance, additive × additive, additive × dominance and dominance × dominance gene effects, respectively. Estimates of gene effects were tested for significance from zero by using t-test as follows:

$$\text{Calculated} \pm t = \frac{\text{Effect}}{\sqrt{\text{Variance of Effect}}}$$

Tabulated (t) was defined with d.f of $\propto$ at 0.05 and 0.01 levels of probability, where the variance of an effect is a linear function of the variance of its mean. The variance of these estimates is obtained as follows:

$V_m = V_{\bar{F}_2}$

$V_a = V_{\overline{BC}_1} + V_{\overline{BC}_2}$

$V_d = 1/4\, V_{\bar{P}_1} + 1/4\, V_{\bar{P}_2} + V_{\bar{F}_1} + 16\, V_{\bar{F}_2} + 4\, V_{\overline{BC}_1} + 4V_{\overline{BC}_2}$

$V_{aa} = 16V_{\bar{F}_2} + 4V_{\overline{BC}_1} + 4V_{\overline{BC}_2}$

$V_{ad} = 1/4\, V_{\bar{P}_1} + 1/4\, V_{\bar{P}_2} + V_{\overline{BC}_1} + V_{\overline{BC}_2}$

$V_{dd} = V_{\bar{P}_1} + V_{\bar{P}_2} + 4V_{\bar{F}_1} + 16V_{\bar{F}_2} + 16V_{\overline{BC}_1} + 16V_{\overline{BC}_2}$

Where,

V_m , V_a , V_d , V_{aa} , V_{ad} and V_{dd} are the variances of the different effects and V_{P_1} , V_{P_2} , V_{F_1} , V_{BC_1} , V_{BC_2} and V_{F_2} are the variances of mean for different six populations.

3.4.2.2. Generations variance analysis

The following genetical parameters were estimated.

1. **Environmental variance (V_E):** Estimated from the variation within the non-segregating populations, e.g., parents and F_1 plants.

$$V_E = (V_{P_1} + V_{P_2} + V_{F_1}) / 3$$

Where:

V_{P_1} = the variance of high parent individuals.

V_{P_2} = the variance of low parent individuals.

V_{F_1} = the variance of first-generation individuals.

2. **Genotypic variance (V_G):** Estimated by subtracting the environmental variance from the phenotypic variance according to the following formula (Falconer 1989):

$$V_G = V_P - V_E$$

Where:

V_G = Genotypic variance of F_2 individuals.

V_P = Phenotypic variance of F_2 individuals.

V_E = Environnemental variance.

Partitioning of variation in F_2 and backcrosses was carried out using the following formula presented by Mather (1949):

$V_{F_2} = ½ D + ¼ H + E$ $\quad\quad$ $V_{B_1} + V_{B_2} = ½ D + ½ H + 2E$

Where:

V_{F_2}: variance within F_2 population,

V_{B_1}: variance within backcross of F_1 to one parent,

V_{B_2}: variance within backcross of F_1 to the other parent,

D: the component of the genetic variance due to the additive effects of genes,

H: the non-additive component of the genetic variance due to dominance and,

E: the environmental component of variation.

Estimates of 1/2 additive and non-additive components were obtained by solving the above two equations.

$½ D = 2V_{F_2} - (V_{B_1} + V_{B_2})$ $\quad\quad$ $¼ H = (V_{B_1} + V_{B_2}) - V_{F_2} - V_E$

3.4.3. Heterosis:

Heterosis was expressed as the deviation of F_1 generation from the mid-parent or the better parent average values by Mather and Jinks (1982), as follows:

Heterosis over mid-parent % (M.P) = $(\bar{F}_1 - \overline{MP}) / \overline{MP} \times 100$

Heterosis over the better-parent % (BP) = $(\bar{F}_1 - \overline{BP}) / \overline{BP} \times 100$

To test the significance of the above estimate of heterosis, the variance of heterosis deviation was calculated as a linear function of three variances.

Variances of heterosis over mid-parent deviation = $V_{\bar{F}_1} + ¼ V_{\bar{P}_1} + ¼ V_{\bar{P}_2}$

Variances of heterosis over the better-parent deviation = $V_{\bar{F}_1} + V_{\overline{B.P}}$

Where: $V_{\bar{F}_1}$, $V_{\bar{P}_1}$ and $V_{\bar{P}_2}$ are the variances of the mean of each generation.

3.4.4. Inbreeding depression

The inbreeding depression percentage was computed **according to Mather and Jinks,1971** as follows:

$$I.D\ \% = \frac{\bar{F}_1 - \bar{F}_2}{\bar{F}_1} \times 100$$

To test the significance of inbreeding depression, "t" test was calculated as follows :

$$t.\ test\ of\ I.D = \frac{Estimate\ Values\ of\ ID}{Standard\ error\ of\ mean}$$

where :

$$Standard\ error\ of\ mean = \sqrt{V_{F_1} + V_{F_2}}$$

V_{F_1} = variance of F_1 mean

V_{F_2} = variance of F_2 mean

3.4.5. Nature degree of dominance (Potence ratio):

The following equation was used to determine potency ratio.

$$Potence\ ratio = \frac{\bar{F}_1 - MP}{½\ (\bar{P}_1 - \bar{P}_2)}$$ …… **Smith (1952)**

Where:

$\bar{F}_1$ is first generation mean

$\bar{P}_2$ is the mean of the smaller parent

$\bar{P}_1$ is the mean of the larger parent

MP is mid-parent value.

1- No dominance is indicated when potency ratio is equal zero.

2- Complete dominance is indicated when potency ratio is equal to $\pm$ 1

3- Partial dominance is considered when the ratio is between +1 and –1, but

not equal zero.

4- Over dominance is indicated if potency ratio exceeds +1 or less than –1.

3.4.6. Heritability

Heritability estimates were computed in both broad (H) and narrow senses (h^2) as follows:

$$H\ (\%) = \frac{\text{Genetic variance}}{\text{Phenotypic variance}} \times 100 \quad \text{…….. } \textbf{Allard (1960)}$$

where :

Genetic variance = $VF_2 - VE$, Phenotypic variance = VF2

$$h^2\ (\%) = \frac{\text{Additive variance}}{\text{Phenotypic variance}} \times 100 \quad \text{…….. } \textbf{Mather (1949)}$$

where:

Additive variance = $2V_{F_2} - V_{BC_1} - V_{BC_2}$

3.4.7. The predicted genetic advance under selection (Δg):-

It was computed according to **Johnson et al. (1955).**

$$\Delta g = K \times \sqrt{V_{F_2} \times h_n^2}$$

Where:

(K) a selection differential with a value of 2.06 under 5 % selection intensity.

Also, this expected gain was expressed as a percentage of F_2 mean (Δg%) according to **Robirson et al. (1951)** as follows:

$$\Delta g\ (\%) = \frac{\Delta g}{\bar{F}} \times 100$$

Where: ($\bar{X}$) mean of the F_2 population.

3.5. Molecular markers associated with stripe and stem rusts resistance:

Two crosses were used one for yellow rust and the other one for stem rust, based on the presence of a large segregation rate in F_2. DNA was isolated using CTAB method from fresh leaves of the used two crosses of breed wheat according to **Doyle and Doyle (1990)**.

Fresh 100-150 mg of bread wheat leaves were collected, placed immediately in liquid nitrogen and grinded to powder under liquid nitrogen using mortar and pestle. The ground material was transferred into 2 ml Eppendorf tubes. The 800 µl of pre-heated (65°C) CTAB extraction buffer were added followed by vigorous vortexing. The tubes were incubated for 30 min., at 60°C. After incubation, 800 µl CI-mix (24 parts chloroform + 1 part isoamylalcohol) were added and tubes were gently mixed by inverting. The mixture was centrifuged at room temperature for 10 min. at 12000 rpm. The aqueous phase (app. 400 µl) was transferred into a fresh 1.5 ml Eppendorf tube. The centrifugation step was repeated to get a clear sample. About 275 µl of pre-cooled (-20°C) isopropanol were added and gently mixed to allow precipitation of DNA. The tubes were centrifuged for 10 min. at 14000 rpm to precipitate the genomic DNA. The supernatant was discarded and the DNA pellet was washed with 200 µl washing buffer (76 % absolute ethanol, 10 mM Na-acetate, 7.5 M NH_4-acetate, 0.5 M EDTA, pH 8) until the pellet floats. Washing buffer was carefully removed and the pellet was resuspended in 200 µl TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) supplemented with RNase A (10 µg/ml). The sample was incubated for 30 min. at 37°C, and then 100 µl of 7.5 M NH_4-acetate and 750 µl absolute ethanol were added and gently mixed. The mixture was centrifuged at maximum speed (1200 rpm) for 10 min. at room-temperature. The supernatant was discarded completely and the pellet was dried for 40-50 min. at

37°C. After drying, the pellet was resuspended in 100 µl TE buffer and stored at 4°C overnight.

After the evaluation of rust disease resistance, the young leaves were used to extract genomic DNA. Each plant of F_2 population was collected and extracted separately. Extracted total DNA were quantified and equal amounts of DNA were taken and bulked to make resistant and susceptible DNA pools based on Michelmore et al., (1991) 10 resistant F_2 plants and 10 susceptible F_2 plants. SSR marker polymorphic analysis between resistant and susceptible DNA pools was carried out with the resistant cultivar and the susceptible cultivar for each selected cross.

Buffers

CTAB extraction buffer

10 ml of 1 M Tris HCl pH 8.0

28 ml of 5 M NaCl

4 ml of 0.5 M EDTA

2 g of CTAB (cetyltrimethyl ammonium bromide)

Bring total volume to 100 ml with ddH_2O.

TE Buffer

10 ml 1 M Tris HCl pH 8.0

2 ml 0.5 M EDTA

Bring total volume to 1 L with ddH_2O.

1 M Tris HCl, pH 8.0

121.1 g Tris dissolve in about 700 ml of H_2O.

Bring pH down to 8.0 by adding concentrated HCl (about 50 ml).

Bring total volume to 1 L with dd H_2O.

0.5 M EDTA

186.12 g EDTA

Add about 700 ml ddH_2O

16-18 g of NaOH pellets

Adjust pH to 8.0 with a few more pellets; EDTA won't dissolve until the pH is near 8.0. Bring total volume to 1 L with dd H_2O.

7.5 M Ammonium acetate

57.81 g ammonium acetate

~50 ml of dd H_2O

Bring to 100 ml total volume.

The PCR reactions using 10 SSR primers were used in this study as shown in **Table 2**. The SSR primers were selected from the database www.graingenes.org, as previous information associated with stripe and stem rusts resistance. The reactions for SSR were optimized and mixtures were prepared (in total volume of 25 µl) as follows:

10 x PCR buffer	3 µl
dNTPs	2.5 µl
MgCl2	1.0 µl
Primer F	0.75 µl
Primer R	0.75 µl
Taq polymerase (5 U/ µl)	0.6 µl
Genomic DNA (40 ng/ µl)	2 µl
Didistilled water up to	25 µl

PCR cycling was carried out as the following program; one cycle at 95°C for 5 min., then 35 cycles were performed as follows: 1 min., at 95°C for denaturation, 45 sec. at (based on primer annealing Tm almost 60°C) for annealing and 30 sec. at 72°C for extension. Reaction was incubated at 72°C for 7 min., then at 4°C for keeping.

The PCR products were separated by electrophoresis using 3% agarose gel in 0.5 × TBE buffer against 100 bp DNA Ladder as a size marker. Bands were detected with ethidium bromide staining and visualized under UV light, then photographed on Gel Documentation. Bands size were detected using gel analyzer.

Table (2): SSR primers and their sequences, gene target, band size, chromosome number and motif.

Primers	Gene target	Sequence	SSR size	Chromosme No.	Motif	Refrences
xgwm 18	Yr26	5' TGGCGCCATGATTGCATTATCTTC 3' 5' GGTTGCTGAAGAACCTTATTTAGG 3'	**186bp**	**1BL**	**$(CA)_{17}GA(TA)_4$**	**Roder MS et al. (1998)**
xgwm 413	Yr26	5' TGCTTGTCTAGATTGCTTGGG 3' 5' GATCGTCTCGTCCTTGGCA 3'	**200-325 bp**	**1B**	**$(GA)_{18}$**	**Roder MS et al. (1998)**
xgwm 501	Yr5	5' GGCTATCTCTGGCGCTAAAA 3' 5' TCCACAAACAAGTAGCGCC 3'	**195bp**	**2B**	**$(CA)_{33}$**	**Roder MS et al. (1998)**
xgwm 382	Yr	5' GTCAGATAACGCCGTCCAAT 3' 5' CTACGTGCACCACCATTTTG 3	**200**	**2D**	**$(GA)_{26}$**	**Lowe I et al. (2011)**
xgwm 44	Yr18	5' GTTGAGCTTTTCAGTTCGGC 3' 5' ACTGGCATCCACTGAGCTG 3	**182bp**	**7D**	**$(GA)_{28}$**	**Roder MS et al. (1998)**
Xwmc 453	Sr6	ACTTGTGTCCATAACCGACCTT ATCTTTTGAGGTTACAACCCGA	**187 bp**	**2A**	**$(CA)_{35}$**	**Somers and Isaac (2004)**
Xgwm 533	Sr2	5' AAGGCGAATCAAACGGAATA 3' 5' GTTGCTTTAGGGGAAAAGCC 3'	**120bp**	**3B**	**$(CT)_{18}(CA)_{20}$**	**Anderson JA et al. (2001)**
Xgwm 319	Sr36	5' GGTTGCTGTACAAGTGTTCACG 3' 5' CGGGTGCTGTGTGTAATGAC 3	**170bp**	**2B**	**$(CT)_{11}(N)_{23}(CT)_6$**	**Lowe I et al. (2011)**
Xgwm 47	Sr9	5' TTGCTACCATGCATGACCAT 3' 5' TTCACCTCGATTGAGGTCCT 3'	**166bp**	**2B**	**$(CT)_7TT(CT)_{16}$**	**Roder MS et al. (1998)**
Xwmc 633	Sr22	5'ACACCAGCGGGGATATTTGTTAC 3' 5'GTGCACAAGACATGAGGTGGATT 3'	**143bp**	**7A**	**---**	**Somers and Isaac (2004)**

TBE buffer (10 X)

Tris	108 gm
Boric acid	55 gm

EDTA	55 gm
Distilled water up to	1 L

Sample preparation

PCR-Product	15 µl
Loading buffer (6X)	3 µl

Loading buffer (6 X)

Bromophenol blue	0.25 gm
Xylene cyanol	0.25 gm
Glycerol (30 %)	100 ml

The run was performed for one hour at 80 volt in Bio-Rad submarine (8 cm x 12 cm).

RESULTS AND DISCUSSION

4. RESULTS AND DISCUSSION

4.1. Inheritance of yield and some agronomical traits:

4.1.1. Mean values and variance of the six populations for all the studied characters.

Mean, variance, and Mean variances for the six populations of the five crosses under investigation for agronomic traits are presented in Tables 3 to 9. These data were used to calculate the scaling test and six parameters as Gamble's procedure **(1962)**.

4.1.1.1 - Days to heading:

Concerning days to heading Table (3), mean performance values were indicated that the F_1 mean values were higher than the mid-parent value towards lateness for the second (103.17), third (102.91) and fifth (104.11) crosses, indicating the presence of partial dominance for late parent for these crosses. While, the F_1 mean value was less than the lowest parent value in the first (90.40) and fourth (101.09) crosses towards earliness, indicating the presence of over dominance for the earliest parent for these crosses. Moreover, the fourth cross was less than the mid parents towards earliness, indicating the presence of partial dominance for early parent for this cross.

With respect to, the F_2 mean the values were intermediate between the two parents and close to F_1 mean values for the second cross (103.99), third cross (100.26) and fifth cross (103.99), indicating the importance of non-additive components of genetic variance for these crosses. However, both BC_1 and BC_2 mean values tended towards the mean of recurrent parent for days to heading with some exceptions in some crosses. These results were in close agreement with those of Hendawy et al (2009).

Table (3): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of days to heading.

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	91.51	93.40	90.83	99.60	99.15	100.99
	S^2	0.26	0.25	0.15	17.54	12.13	13.88
	$S^2_{\bar{X}}$	0.01	0.01	0.004	0.06	0.16	0.19
2	$\bar{X}$	104.89	99.42	103.17	103.99	107.27	100.01
	S^2	0.10	0.25	0.15	18.72	15.41	13.34
	$S^2_{\bar{X}}$	0.002	0.01	0.004	0.06	0.21	0.18
3	$\bar{X}$	101.11	97.96	102.91	100.26	103.07	103.45
	S^2	0.92	0.59	0.61	26.73	21.63	22.44
	$S^2_{\bar{X}}$	0.02	0.01	0.02	0.09	0.29	0.30
4	$\bar{X}$	104.62	98.76	101.09	104.87	105.17	102.39
	S^2	0.24	0.19	0.08	15.81	14.50	10.83
	$S^2_{\bar{X}}$	0.01	0.004	0.002	0.05	0.19	0.14
5	$\bar{X}$	105.09	103.11	104.11	103.99	106.05	104.23
	S^2	0.08	0.10	0.10	21.24	16.02	18.61
	$S^2_{\bar{X}}$	0.002	0.002	0.003	0.07	0.21	0.25

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

4.1.1.2- Days to maturity (day):

Regarding the days to maturity, results in Table 4 showed that the F_1 mean value for the first cross (147.63) was less than the early parent, indicating the presence of over dominance for the early parent. Furthermore, the F_1 mean value was less than the mid-parent for the second cross (148.03) and third cross (148.89) indicating the presence of partial dominance for an earliest parent for these crosses. On the other hand, the F_1 mean values were more than the late parents for the fourth cross (149.17) and fifth cross (149.94) indicating the presence of over dominance for the late parent.

As to the F_2, mean values were more than the late parent for all the studied

crosses except for the third one (148.95), indicating the presence of partial dominance for the late parent for these crosses.

With regards to both BC_1 and BC_2 mean values tended towards the mean of recurrent parent for all the studied crosses with some exceptions. This finding was also found by Abd El-Aty et al (2005), Hendawy et al (2009) and Sharshar (2015).

Table (4): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of days to maturity (day).

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	149.89	148.87	147.63	150.37	150.27	149.09
	S^2	0.10	0.12	0.24	5.37	3.85	3.95
	$S^2_{\bar{X}}$	0.002	0.003	0.01	0.02	0.05	0.05
2	$\bar{X}$	150.93	147.09	148.03	151.75	153.60	150.57
	S^2	0.06	0.08	0.09	7.33	5.14	5.92
	$S^2_{\bar{X}}$	0.001	0.002	0.002	0.02	0.07	0.08
3	$\bar{X}$	150.91	148.93	148.89	148.95	150.00	150.99
	S^2	0.08	0.09	0.10	4.87	3.30	3.09
	$S^2_{\bar{X}}$	0.002	0.001	0.003	0.02	0.04	0.04
4	$\bar{X}$	147.96	148.82	149.17	150.99	150.19	152.52
	S^2	0.04	0.08	0.15	5.18	2.86	4.14
	$S^2_{\bar{X}}$	0.001	0.003	0.004	0.02	0.04	0.06
5	$\bar{X}$	148.07	147.11	149.94	151.19	150.67	150.32
	S^2	0.06	0.10	0.29	6.87	5.33	5.41
	$S^2_{\bar{X}}$	0.001	0.002	0.01	0.02	0.07	0.07

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

4.1.1.3- Plant height (cm):

Concerning the plant height as shown in Table 5, the F_1 mean values for the second (112.17 cm), Fourth (114.29 cm) and fifth (122.09 cm) crosses, indicating over dominance role in inheritance this character for these crosses. Meanwhile, the F_1 mean values exceeded the mid values of the two parental mean for the first cross

(109.57 cm), indicating the presence of partial dominance for tallest parent for these crosses.

The obtained F_2 mean was lower than that of F_1 in most crosses, indicating the occurrence of inbreeding depression in F_2 generation. However, both BC_1 and BC_2 mean values tended toward the mean of recurrent parent for all the studied crosses with some exception. These results are in agreement with those of Abd El-Aty et al (2005) and Darwesh (2011).

Table (5): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of plant height (cm).

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	94.62	111.78	109.57	107.53	102.53	110.60
	S^2	0.65	4.04	3.49	40.72	23.90	31.05
	$S^2_{\bar{X}}$	0.01	0.09	0.10	0.14	0.32	0.41
2	$\bar{X}$	116.36	115.78	112.17	110.10	111.33	116.87
	S^2	1.33	2.22	17.97	155.01	121.85	135.66
	$S^2_{\bar{X}}$	0.03	0.05	0.51	0.52	1.62	1.81
3	$\bar{X}$	114.71	109.31	113.43	116.82	116.60	110.00
	S^2	0.44	0.72	8.61	389.58	273.76	364.19
	$S^2_{\bar{X}}$	0.01	0.02	0.25	1.30	3.65	4.86
4	$\bar{X}$	117.60	118.89	114.29	117.25	117.47	116.47
	S^2	5.65	1.01	6.09	62.06	51.60	30.93
	$S^2_{\bar{X}}$	0.13	0.02	0.17	0.21	0.69	0.41
5	$\bar{X}$	120.22	121.96	122.09	119.03	119.80	120.47
	S^2	1.09	1.00	8.26	196.05	144.89	137.28
	$S^2_{\bar{X}}$	0.02	0.02	0.24	0.65	1.93	1.83

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

4.1.1.4. Number of spikes per plant:

Data in Table 6 indicated that, the F_1 mean values for the first cross (27.49), second cross (27.26), third cross (24.86) and fourth cross (26.86) were

approximately equal to the mid-parent values, indicating the presence of non-additive components of genetic variance for this trait. Meanwhile, for the fifth cross (26.14) the F_1 mean value was lower than the mid-parent, indicating partial dominance for this cross.

Table (6): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of number of spikes/plant.

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	31.24	23.64	27.49	26.03	25.12	24.05
	S^2	1.28	1.10	7.32	104.36	82.43	76.78
	$S^2_{\bar{X}}$	0.03	0.02	0.21	0.35	1.10	1.02
2	$\bar{X}$	22.04	31.71	27.26	23.68	17.92	25.47
	S^2	0.91	1.07	4.84	120.10	67.45	84.50
	$S^2_{\bar{X}}$	0.02	0.02	0.14	0.40	0.90	1.13
3	$\bar{X}$	22.09	24.84	24.86	23.50	21.44	20.79
	S^2	1.72	1.41	5.42	65.29	53.76	49.60
	$S^2_{\bar{X}}$	0.04	0.03	0.15	0.22	0.72	0.66
4	$\bar{X}$	26.40	27.24	26.86	26.91	23.45	25.48
	S^2	1.43	1.37	1.83	106.78	99.98	78.98
	$S^2_{\bar{X}}$	0.03	0.03	0.05	0.36	1.33	1.05
5	$\bar{X}$	27.47	33.60	26.14	30.42	23.20	24.03
	S^2	1.25	1.70	3.54	100.06	69.68	82.76
	$S^2_{\bar{X}}$	0.03	0.04	0.10	0.33	0.93	1.10

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

The F_2, BC_1 and BC_2 mean values were less than the mid- parent for all the studied crosses except for F_2 in the fourth cross (26.91), indicating the presence of transgressive segregation in these generations. Similar trend was previously reported by Abd El-Aty et al (2005) and Hamam (2013).

4.1.1.5. Number of kernels per spike:

The data presented in Table 7 showed that, for number of kernels/spike the F_1 mean values exceeded the mid parents for the first cross (57.63) and second cross (67.29), indicating the presence of dominance towards the better parent. On the other hand, the F_1 mean values for the third (66.69), the fourth (59.71) and the fifth (65.43) crosses were lower than the mid-parent, indicating partial dominance played major role in inheritance this character for these crosses.

Table (7): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of number of kernels/spike.

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	46.24	62.76	57.63	64.58	49.59	59.61
	S^2	0.73	0.64	0.83	460.87	277.27	350.67
	$S^2_{\bar{X}}$	0.02	0.01	0.02	1.54	3.70	4.68
2	$\bar{X}$	43.60	68.40	67.29	63.94	62.19	65.61
	S^2	0.47	0.61	0.80	363.24	275.75	245.13
	$S^2_{\bar{X}}$	0.01	0.01	0.02	1.21	3.68	3.27
3	$\bar{X}$	74.07	68.29	66.69	63.86	69.35	66.81
	S^2	1.34	0.80	0.69	308.38	221.20	194.40
	$S^2_{\bar{X}}$	0.03	0.02	0.02	1.03	2.95	2.59
4	$\bar{X}$	66.58	68.98	59.71	57.02	69.35	65.12
	S^2	0.61	0.93	1.03	242.14	114.91	176.22
	$S^2_{\bar{X}}$	0.01	0.02	0.03	0.81	1.53	2.35
5	$\bar{X}$	70.69	72.33	65.43	57.21	56.33	54.63
	S^2	0.86	33.36	0.61	332.34	220.66	265.51
	$S^2_{\bar{X}}$	0.02	0.74	0.02	1.11	2.94	3.54

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

The obtained F_2 mean was lower than the F_1 in most crosses, indicating the occurrence of inbreeding depression in F_2 generation. However, both BC_1 and BC_2 mean values tended toward the mean of recurrent parent for all the studied crosses

with some exception. These results are in agreement with those of Abd El-Aty et al (2005) and Darwesh (2011).

4.1.1.6. 100-kernel weight (g)

Data in Table 8 showed that the F_1 mean values was heavier than the mid-parent for all the studied crosses, except for the third (3.28 g), indicating dominance towards the better parent, suggesting cross vigor for 100-kernel weight.

Table (8): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of 100-kernel weight (g).

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	2.73	3.54	3.95	3.63	3.31	3.73
	S^2	0.01	0.005	0.01	0.55	0.42	0.36
	$S^2_{\bar{X}}$	0.0002	0.0001	0.0002	0.002	0.01	0.005
2	$\bar{X}$	2.62	4.10	3.63	3.46	2.46	3.90
	S^2	0.005	0.02	0.002	0.43	0.34	0.31
	$S^2_{\bar{X}}$	0.0001	0.0004	0.0001	0.0014	0.0046	0.0041
3	$\bar{X}$	3.25	3.42	3.28	3.26	3.40	3.64
	S^2	0.01	0.001	0.01	0.85	0.58	0.52
	$S^2_{\bar{X}}$	0.0002	0.00003	0.0002	0.003	0.01	0.01
4	$\bar{X}$	3.74	3.55	4.05	3.75	3.93	4.15
	S^2	0.004	0.004	0.01	0.46	0.30	0.30
	$S^2_{\bar{X}}$	0.0001	0.0001	0.0003	0.002	0.004	0.004
5	$\bar{X}$	3.78	3.99	4.16	3.50	3.71	3.92
	S^2	0.003	0.005	0.004	0.49	0.33	0.34
	$S^2_{\bar{X}}$	0.0001	0.0001	0.0001	0.002	0.004	0.005

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

The F_2 mean was lower than that of F_1 in all studied crosses, indicating the occurrence of inbreeding depression in F_2 generation. However, both BC_1 and BC_2 mean values tended toward the mean of recurrent parent for all the studied crosses with some exception. These results are in agreement with those of Abd El-Aty et al

(2005), Darwish (2011) and Sharshar (2015).

4.1.1.7. Grain yield per plant (g):

The F_1 mean values exceeded the highest parents for the first cross (43.91 g), third cross (41.74 g) and fourth cross (35.39 g), indicating over dominance played major role in the inheritance for this trait. For remaining crosses the F_1 mean values were less than the mid parents, indicating the presence of dominance towards the lowest parent.

Table (9): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of grain yield/plant(g).

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	22.02	36.93	43.91	37.34	28.22	41.17
	S^2	3.20	1.25	15.90	343.74	257.26	367.62
	$S^2_{\bar{X}}$	0.07	0.03	0.45	1.15	3.43	4.90
2	$\bar{X}$	22.33	54.13	36.34	37.56	19.77	37.60
	S^2	0.98	3.57	19.11	457.14	365.77	416.06
	$S^2_{\bar{X}}$	0.02	0.08	0.55	1.52	4.88	5.55
3	$\bar{X}$	40.98	35.33	41.74	39.12	38.68	33.56
	S^2	1.66	1.45	3.96	591.16	552.91	393.50
	$S^2_{\bar{X}}$	0.04	0.03	0.11	1.97	7.37	5.25
4	$\bar{X}$	28.33	35.00	35.39	41.18	38.71	43.15
	S^2	2.41	4.57	12.14	447.20	291.41	359.06
	$S^2_{\bar{X}}$	0.05	0.10	0.35	1.49	3.89	4.79
5	$\bar{X}$	27.33	54.53	40.63	43.41	36.19	40.43
	S^2	1.91	2.03	19.30	486.58	363.20	402.82
	$S^2_{\bar{X}}$	0.04	0.05	0.55	1.62	4.84	5.37

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

Data in Table 9 showed that, the F_2 mean values were more than the mid-parent for all the studied crosses except for the second cross (37.56 g), indicating dominance towards the better parent.

Regarding, both BC_1 and BC_2 mean values varied according to the cross itself, it was tended towards the mean of recurrent parent for this trait with some

exceptions. These results are in close agreements with those of Tammam (2005) and Abd El-Aty et al (2005) .

4.1.2. Heterosis, Inbreeding depression and Potence ratio:

Heterosis percentage relative to mid and better parents, inbreeding depression and potence ratio for all the studied characters in the five crosses are presented in Tables 10-11.

4.1.2.1. Days to Heading (day):

Data in Table 10 showed highly significant negative heterosis (desirable) relative to mid parents for the first cross (Line 1 × Misr 1) and the fourth cross (Sakha 94 × Misr 1) for days to heading. On the other hand, all crosses except for the third one (Shandweel 1× Misr 1) showed highly significant negative heterosis (desirable) relative to better parents. These results are in harmony with those of Salgotra et al (2002), Abd-El Aty et al (2005) and El-Hawary (2010). They reported that significant negative heterosis effects over the mid parents and better parents in many cases for days to heading also, they reported significant positive heterosis over the mid and better parents in many cases.

Regarding to inbreeding depression percent for days to heading, data presented in Table 10 showed significant positive or negative inbreeding depression for all the studied crosses except for the fifth cross (Sakha 94 × Sakha 95). These results agreed with those obtained by Shehab El-deen (2008), Ragab (2010) and Darwesh (2011).

Concerning days to heading, values of potence ratio were less than unity either with positive or negative sign, indicating that partial dominance existed in the heredity of this trait. Meanwhile, the values were more than unity for first (Line1 × Misr1) and third (Shandweel 1 × Misr 1) with negative and positive sign respectively, indicating the presence of over dominance controlling the inheritance

of this trait. These results were in close agreement with those of Abd El-Aty and katta (2002), Abd El-Aty et al (2005). While, Darwesh (2011) obtained over dominance for this trait.

Table (10):Heterosis, potence ratio and inbreeding depression for days to heading, days to maturity and plant height in the five studied crosses.

Traits	Crosses	Heterosis MP%	Heterosis BP%	Potence ratio	Inbreeding depression %
Days to heading (day)	1	-1.76**	-2.75**	-1.72	-9.66**
	2	0.99**	-1.64**	0.37	-0.79**
	3	3.4**	1.78**	2.14	2.58**
	4	-0.59**	-3.38**	-0.21	-3.74**
	5	0.01	-0.93**	0.01	0.12
Days to maturity (day)	1	-1.17**	-1.51**	-3.42	-1.86**
	2	-0.66**	-1.92**	-0.51	-2.52**
	3	-0.69**	-1.34**	-1.05	-0.04
	4	0.53**	0.23**	-1.81	-1.22**
	5	1.59**	1.27**	4.93	-0.83**
Plant height (cm)	1	6.17**	-1.97**	0.74	1.86**
	2	-3.36**	-3.6**	-13.48	1.85
	3	1.27**	-1.12*	0.52	-2.99*
	4	-3.35**	-3.87**	-6.14	-2.59**
	5	0.82	0.11	1.15	2.5**

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

4.1.2.2. Days to maturity (day):

Data in Table 10, showed highly significant negative heterosis percent, relative to mid-parent and better parent for the first cross (Line 1 × Misr 1), second (Line 2 × Sakha 95) and the third cross (Shandweel 1 × Misr 1), while the other

crosses exhibited highly significant positive heterosis percentage over mid-parent and better parent. These results agreed with those of Hamada (2003), Abd El-Aty et al (2005), Hendawy and Seleem (2007) they obtained significant heterosis values for Days to maturity.

With regard to the inbreeding depression percent, highly significant negative values were detected for all studied crosses except for the third one.

The potence ratio, indicated that the over dominance towards earliness for days to maturity in the first cross (Line 1 × Misr 1), third cross (Shandweel 1 × Misr 1) and fourth cross (Sakha 94 × Misr 1), while over dominance towards lateness detected for the fifth cross (Sakha 94 × Sakha 95). On the other hand, for the second cross (Line 2 × Sakha 95) the value of potence ratio was less than unity with negative sign, indicating that partial dominance existed in the heredity of this trait in this cross.

4.1.2.3. Plant height (cm):

Heterotic effect values over mid-parent were highly significant and positive in first (Line 1 × Misr 1) and third (Shandweel 1 × Misr 1) crosses. While, highly significant and negative values were obtained from second (Line 2 × Sakha 95) and fourth (Sakha 94 × Misr 1) crosses (Table 10). Over better parent, all crosses showed highly significant and negative values except for the fifth on showed insignificant and postive value. These results agreed with those obtained by Shehab El-Deen (2008), Aboshosha and Hammad (2009) and Sharshar (2015) they found significant positive and negative heterotic effects for plant height.

With respect to inbreeding depression, highly significant positive or negative values were detected for all the studied crosses except for the second cross (Line 2 × Sakha 95) which had positive and non-significant value. Abd El-Aty et al (2005).

Potence ratio values were exceeding unity in third (Shandweel 1 × Misr 1), fourth (Sakha 94 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses indicating over dominance in these cases. While, potence ratio values were less than unity in the remain crosses indicating partial dominance in this case. The same results were obtained by Menon and Sharma (1995), Darwish and Ashoush (2003) and Aglan (2003) who reported over and partial dominance in this cases.

4.1.2.4. Number of spikes per plant:

Highly significant positive heterosis percent, relative to mid-parent for the second (Line 2 × Sakha 95) and third (Shandweel 1× Misr 1) crosses for number of spike/plant (Table 11), while the fifth one (Sakha 94 × Sakha 95) exhibited highly significant negative heterosis percentage over mid-parent. On the other hand, highly significant and negatively heterotic effects over better parents were obtained for all crosses except for the third one (Shandweel 1 × Misr 1). These results agreed with those of Hamada (2003), Abd El-Aty et al (2005) and Hendawy and Seleem (2007) they obtained significant heterotic values for number of spikes/ plant.

With respect to the inbreeding depression percent, highly significant positive values were detected for the first (Line 1 × Misr1), second (Line 2 × Sakha 95) and third (Shandweel 1 × Misr 1) crosses. Meanwhile, the fifth cross (Sakha 94 × Sakha 95) had negative and high significant value for inbreeding depression **(**Table 11). Similar trend with those obtained by, Abd El-Aty and Katta (2002), Darwish (2011) and Koumber and El-Gammaal (2012), while El-Hawary (2010) obtained positive and significant values of inbreeding depression for this character. Significant effects for both heterosis and inbreeding depression were associated in cross 2 (Line 2 × Sakha 95) and cross 3 (Shandweel 1 × Misr 1) . In this case, the expression of heterosis in F_1 was followed by considerable reduction in F_2

performance and indicating the importance role of over dominance inheritance of this trait in this cross.

Potence ratio values were exceeding unity in third cross (Shandweel 1 × Misr 1) and fifth cross (Sakha 94 × Sakha 95) indicating over dominance in this case. While, potence ratio values were less than unity in the remaining crosses indicating partial dominance in this cases. Over dominance were reported by Darwish and Ashoush (2003).

4.1.2.5. Number of kernels per spike:

With regard to number of kernels/spike (Table 11), all crosses expressed highly significant negative heterotic effects relative to mid-parent and the better parent, except the first cross (Line 1 × Misr 1) and the second cross (Line 2 × Sakha 95) for mid-parent which had highly significant postive heterotic effect. These results agreed with those recorded by Zaazaa, et al. (2012), Koumber and El-Gammaal (2012) and Sharshar (2015).

Inbreeding depression percent values were highly significant and positive in all crosses except the first one (Line 1 × Misr 1) which had negative and high significant value.

Potence ratio values were exceeding unity in all crosses except cross 1 (Line 1× Misr 1) and cross 2 (Line 2 × Sakha 95) indicating over dominance and partial dominance, respectively.

4.1.2.6. 100-kernel weight (g):

Highly significant positive heterosis relative to mid-parent and the better parent were detected for all the studied crosses, except for the third cross (Shandweel 1 × Misr 1) which had highly significant negative heterotic effects relative to the mid-parent and the better parent, and the second cross (Line 2 ×

Sakha 95) relative to better parent (Table 11). These results agreed with those obtained by Abd El-Aty et al (2005), Koumber and El-Gammaal (2012) and Hamam (2013) obtained significant and positive heterosis respecting for this character.

Table (11):Heterosis, potence ratio and inbreeding depression for number of spikes/plant, number of kernels /spike, 100-kernel weight and grain yield/plant in the five studied crosses.

Traits	Crosses	Heterosis MP%	Heterosis BP%	Potence ratio	Inbreeding depression %
Number of spikes/plant	1	0.15	-12.03**	0.01	5.3**
	2	1.41**	-14.05**	0.08	13.11**
	3	5.93**	0.05	1.01	5.45**
	4	0.13	-1.42**	0.08	-0.2
	5	-14.38**	-22.19**	-1.43	-16.35**
Number of kernels /spike	1	5.74**	-8.17**	0.38	-12.07**
	2	20.15**	-1.63**	0.91	4.98**
	3	-6.31**	-9.97**	-1.55	4.24**
	4	-11.9**	-13.43**	-6.72	4.52**
	5	-8.51**	-9.55**	-7.4	12.56**
100-kernel weight	1	25.89**	11.48**	2	8.05**
	2	8.15**	-11.43**	0.37	4.86**
	3	-1.48**	-3.89**	-0.59	-0.07
	4	11.1**	8.2**	4.14	7.49**
	5	7.22**	4.46**	2.73	15.95**
Grain yield/plant (g)	1	48.97**	18.9**	-1.94	14.96**
	2	-4.56**	-32.86**	-0.11	-3.34*
	3	9.4**	1.87**	1.27	6.28**
	4	10.86**	-0.35	0.97	-16.36**
	5	-0.74	-25.5**	-0.02	-6.84**

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

Inbreeding depression percent values were highly significant and positive in all crosses except the third cross (Shandweel 1 × Misr 1) was insignificant with negative sign.

Potence ratio values were less than unity in the second cross (Line 2 × Sakha 95) and third cross (Shandweel 1 × Misr 1) indicating partial dominance in these crosses. While, potence ratio values were more than unity for the others indicating over dominance for these cases.

4.1.2.7. Grain yield per plant (gm):

Highly significant positive heterosis relative to mid-parent and the better parent were detected for the first cross (Line 1 × Misr 1) and the third cross (Shandweel 1 × Misr 1) also, for the fourth cross (Sakha 94 × Misr 1) which had highly significant positive heterotic effects relative to the mid-parent. Meanwhile, heterosis relative to mid-parent and the better parent were negative and high significant or insignificant for the other crosses. These results agreement with those obtained by Abd El-Aty and Katta (2002), Abd El-Aty et al (2005), Abd-El-Nour and Mosherf (2006), Shehab El-Deen (2008), Khattab (2009), Darwesh (2011), Hamam (2013) and Sharshar (2015) they obtained positive and/or negative significant heterosis respecting this trait.

Regarding to inbreeding depression percent for Grain yield per plant, data presented in Table 11 showed significant or/and high significant positive or negative inbreeding depression for all the studied crosses.

Potence ratio values were less than unity in all crosses except for the first (Line 1× Misr 1) and third (Shandweel 1× Misr 1) crosses, indicating partial and over dominance, respectively.

4.1.3. Estimation of type of gene Action:

4.1.3.1- Scalling Test:

The scale tests of the studied traits for all the studied crosses are presented in Table 12. Generation mean analysis belong to quantitative biometrical methods based on measurements of phenotypic performance of certain quantitative traits on-as many as-possible plant individuals in basic experimental breeding generations (parental, filial, back crosses and first segregating generation). As it was outlined by Kearsey and Pooni (1996), generation mean analysis is a useful technique in plant breeding for estimating gene effects (additive and dominance) and their digenic: additive × additive, additive × dominance, dominance × dominance interactions responsible for inheritance of quantitative traits. It helps us in understanding the performance of the parents used in crosses and potential of crosses to be used either for heterosis exploitation or pedigree selection Sharma and Sain (2003).

To test the presence or absence of non-allelic interactions, scaling test was used. The significance of A and B scales indicate the presence of all types of non-allelic interactions. The significance of C scale suggests (aa) and (dd) types of epistasis Singh and Narayanan (1993). However, the significance of at least one of the scales indicates the presence of non-allelic interaction which could be estimated by six parameters model as Gamble procedure, while the insignificant of all scales, indicates the absence of non-allelic interaction and hence, a simple additive-dominance model would be adequate for estimating the genetical components of variance.

Table (12): Scaling test parameters A , B and C for days to heading, days to maturity, plant height, number of spikes/plant, number. of kernels/spike, 100-kernel weight(g) and grain yield / plant(g) in the five studied crosses.

Traits	Crosses	Scaling test		
		A	B	C
Days to heading (day)	1	15.95**	17.74**	31.85**
	2	6.47**	-2.57**	5.29**
	3	2.11	6.04**	-3.86**
	4	4.64**	4.93**	13.93**
	5	2.9**	1.23	-0.48
Days to maturity (day)	1	3.02**	1.69**	7.48**
	2	8.24**	6.03**	12.93**
	3	0.2	4.15**	-1.83**
	4	3.25**	7.05**	8.85**
	5	3.32**	3.59**	9.68**
Plant height (cm)	1	0.87	-0.15	4.59**
	2	-5.86*	5.78*	-16.08**
	3	5.06	-2.74	16.39**
	4	3.05	-0.24	3.94
	5	-2.71	-3.11	-10.22**
Number of spikes/plant	1	-8.49**	-3.02	-5.74*
	2	-13.46**	-8.03**	-13.54**
	3	-4.07*	-8.13**	-2.63
	4	-6.35**	-3.14	0.28
	5	-7.21**	-11.69**	8.31**
Number of kernels /spike	1	-4.7	-1.16	34.08**
	2	13.49**	-4.46	9.18*
	3	-2.06	-1.35	-20.3**
	4	12.4**	1.55	-26.92**
	5	-23.45**	-28.51**	-45.03**
100-kernel weight	1	-0.07	-0.04	0.35*
	2	-1.33**	0.07	-0.16
	3	0.27	0.58**	-0.09
	4	0.05	0.7**	-0.4*
	5	-0.53**	-0.31*	-2.1**
Grain yield/plant (g)	1	-9.49*	1.48	2.59
	2	-18.82**	-15.27**	1.39
	3	-5.37	-9.96*	-3.32
	4	13.7**	15.4**	30.1**
	5	4.41	-14.3**	10.51*

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

The results revealed the presence of non-allelic interaction for all the studied characters in all the studied crosses, except in the fourth one (Sakha 94 × Misr 1) for plant height. It is worth to mention that, at least one of the A, B and C scales was significant for the previous characters, indicating the adequacy of the six parameter model to explain the type of gene action controlling the traits in these crosses. However, for the excepted cases, the simple additive-dominance model would be adequate. These results agreement with Abd El-Aty et al (2005), Aboshosha and Hammad (2009) and Hassan et al (2013).

4.1.3.2.Type of gene action:

The effective breeding program is dependent upon the relative amount and type of genetical variability available in the breeder's materials. If the estimates of the genetical variance and its components, indicated that additive genetic variance is major importance in the population, selection will be the most effective procedure. If the non-additive genetic variability is the major component of genetic variance, inbred-hybrid program may be the appropriate choice (Cockerhan, 1961). Therefore, studies of types of gene action in the materials used in this investigation were taking into consideration.

Genetical analysis of generation means to give estimates of the six parameters model i.e. (m), (a), (d), (aa), (ad) and (dd) which were calculated according to relationships illustrated by Gamble (1962). Type of gene action for all the studied traits in five studied crosses are shown in Table 13.

The estimated mean effects (m), which reflect the contribution due to overall mean plus the locus effects and interaction of the fixed loci was found to be highly significant for all the studied characters in all crosses, indicted that these characters were quantitatively inherited. These results are in harmony with those of Hendawy (1998), Afiah (1999), El-Hosary et al. (2000), Shehab El-Deen (2008) and

Sharshar (2015).

From the obtained results (Table 13), the estimates of additive (a) effects which significant or highly significant with positive signs were obtained for; days to heading in the second (Line 2 × Sakha 95), fourth (Sakha 94 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, days to maturity in the first cross (Line 1 × Misr 1) and the second cross (Line 2 × Sakha 95), plant height in the third cross (Shandweel 1 × Misr 1), 100- kernel weight in the fourth cross (Sakha 94 × Misr 1). Meanwhile, it was negatively significant or highly significant for; days to heading in the first cross (Line 1 × Misr 1), days to maturity in the third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses, plant height in the first (Line 1 × Misr 1) and second (Line 2 × Sakha 95), number of spikes/plant in the second cross (Line 2 × Sakha 95), number of kernels/spike in the first cross (line 1× Misr 1), grain yield/plant in first (Line 1× Misr 1) and second (Line 2 × Sakha 95) crosses as well as for all crosses in 100-kernel weight. These results indicate the importance of additive gene effects in the inheritance and play the major role in controlling the genetical variation of these characters.

The estimates of (d) effects were positively significant or highly significant for; days to heading in third (Shandweel 1 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, days to maturity in third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses, plant height in the second one (Line 2 × Sakha 95), number of kernels/spike in third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses as well as for 100-kernel weight in the third (Shandweel 1 × Misr 1), fourth (Sakha 94 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses. On the other hand, it was negatively significant or highly significant for; days to heading and days to maturity in the first cross (Line 1 × Misr 1), number of spikes/plant in all crosses except for the first one (Line 1 × Misr 1), number of kernels/spike in first (Line 1 ×

Table (13): Type of gene action for days to heading, days to maturity, plant height, number of spikes/plant, number. of kernels/spike, 100-kernel weight(g) and grain yield / plant(g) in the five studied crosses.

Traits	Crosses	Type of gene action					
		(m)	(a)	(d)	(aa)	(ad)	(dd)
Days to heading (day)	1	99.6**	-1.84**	0.23	1.85	-0.9	-35.55**
	2	103.99**	7.25**	-0.37	-1.39	4.52**	-2.52
	3	100.26**	-0.39	15.38**	12**	-1.96*	-20.14**
	4	104.87**	2.79**	-4.96**	-4.36**	-0.15	-5.21*
	5	103.99**	1.83**	4.63**	4.61**	0.84	-8.74**
Days to maturity (day)	1	150.37**	1.17**	-4.52**	-2.77**	0.66*	-1.93
	2	151.75**	3.03**	0.35	1.33	1.1**	-15.6**
	3	148.95**	-0.99**	5.15**	6.19**	-1.98**	-10.54**
	4	150.99**	-2.33**	2.22**	1.44	-1.9**	-11.73**
	5	151.19**	0.35	-0.42	-2.77**	-0.13	-4.14*
Plant height (cm)	1	107.53**	-8.07**	2.5	-3.87	0.51	3.14
	2	110.1**	-5.53**	12.1*	16**	-5.82**	-15.92*
	3	116.82**	6.6*	-12.65	-14.07	3.9	11.75
	4	.....	.....	.....	.....	.....	.....
	5	119.03**	-0.67	5.4	4.4	0.2	1.42
Number of spikes/plant	1	26.03**	1.07	-5.73	-5.77	-2.73	17.29**
	2	23.68**	-7.55**	-7.58*	-7.96*	-2.71	29.46**
	3	23.5**	0.65	-8.17**	-9.56**	2.03	21.75**
	4	26.91**	-2.03	-9.74*	-9.77*	-1.6	19.27**
	5	30.42**	-0.83	-31.6**	-27.21**	2.24	46.11**
Number of kernels /spike	1	64.58**	-10.03**	-36.8**	-39.93**	-1.77	45.79**
	2	63.94**	-3.43	11.14	-0.15	8.97**	-8.88
	3	63.86**	2.53	12.4*	16.89**	-0.36	-13.49
	4	57.02**	4.23*	32.8**	40.87**	5.43**	-54.82**
	5	57.21**	1.71	-13.02*	-6.93	2.53	58.89**
100-kernel weight	1	3.63**	-0.42**	0.34	-0.47	-0.01	0.58
	2	3.46**	-1.44**	-0.83**	-1.1**	-0.7**	2.36**
	3	3.29**	-0.24*	0.89**	0.94**	-0.16	-1.79**
	4	3.75**	-0.23*	1.57**	1.16**	-0.32**	-1.92**
	5	3.5**	-0.21*	1.55**	1.27**	-0.11	-0.44
Grain yield/plant (g)	1	37.34**	-12.94**	3.84	-10.6	-5.49	18.61
	2	37.56**	-17.83**	-37.22**	-35.48**	-1.77	69.57**
	3	39.12**	5.12	-8.42	-12.01	2.3	27.34
	4	41.18**	-4.44	2.48	-0.99	-0.85	-28.12*
	5	43.41**	-4.25	-20.7*	-20.39*	9.35**	30.27*

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, 100-kernel weight in the second one (Line 2 × Sakha 95), grain yield/plant in second (Line 2 × Sakha 95) and fifth (Sakha 94 × Sakha 95) crosses.

In some cases ,where the absence of significant (d) component imply no dominance genetic differences between the two parents and the dominant effects seems to be not important in the genetical control of these cases.

However, in quantitative inherited traits, gene action described as additive, dominance and epistatic effects. Additive effect is defined as the average effect of genes; dominance as the interaction of allelic genes and epistasis as interaction of non-allelic genes that influence particular trait.

Snape (1987), pointed out that a very common situation, when analyzing yield and yield components, is to find that the additive effect is slight and non-significant, while the dominance estimate is large and highly significant. Estimates of slight additive effects are possible due to high degree of dispersion of increasing alleles between parents. Similarity, dominance could be small due to its ambidirectional nature. This might explain why additive genetic component of variance varied to a great extent. On the other hand, negative and non-significant estimates of dominance variance could be due to micro-environmental variation, sampling errors and/or the fact that basic generations are inefficient for determining dominance variance.

For non-allelic interactions *i.e.*, additive × additive (aa), additive × dominance (ad) and dominance × dominance (dd), the data showen in Table 13, indicated that positively significant or highly significant additive × additive effects (aa) were detected for; days to heading in the third (Shandweel 1 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, days to maturity in the third one (Shandweel 1 × Misr 1), plant height in the second one (Line 2 × Sakha 95), number of kernels/spike in the

third (Shandweel 1 × Misr 1) and the fourth (Sakha 94 × Misr 1) crosses, 100-kernel weight in the third (Shandweel 1 × Misr 1), the fourth (Sakha 94 × Misr 1) and the fifth (Sakha 94 × Sakha 95) crosses. Meanwhile, negatively significant or highly significant additive × additive type of gene action was found for; days to heading in the fourth cross (Sakha 94 × Misr 1), days to maturity in first (Line 1× Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, number of spikes / plant in all studied crosses except for the first one (Line 1× Misr 1), number of kernels / spike in the first cross (Line 1× Misr 1), 100-kernel weight in the second cross (Line 2 × Sakha 95), grain yield / plant in second (Line 2 × Sakha 95) and fifth (Sakha 94 × Sakha 95) crosses. For the excepted traits in certain crosses, where (aa) epistatice gene action was more important and higher in magnitude those of (dd) ones, the isolation of superior recombinations from segregating generations in these crosses would be enhanced.

In addition, positively significant or highly significant additive × dominance effected (ad) were found for; days to maturity in the second cross (Line 2 × Sakha 95), days to maturity in first (Line 1× Misr 1) and second (Line 2 × Sakha 95) crosses, number of kernels / spike in the second (Line 2 × Sakha 95) and fourth (Sakha 94 × Misr 1) crosses as well as for grain yield / plant in the fifth one (Sakha 94 × Sakha 95). On the other hand, negatively Significant or highly significant additive × dominance types of epistasis were found for; days to heading in the third cross (Shandweel 1 × Misr 1), days to maturity in third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses, plant height in the second cross (Line 2 × Sakha 95), 100-kernel weight in second (Line 2 × Sakha 95) and fourth (Sakha 94 × Misr 1) crosses as well as grain yield / plant in the fifth one (Sakha 94 × Sakha 95). Ramalingam and Sivasamy (2002) demonstrated that the preponderance of (aa) epistatic effect when higher in magnitude for any trait, this might suggesting

delayed selection and inter-mating the segregates, followed by pedigree selection for improvement of these traits in these crosses. While, the negative sign of (ad) interaction for some traits in some crosses may be suggested dispersion of genes in the parents.

The dominance × dominance types of effects (dd) were positively significant or highly significantly for; number of kernels/spike in the first (Line 1 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, 100-kernel weight in the second cross (Line 2 × Sakha 95) as well as for grain yield/plant in second (Line 2 × Sakha 95) and fifth (Sakha 94 × Sakha 95) crosses. Moreover, it was highly significantly and positive for number of spikes/plant. Meanwhile, negatively significant or highly significant dominance × dominance types of epistasis were found for; days to heading in all studied crosses except for the second one (Line 2 × Sakha 95), days to maturity in all studied crosses except for the first one (Line 1 × Misr 1), plant height in the second one (Line 2 × Sakha 95), number of kernels / spike as well as grain yield/plant in the fourth cross (Sakha 94 × Misr 1), 100-kernel weight in third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses. In some cases, (dd) epistatic effect was more important and higher in magnitude than (aa) epistatic effects in the inheritance of these traits in these crosses. This might indicate that the selection would be fruitful if delayed till dominance and their epstatic effects reduce to the minimum and resulted the slow down of the selection. Similar rustles which recorded the presence of the additive, dominance and the epistasis (additive × additive, additive × dominance and dominance × dominance) were reported by Aglan (2003) and Sharshar (2015).

However, when epistatic effects were significant for a trait, the possibility of obtaining desirable segregates through inter-mating in early segregations by breaking undesirable linkage could be available or it is suggested to adopt

recurrent selection for handling the above crosses for rapid improvement. These results are in agreement with those of Monir et al.(2007), Khattab et al.,(2010) and Aykuttonk et al.,(2011).

4.1.4. Heritability estimates and predicted genetic advance from selection:

The most important function of the heritability in genetical study of quantitative characters is as its play a predictive role. It express the reliability of the phenotypic value as a guide to the breeding value. The possible advance through selection based on phenotypic value can, therefore, be predicted only from knowledge of the degree of correspondence between phenotypic value and breeding value. The degree of correspondence is measured by heritability estimates. Heritability estimates in both broad and narrow senses and expected genetic advance from selection for agronomic traits are represented in Tables 14-15.

4.1.4.1.Days to heading:

High estimates of heritability in broad sense were detected in all crosses (Table 14). It ranged from 97.45 % for the third cross (Shandweel 1 × Misr 1) to 99.54% for the fifth cross (Sakha 94 × Sakha 95). This results indicating that genotypic variances played the major part of phenotypic variances. Similar results were obtained by Senapati et al., (1994), Salama (2002) and Said (2003) who found high values of broad sense heritability ranged from 80 to 92%.

Narrow sense heritability values were moderate for all crosses, indicating that additive genetic variances played the major part of genotypic variances and goodness of selection for this trait in early generation. The same results were obtained by Al-Kadoussi (1996) who found moderate values of narrow sense heritabilty 50%. On the other hand, Shehab El- Din (1997) obtained intermediate

to low narrow sense heritability valves.

The estimates of the genetic advance from selection as percent of F_2 mean (Δg%) ranged from 3.10% for the fourth cross (Sakha 94 × Misr 1) to 4.49% for the first cross (Line 1 × Misr 1).

Table (14): Estimates of variance, heritability percentage in broad (H^2) and narrow (h^2) senses and expected (Δg) genetic advance from selection in five bread wheat crosses.

Traits	Crosses	V(1/2D)	V(1/4H)	VE	Heritability		Genetic advance	
					H%	h^2%	Δg	Δg %
Days to heading (day)	1	98.87**	8.26**	0.2	98.87	51.78	4.47	4.49
	2	99.14**	9.87**	0.16	99.14	46.43	4.14	3.98
	3	97.45**	16.65**	0.68	97.45	35.16	3.74	3.73
	4	99.07**	9.38**	0.15	99.07	39.73	3.25	3.1
	5	99.54**	13.29**	0.1	99.54	36.97	3.51	3.38
Days to maturity (day)	1	96.74**	2.26*	0.17	96.74	54.66	2.61	1.73
	2	98.9**	3.65**	0.08	98.9	49.14	2.74	1.81
	3	98.18**	1.44	0.09	98.18	68.66	3.12	2.1
	4	97.66**	1.7	0.12	97.66	64.94	3.05	2.02
	5	97.28**	3.69**	0.19	97.28	43.58	2.35	1.56
Plant height (cm)	1	92.84**	11.32**	2.92	92.84	65.04	8.55	7.95
	2	93.63**	92.63**	9.87	93.63	33.88	8.69	7.89
	3	98.82**	243.77**	4.59	98.82	36.25	14.74	12.62
	4	92.41**	15.76**	4.71	92.41	67.02	10.88	9.28
	5	97.63**	81.47**	4.65	97.63	56.07	16.17	13.59

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

4.1.4.2.Days to maturity:

Data presented in Table 14 showed that, high values of broad sense heritability were detected and ranged from 96.74% for the first cross (Line 1 × Misr 1) to 98.90% for the second cross (Line 2 × Sakha 95). Similar results were obtained by Hamada (2003) and Said (2003) reported high broad sense heritability with values ranged from 89% to 90%.

With respect to heritability in narrow sense, the values were moderate to high

with values ranged from 43.58% for the fifth cross (Sakha 94 × Sakha 95) to 68.66% for the third cross (Shandweel 1 × Misr 1).

The estimates of genetic advance from selection as percent of F_2 mean (Δg%) ranged from 1.56% for the fifth cross (Sakha 94 × Sakha 95) to 2.10% for the third cross (Shandweel 1 × Misr 1).

4.1.4.3.Plant height:

High values of broad sense heritability were detected in all crosses with values ranged from 92.41% for the fourth cross (Sakha 94 × Misr 1) to 98.82% for the third cross (Shandweel 1 × Misr 1) Table 14. Similar results were obtained by Liu and Ma (1994) and Ozkan et al.,(1997) who reported high broad sense heritability with values ranged from 76% to 90% for this trait. Also, many investigators such as Shehab El-Din (1997), Salama (2002) and Said (2003) obtained high broad sense heritability for this trait.

Narrow sense heritability values were moderate to high with values varied from 33.88 % for the second cross (Line 2 × Sakha 95) to 67.02 % for the fourth cross (Sakha 94 × Misr 1). Similar resultes were obtained by Al-Kadoussi (1996), Awaad (2002) and Shehab El Din (1997) who reported that narrow sense heritability was more than 50%. On the other hand, high values of narrow sense heritability were reported by said (2003).

The estimates of genetic advance from selection as percent of F_2 (Δg%) ranged from 7.89 for the second cross (Line 2 × Sakha 95) to 13.59% for the fifth cross (Sakha 94 × Sakha 95).

4.1.4.4.Number of spike per plant:

Concerning broad sense heritability Table 15, values were high with values ranged from 94.65% for the third cross (Shandweel 1 × Misr 1) to 98.49% for the

fourth cross (Sakha 94 × Misr 1). Similar results were obtained by Hamada (2003) reported high broad sense heritability estimate with values ranged from 72% to 88%.

Narrow sense heritability estimates varied from moderate to high with values ranged 32.40% for the second cross (Line 2 × Sakha 95) to 73.49% for the fourth cross (Sakha 94 × Misr 1). The same results were obtained by Salem et al., (2000), Hamada (2003) and Said (2003) who reported low narrow sense heritability with values ranged from 15% to 69%. On the other hand , high values of narrow sense heritability were reported by Al-Kadossi (1990).

Table (15): Estimates of variance, heritability percentage in broad (H^2) and narrow (h^2) senses and expected (Δg) genetic advance from selection in five bread wheat crosses.

Traits	Crosses	V(1/2D)	V(1/4H)	VE	Heritability		Genetic advance	
					H%	h^2%	Δg	Δg %
Number of spikes/plant	1	95.93**	50.6**	4.25	95.93	47.44	9.98	38.36
	2	97.57**	28.93**	2.92	97.57	73.49	16.59	70.05
	3	94.65**	34.58**	3.49	94.65	41.69	6.94	29.53
	4	98.49**	70.57**	1.62	98.49	32.40	6.90	25.63
	5	97.49**	49.86**	2.51	97.49	47.66	9.82	32.29
Number of kernels /spike	1	99.84**	166.31**	0.76	99.84	63.75	28.19	43.65
	2	99.82**	156.97**	0.67	99.82	56.6	22.22	34.76
	3	99.71**	106.34**	0.88	99.71	65.23	23.6	36.96
	4	99.63**	48.08**	0.9	99.63	79.77	25.57	44.85
	5	97.33**	144.97**	8.86	97.33	53.71	20.17	35.26
100-kernel weight	1	98.95**	0.22	0.01	98.95	58.11	0.89	24.44
	2	98.5**	0.21	0.01	98.5	48.72	0.66	19.03
	3	99.32**	0.24	0.01	99.32	70.94	1.35	41.05
	4	98.47**	0.14	0.01	98.47	68.66	0.96	25.53
	5	99.18**	0.17	0	99.18	63.6	0.92	26.23
Grain yield/plant (g)	1	97.36**	272.08**	9.06	97.36	18.21	6.96	18.62
	2	97.66**	314**	10.69	97.66	28.97	12.76	33.98
	3	99.53**	352.49**	2.76	99.53	39.91	19.99	51.09
	4	98.25**	195.45**	7.82	98.25	54.55	23.76	57.70
	5	97.81**	268.81**	10.63	97.81	42.57	19.34	44.56

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

The expected genetic advance from selection as percent of F2 mean (Δg%) ranged from 25.63% for the fourth cross (Sakha 94 × Misr 1) to 70.05% for the second cross (Line 2 × Sakha 95). Ghimiray and Sarker (2000) recorded high values of expected genetic advance from selection for this trait.

4.1.4.5.Number of kernels per spike:

With respect to broad sense heritability Table 15, values were high with values varied from 97.33 % for the fifth cross (Sakha 94 × Sakha 95) to 99.84 % for the first cross (Line 1 × Misr 1) indicating genetic variance played the major portion from phenotypic variance. The same results were obtained by Hamada (2003) and Said (2003) who reported high broad sense heritability for this trait. On the other hand, Liu and Ma (1994) recorded low broad sense heritability with value 70% for this trait.

Narrow sense heritability values were moderate to high with values ranged from 53.71% for the fifth cross (Sakha 94 × Sakha 95) to 79.77% for the fourth cross (Sakha 94 × Misr 1) indicating the main portion of genetic variance due to additive variance. The same findings were obtained by many authers i.e., Al-Kadoussi (1996) reported that, narrow sense heritabilty values were more than 50%, Salama (2002) obtained moderate narrow sense heritability with values ranged from 24% to 40%. On the other hand Said (2003) reported that narrow sense heritability was high for this trait.

The expected genetic advance from selection as percent of F_2 mean (Δg%) ranged from 34.76% for the second cross (Line 2 × Sakha 95) to 44.85% for the fourth cross (Sakha 94 × Misr 1).

4.1.4.6.100-Kernel weight:

Regarding the broad sense heritability Table 15, values were high with values

ranged from 98.47% for the fourth cross (Sakha 94 × Misr 1) to 99.32% for the third cross (Shandweel 1 × Misr 1). Similar findings were obtained by Hamada (2003) and Said (2003) who reported high broad sense heritability with vales ranged from 69% to 92%.

Narrow sense heritability values were high to moderate with values varied from 48.72% for the second cross (Line 2 × Sakha 95) to 70.94% for the third cross (Shandweel 1 × Misr 1). The same results were obtained by Said (2003) who reported high narrow sense heritability for this trait.

The expected genetic advance from selection as a percent of F_2 mean (Δg%) values were high in all cross with values ranged from 19.03% for the second cross (Line 2 × Sakha 95) to 41.05% for the third cross (Shandweel 1 × Misr 1).

4.1.4.7.Grain yield per plant:

The data presented in Table 15 indicated that, heritability in broad sense values were high in all crosses with values ranged from 97.36% for the first cross (Line 1 × Misr 1) to 99.53% for the third cross (Shandweel 1 × Misr 1). The same results were obtained by Ozkan et al., (1997), Hamada (2003) and Said (2003) who reported high broad sense heritability.

Narrow sense heritability values were low to moderate with values ranged from 18.21% for the first cross (Line 1 × Misr 1) to 54.55% for the fourth cross (Sakha 94 × Misr 1). Similar results were obtained by Awaad (2002), Hamada (2003) and said (2003) who reported moderate narrow sense heritability (46% - 53%) to low (8%- 32%) for this trait.

The expected genetic advance from selection as percent of F_2 mean (Δg%) ranged from 18.62% for the first cross (Line 1 × Misr 1) to 57.70 for the fourth cross (Sakha 94 × Misr 1). Said (2003) obtained high values of (Δg%) for this trait.

The highest values of predicted genetic advance were coupled with high and moderate narrow-sense heritability values in the same crosses and for the same traits referred before under study. This may concede with a conclusion of Johnson et al., (1955) who reported that heritability estimates along with genetic advance upon selection were more valuable in predicting selection in early generation and obtain high yielding genotypes. Therefore, selection in these particular populations should be effective and satisfactory for successful breeding purposes.

As it is well known, expected improvement *via* selection is directly proportional to heritability. This figure is a measure of low total variability in these traits and therefore, the low of total response that could be realized by breeding techniques.

Low expected (Δg) and predicted (Δg %) genetic advance estimates were found to be associated with low narrow-sense heritability values in the same crosses and the same traits mentioned before as shown in Tables 14-15. However, this is an expected and logic results, where the expected genetic advance equation depended mainly of value of narrow-sense heritability estimate. However, these traits in these crosses may be more control in their inheritance by non-additive gene effects which confirmed the previous results in this study related to the gene action. So, these traits could be improved by acting the selection in the late segregating generations of wheat breeding under study. However, these information are of importance for wheat breeders to improve earliness and yield potential, release new wheat genotypes and enhancement of Egyptian wheat germplasm. This may coincide with a conclusion of El-Refaey et al. (2015) who indicated that heritability in narrow-sense and genetic advance were low in most cases due to the opposite directions of dominance and dominance × dominance effects resulted in lower overall dominance variance.

Based on the obtained results, for obtaining new promising line, the fourth cross (Sakha 94 × Misr 1) is highly recommended to be used in Egyptian wheat breeding programs for grain yield.

4.2. Inheritance of stripe and stem rust diseases:

4.2.1.The frequency distribution of different infection types and the phenotypic classes for stripe and stem rust diseases.

4.2.1.1. Stripe rust disease:

The infection type frequency distribution and the phenotypic classes of parents, F_1, F_2, BC_1 and BC_2 populations of the five studied crosses are presented in Table 15. These crosses included these categories: Susceptible (S) × Susceptible (S), Susceptible (S) × Resistant (R), Resistant (R) × Susceptible (S) and Resistant (R) × Resistant (R).

Cross 1: Line 1 (S) × Misr 1 (S)

Data presented in Table 16 indicated that the parent Line 1expressed high susceptibility to stripe rust, where all tested plants (45 plants) showed (S) infection types. On the other hand, Misr 1 expressed moderate susceptibility to stripe rust, where all tested plants (45 plants) showed (MS) infection types. Also, the F_1 tested plants (45 plants) were highly susceptible with infection type (S). Accordingly, these data suggested the complete dominance for susceptibility.

Regarding the F_2, the infection types ranged from (0) to (S) in 300 tested plants. However, numbers of F_2 resistant : susceptible plants were 85 : 215. These numbers fitted the theoretical expected ratio of 1 : 3 with P. value = 0.182, indicating that two interacting gene pairs are controlling the wheat stripe rust resistance in this cross. In addition, the infection types of BC_1 plants ranged from (MS) to (S) and BC_2 plants ranged from (R) to (S). However, for BC_1, the observed

ratio of resistant : susceptible plants was 0 : 75. This ratio fitted the theoretical ratio of 1 : 15 and supported the results obtained from the F_2 data. Whereas, the observed resistant : susceptible ratio of the BC_2 was 45 : 30 which fitted the expected ratio 9 : 7 and suggesting the operation of two interacting gene pairs and supported the expected ratio indicated from the F_2.

Cross 2: Line 2 (S) × Sakha 95 (R)

At the level of parents Table 16, Line 2 expressed high susceptibility to stripe rust, where all the tested plants (45 plants) recorded infection types (S). On the other hand, the parent Sakha 95 expressed high resistant to stripe rust, where all the tested plants (45 plants) recorded infection types (R) Also, the F_1 tested plants(45 plants) were high susceptibility with infection type (S), indicating the complete dominance for highly susceptibility over high resistance.

The F_2 infection types ranged from (0) to (S) for the tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 54 : 246. These numbers fitted the theoretical expected ratio of 3 : 13 with P. value = 0.740, indicating that two interacting gene pairs are controlling the wheat stripe rust resistance in this cross. Moreover, the infection types of BC_1 plants ranged from (MS) to (S). The observed ratio of resistant : susceptible plants was 0 : 75. This ratio fitted the theoretical ratio of 1 : 15 and confirm the results obtained from the F_2 data. Whereas, the BC_2 infection types ranged from (0) to (S). the observed resistant : susceptible ratio of the BC_2 was 52 : 23 fitting the expected ratio 3 : 1 and indicating the functioning of two double dominant gene pairs.

Cross 3: Shandweel 1 (R) × Misr 1(S)

The results presented in Table 16 clearly showed that the parent Shandweel 1 expressed moderate resistance to stripe, where all the tested plants (45 plants)

Table (16): Infection type frequency distribution and phenotypic classes of parents, F_1, F_2, BC_1 and BC_2 populations of five bread wheat crosses of stripe rust disease in 2016/17 season.

Crosses	Cross name	No. of tested plants		Infection type					Phenotypes		Expected ratio	x^2	P. value
				Resistant (R)			Susceptible (S)						
				0	R	MR	MS	S	Res	Sus			
1	Susceptible × Susceptible	P_1	45					45	-	45	-	-	-
		P_2	45				45		-	45	-	-	-
		F_1	45					45	-	45	-	-	-
		F_2	300	68	4	13	86	129	85	215	1:3	1.78	0.182
	Line 1× Misr1	B.C1	75				8	67	0	75	1 :15	5.00	0.025
		B.C2	75	35		10	19	11	45	30	9 : 7	0.63	0.427
2	Susceptible × Resistant	P_1	45					45	-	45	-	-	-
		P_2	45		45				45	-	-	-	-
		F_1	45					45	-	45	-	-	-
		F_2	300	31	8	15	37	209	54	246	3 : 13	0.11	0.740
	Line 2 × Sakha 95	B.C1	75				3	72	0	75	1 :15	5.00	0.025
		B.C2	75	29	8	15	11	12	52	23	3 : 1	1.28	0.258
3	Resistant × Susceptible	P_1	45			45			45	-	-	-	-
		P_2	45				45		-	45	-	-	-
		F_1	45			45			45	-	-	-	-
		F_2	300	200	7	39	25	29	246	54	13:3	0.11	0.740
	Shandweel 1 × Misr 1	B.C1	75	31	5	15	13	11	51	24	3 : 1	1.96	0.162
		B.C2	75	20	1	4	36	14	25	50	1 : 3	2.78	0.095
4	Resistant × Susceptible	P_1	45		45				45	-	-	-	-
		P_2	45				45		-	45	-	-	-
		F_1	45			45			45	-	-	-	-
		F_2	300	189	15	26	41	29	230	70	3 : 1	0.44	0.507
	Sakha 94 × Misr 1	B.C1	75	32	3	6	15	19	41	34	9 : 7	0.08	0.777
		B.C2	75	16	3	6	26	24	25	50	1 : 3	2.78	0.095
5	Resistant ×Resistant	P_1	45		45				45	-	-	-	-
		P_2	45		45				45	-	-	-	-
		F_1	45		45				45	-	-	-	-
		F_2	300	190	25	37	27	21	252	48	13:3	1.49	0.222
	Sakha 94 × Sakha 95	B.C1	75	35	14	11	12	3	60	15	13:3	0.08	0.777
		B.C2	75	51	7	8	5	4	66	9	13:3	2.24	0.134

showed (MR) infection types. On the other hand, the parent Misr 1 expressed moderate susceptibility to stripe rust, where all the tested plants (45 plants) recorded infection types (MS) Also, the F_1 tested plants (45 plants) were resistant with infection type (MR), indicating the complete dominance for resistance over susceptibility.

According the F_2 infection types, it ranged from (0) to (S) in 300 tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 246: 54. This ratio fitted the theoretical expected ratio of 13 : 3 with P. value = 0.740, indicating that two interacting gene pairs are controlling the wheat stripe rust resistance in this cross. Furthermore, the infection types of BC_1 and BC_2 plants ranged from (0) to (S). With respect to BC_1, the observed ratio of resistant : susceptible plants was 51 : 24. These numbers fitted the theoretical ratio of 3 : 1 and confirm the results obtained from the F_2 data. Whereas, the observed resistant : susceptible ratio of the BC_2 was 25 : 50 fitting the expected ratio 1 : 3 and suggesting the operation of two interacting gene pairs.

Cross 4: Sakha 94 (R) × Misr 1 (S)

Taking parents into consideration, data presented in Table 16 indicated that the parents Sakha 94 expressed highly resistant to stripe rust, where all the tested plants (45 plants) recorded infection types (R). On the other hand, the parent Misr 1 expressed moderate susceptibility to stripe rust, where all the tested plants (45 plants) recorded infection types (MS). Also, the F_1 tested plants (45 plants) were resistant with infection type (MR), indicating the complete dominance for resistance.

According the F_2, the types ranged from (0) to (S) for the tested plants. However, numbers of F_2 resistant : susceptible plants were 230 : 70. These

numbers fitted the theoretical expected ratio of 3 : 1 with P. value = 0.507, indicating that two interacting gene pairs are controlling the wheat stripe rust resistance in this cross.

The infection types of BC_1 plants ranged from (0) to (S). The observed ratio of resistant : susceptible plants were 41 : 34. This ratio fitted the theoretical ratio of 9 : 7 and emphasize the results obtained from the F_2 data. Whereas, the BC_2 infection types ranged from (0) to (S). the observed resistant : susceptible ratio of the BC_2 was 25 : 50 which fitted the expected ratio 1 : 3 and indicating the functioning of two double dominant gene pairs.

Cross 5: Sakha 94 (R) × Sakha 95 (R)

Data presented in Table 16 indicated that the parent Sakha 94 expressed high resistant to stripe rust, where all the 45 tested plants recorded infection types (R), whereas, the parent Sakha 95 expressed high resistant to stripe rust, where all the tested plants (45 plants) recorded infection types (R), Also, the F_1 tested plants (45 plants) were high resistant with infection type (R). These data suggested the presence of dominance for resistance.

The F_2 infection types ranged from (0) to (S) in 300 tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 252 : 48. This ratio fitted the theoretical expected ratio of 13 : 3 with P. value = 0.222, indicating that two interacting gene pairs are controlling the wheat stripe rust resistance in this cross. In addition to, the infection types of BC_1 and BC_2 plants ranged from (0) to (S). According to BC_1, the observed ratio of resistant : susceptible plants was 60 : 15. These numbers fitted the theoretical ratio of 13 : 3 and confirmed the results obtained from the F_2 data. Whereas, the observed resistant : susceptible ratio of the BC_2 was 66 : 9 fitting the expected ratio 13 : 3 and suggesting the operation of two interacting gene pairs.

4.2.1.2. Stem rust disease:

The infection type frequency distribution and the phenotypic classes of parents, F_1, F_2, BC_1 and BC_2 populations of the five studied crosses are presented in Table 16. These crosses included these categories: Susceptible (S) × Susceptible (S) and Resistant (R) × Susceptible (S).

Cross 1: Line 1 (S) × Misr 1 (S)

Data presented in Table 17 indicated that the parent Line 1expressed moderate susceptibility to stem rust, where all tested plants (45 plants) showed (MS) infection types. On the other hand, Misr 1 expressed high susceptibility to stem rust, where all tested plants (45 plants) showed (S) infection types. Also, the F_1 tested plants (45 plants) were highly susceptible with infection type (S). Accordingly, these data suggested the complete dominance for susceptibility.

Regarding the F_2, the infection types ranged from (R) to (S) in 300 tested plants. However, numbers of F_2 resistant : susceptible plants were 30 : 270. These numbers fitted the theoretical expected ratio of 1 : 15 with P. value = 0.007, indicating that two interacting gene pairs are controlling the wheat stem rust resistance in this cross. In addition, the infection types of BC_1 plants ranged from (MR) to (S) and BC_2 plants ranged from (MS) to (S). However, for BC_1, the observed ratio of resistant : susceptible plants was 3 : 72. This ratio fitted the theoretical ratio of 1 : 15 and supported the results obtained from the F_2 data. Whereas, the observed resistant : susceptible ratio of the BC_2 was 0: 75 which fitted the expected ratio 1 : 15 and suggesting the operation of two interacting gene pairs and supported the expected ratio indicated from the F_2.

Table (17): Infection type frequency distribution and phenotypic classes of parents, F_1, F_2, BC_1 and BC_2 populations of five bread wheat crosses of stem rust disease in 2016/17 season.

Crosses	Cross name	No. of tested plants		Infection type					Phenotypes		Expected ratio	x^2	P. value
				Resistant (R)			Susceptible (S)						
				0	R	MR	MS	S	Res	Sus			
1	Susceptible × Susceptible	P_1	45				45		-	45	-	-	-
		P_2	45					45	-	45	-	-	-
		F_1	45					45	-	45	-	-	-
		F_2	300		13	17	28	242	30	270	1 :15	7.200	0.007
	Line 1× Misr1	B.C1	75			3	40	32	3	72	1 :15	0.648	0.421
		B.C2	75				5	70	0	75	1 :15	5.000	0.025
2	Susceptible × Susceptible	P_1	45					45	-	45	-	-	-
		P_2	45					45	-	45	-	-	-
		F_1	45					45	-	45	-	-	-
		F_2	300	5	3	14	37	241	22	278	1 :15	0.601	0.438
	Line 2 × Sakha 95	B.C1	75				2	73	0	75	1 :15	5.000	0.025
		B.C2	75				7	68	0	75	1 :15	5.000	0.025
3	Susceptible × Susceptible	P_1	45					45	-	45	-	-	-
		P_2	45					45	-	45	-	-	-
		F_1	45					45	-	45	-	-	-
		F_2	300	3	15	12	49	221	30	270	1 :15	7.200	0.007
	Shandweel 1 × Misr 1	B.C1	75	5	6	9	18	37	20	55	1:3	0.111	0.739
		B.C2	75				10	65	0	75	1 :15	5.000	0.025
4	Resistant × Susceptible	P_1	45			45			45	-	-	-	-
		P_2	45					45	-	45	-	-	-
		F_1	45				45		-	45	-	-	-
		F_2	300	73	51	32	40	104	156	144	9 : 7	2.202	0.138
	Sakha 94 × Misr 1	B.C1	75	14	32	9	16	4	55	20	3 : 1	0.111	0.739
		B.C2	75				12	63	0	75	1 :15	5.000	0.025
5	Resistant × Susceptible	P_1	45			45			45	-	-	-	-
		P_2	45					45	-	45	-	-	-
		F_1	45				45		-	45	-	-	-
		F_2	300	106	69	43	35	47	218	82	3 : 1	0.871	0.351
	Sakha 94 × Sakha 95	B.C1	75	10	18	24	17	6	52	23	3 : 1	1.284	0.257
		B.C2	75		14	9	14	38	23	52	1:3	1.284	0.257

Cross 2: Line 2 (S) × Sakha 95 (S)

Data presented in Table 17 indicated that the parents Line 2 and Sakha 95 expressed high susceptibility to stem rust, where all the tested plants (45 plants) for two parents recorded infection types (S). Also, the F_1 tested plants (30 plants) were susceptible with infection type (S), indicating the complete dominance for susceptibility.

The F_2 infection types ranged from (0) to (S) for the 300 tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 22 : 278. This ratio fitted the theoretical expected ratio of 1 : 15 with P. value = 0.438, indicating that two interacting gene pairs are controlling the wheat stem rust resistance in this cross. Furthermore, the infection types of BC_1 and BC_2 plants ranged from (MS) to (S) for all tested plants. The observed ratio of resistant : susceptible plants was 0 : 75. These numbers fitted the theoretical ratio of 1:15 and supported the results obtained from the F_2 data.

Cross 3: Shandweel 1 (S) × Misr 1(S)

The results presented in Table 17 clearly showed that the parent Shandweel 1expressed high susceptibility to stem, where all the tested plants (45 plants) showed (S) infection types. Also, the parent Misr 1expressed high susceptibility to stem rust, where all the tested plants (45 plants) recorded infection types (S). Furthermore, the F_1 tested plants (45 plants) were high susceptibility with infection type (S). Accordingly, these data suggested the complete dominance for high susceptibility.

With respect to the F_2 infection types, it ranged from (0) to (S) for the tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 30 : 270. These numbers fitted the theoretical expected ratio of 1 : 15 with P. value =

0.007, indicating that two interacting gene pairs are controlling the wheat stem rust resistance in this cross. Moreover, the infection types of BC_1 plants ranged from (0) to (S). The observed ratio of resistant : susceptible plants was 20 : 55. This ratio fitted the theoretical ratio of 1:3 and supported the results obtained from the F_2 data. Whereas, the BC_2 infection types ranged from (MS) to (S). the observed resistant : susceptible ratio of the BC_2 was 0:75 which fitted the expected ratio 1:15 and indicating the functioning of two double dominant gene pairs.

Cross 4: Sakha 94 (R) × Misr 1 (S)

The results presented in Table 17 clearly showed that the parent Sakha 94 expressed resistance to stem rust, where all tested plants (45 plants) showed (MR) infection types. On the other hand, the parent Misr 1 expressed highly susceptible to stem rust, where all tested plants (45 plants) recorded infection types (S). Also, the 45 F_1 tested plants were susceptible with infection type (Ms). Accordingly, these data suggested the existence of partial dominance for susceptibility over the resistance.

With respect to the F_2 infection types, it ranged from (0) to (S) for the 300 tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 156:144. This ratio fitted the theoretical expected ratio of 9:7 with P. value = 0.138, indicating that two interacting gene pairs are controlling the wheat stem rust resistance in this cross. Furthermore, the infection types of BC_1 plants ranged from (0) to (S). The observed ratio of resistant : susceptible plants was 55:20. These numbers fitted the theoretical ratio of 3:1 and confirm the results obtained from the F_2 data. Whereas, the observed resistant : susceptible ratio of the BC_2 was 0:75 which fitted the expected ratio 1:15 and indicating the functioning of two double dominant gene pairs.

Cross 5: Sakha 94 (R) × Sakha 95 (S)

Data presented in Table 17 indicated that the parent Sakha 94 expressed moderate resistant to stem rust, where all the 45 tested plants recorded infection types (MR), while, the parent Sakha 95 expressed high susceptibility to stem rust, where all the tested plants (45 plants) recorded infection types (S), Also, the F_1 tested plants (45 plants) were moderate susceptibility with infection type (MS).

The F_2 infection types ranged from (0) to (S) in 300 tested plants. However, the observed numbers of F_2 resistant : susceptible plants were 218 : 82. This ratio fitted the theoretical expected ratio of 3:1 with P. value = 0.351, indicating that two interacting gene pairs are controlling the wheat stripe rust resistance in this cross. In addition to, the infection types of BC_1 plants ranged from (0) to (S). The observed ratio of resistant : susceptible plants was 52 : 23. These numbers fitted the theoretical ratio of 3:1 and confirmed the results obtained from the F_2 data. Whereas, the BC_2 infection types ranged from (R) to (S). the observed resistant : susceptible ratio of the BC2 was 23:52 which fitted the expected ratio 1:3 and indicating the functioning of two double dominant gene pairs.

4.2.2. Mean of the average coefficient infection (ACI) and variances for strip and stem rusts disease resistance.

The mean of the average coefficient infection (ACI) of strip and stem rust diseases for the six populations of the five studied crosses are presented in Tables (18-19).

4.2.2.1- Strip rust disease resistance:

With respect to the first cross Line 1 (S) × Misr 1 (S), the data in Table 18 indicated that the F_1 mean value (20.29) was less than the mid parent (25.83) and less than the first parent (Line 1) indicating partial dominance towards the parent

of low disease severity. The F_2 mean values were higher than the $F_1$and lower than the mid-parent, indicating the partial dominance towards the parent of low disease severity. The BC_2 populations recorded diseases severities lower than the mid-parent, suggesting the importance of non-additive component (partial dominance) in the inheritance o this trait.

In the second cross Line 2 (Susceptible) × Sakha 95 (resistant) the results indicated that the F_1 mean value was less than the mid parent value and less than the first parent (Line 2) with value (59.11) indicating partial dominance for the Susceptible parent. The F_2 mean values were higher than the F_1 and lower than the mid-parent, indicating the partial dominance towards the resistant parent. The BC_2 populations recorded diseases severities lower than the mid-parent, suggesting the importance of non-additive component (partial dominance) in the inheritance o this trait.

For the third cross Shandweel 1 (R) × Misr 1 (S) the results indicated that the F_1 mean value (0.58) was less than the mid- parent and less than the lower parent (Shandweel 1) indicating over dominance towards the resistant parent. On the other hand, the F_2 mean value (0.89) was less than the mid parent (1.95), indicating partial dominance towards the resistant. BC_1 and BC_2 mean values indicated that segregation were in the direction of their respective recurrent parents.

Regarding to the fourth cross Sakha 94 (R) × Misr 1 (S), the results indicated that the F_1 mean value (0.45) was less than the lower parent (0.93) indicating over-dominance for resistance. The F_2 and BC_1 mean values (1.13) and (0.95), respectively, was higher than the F_1 mean value (0.45) indicating partial dominance for resistance. With regard to the BC_2 mean value, it was tended towards the mean of recurrent parent.

With respect to the fifth cross; Sakha 94 (R) × Sakha 95 (R), the data in Table 18 indicated that the F_1 mean value (0.84) was less than the mid parent value (0.93), indicating over dominance controlling the inheritance of resistance of this trait. The F_2, BC_1 and BC_2 mean values were higher than the F_1 mean value, indicating partial dominance for resistance.

Table (18): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of stripe rust.

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	48.44	3.22	20.29	21.18	57.17	8.28
	S^2	13.43	1.93	2.86	911.49	754.37	616.63
	$S^2_{\bar{X}}$	0.30	0.04	0.08	3.04	10.06	8.22
2	$\bar{X}$	59.11	0.91	19.43	28.46	75.63	9.22
	S^2	8.28	0.06	5.55	821.98	627.43	529.77
	$S^2_{\bar{X}}$	0.18	0.001	0.16	2.74	8.37	7.06
3	$\bar{X}$	0.61	3.29	0.58	0.89	0.48	2.78
	S^2	0.30	1.81	0.27	5.20	0.50	8.37
	$S^2_{\bar{X}}$	0.01	0.04	0.01	0.02	0.01	0.11
4	$\bar{X}$	0.93	3.43	0.45	1.13	0.95	2.82
	S^2	0.05	1.53	0.07	7.90	3.17	8.67
	$S^2_{\bar{X}}$	0.001	0.03	0.002	0.03	0.04	0.12
5	$\bar{X}$	0.91	0.95	0.84	1.59	1.19	1.10
	S^2	0.06	0.04	0.11	13.05	9.27	8.47
	$S^2_{\bar{X}}$	0.001	0.0009	0.003	0.04	0.12	0.11

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

4.2.2.2.Stem rust disease resistance:

The mean of the average coefficient infection (ACI), variances of stem rust disease in the six populations of the five studied crosses are presented in Table 19.

For the first cross Line 1 (S) × Misr 1 (S) the data revealed that the F_1 mean value 9.00 was less than the mid parent indicating partial dominance towards parent of low disease severity. The F_2 and BC_1 populations recorded disease

severities were low than mid-parent, suggesting the importance of partial dominance in the inheritance o this trait.

With respect to the second cross; Line 1 (S) × Sakha 95 (S), the data in Table 19 indicated that the F_1 mean value was less than the mid- parent , indicating partial dominance controlling the inheritance of this trait. On the other hand, the F_2 mean value was approximately equal to the mid-parent value, indicating the presence of transegressive segregation in F_2 generation. The BC_1 and BC_2 mean values were higher than the F_1 mean value, indicating partial dominance for susceptibility.

Table (19): Mean($\bar{X}$), variance (S^2) and mean variance ($S^2_{\bar{X}}$) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of stem rust.

Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2
1	$\bar{X}$	0.94	30.89	9.00	5.84	1.89	26.22
	S^2	0.44	8.28	4.12	44.62	4.47	66.96
	$S^2_{\bar{X}}$	0.01	0.18	0.12	0.15	0.06	0.89
2	$\bar{X}$	29.56	1.18	5.71	15.05	9.15	6.91
	S^2	4.34	0.69	3.15	314.86	172.17	250.05
	$S^2_{\bar{X}}$	0.10	0.02	0.09	1.05	2.30	3.33
3	$\bar{X}$	1.09	39.56	1.57	16.65	7.38	16.98
	S^2	0.36	4.34	2.02	409.33	364.49	262.15
	$S^2_{\bar{X}}$	0.01	0.10	0.06	1.36	4.86	3.50
4	$\bar{X}$	0.47	40.44	4.00	4.07	1.41	8.27
	S^2	0.11	4.34	0.29	79.73	34.49	70.49
	$S^2_{\bar{X}}$	0.002	0.10	0.01	0.27	0.46	0.94
5	$\bar{X}$	0.44	1.09	1.07	0.84	0.69	2.11
	S^2	0.06	0.36	0.83	8.62	5.20	5.40
	$S^2_{\bar{X}}$	0.001	0.01	0.02	0.03	0.07	0.07

(Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95.

With respect to the third cross; Shandweel 1 (S) × Misr 1 (S), the data in Table 19 indicated that the F_1 mean value (1.57) was less than the mid-parent mean

value (20.32), revealing the presence of dominance towards the parent of low disease severity. The F_2, $BC_1$and BC_2 populations recorded disease severity lower than the mid-parents, suggesting the importance of non-additive (partial dominance) in the inheritance of this trait.

Regarding the fourth cross; Sakha 94 (R) × Misr 1 (S), the results indicated that the F_1 mean value (4.00) was less than the mid-parents, indicating dominance for susceptibility. The F_2, BC_1 and BC_2 mean values were less than the mid-parent, indicating partial dominance controlling the inheritance of this trait.

With respect to the fifth cross; Sakha 94 (R) × Sakha 95 (S), the data in Table 19 indicated that the F_1 mean value (1.07) was higher than the mid-parent (0.77), indicating partial dominance towards the susceptible parent. The F_2 and BC_1 mean values were less than the F_1 mean value, indicating partial dominance for resistance.

4.2.3.Heterosis, Inbreeding Depression and Potence Ratio:

Heterosis expressed as the percentage deviation of F_1. Mean performance from its mid parents and better parent average values, inbreeding depression and potence ratio for stripe and stem rust diseases in the our crosses are presented in Table 20.

4.2.3.1.Stripe rust disease resistance

The resistant crosses to stripe rust diseases (Desirable) should have significant negative heterotic effects relative to mid-parent and the better parent.

In the present study, data in Table 20 showed that all crosses exhibited highly significant negative heterotic effects relative to mid-parent and better parent. These superior and promising genotypes and their progenies might be used in the future in wheat breeding programs for improving the resistance to stripe rust

disease. Said (2003), Ragab (2005) and Yasen (2008) obtained highly significant heterotic effects in negative direction for resistance to stripe rust disease.

Table (20):Heterosis, potence ratio and inbreeding depression for stripe rust resistance and stem rust resistance in the five studied crosses.

Traits	Crosses	Heterosis MP%	Heterosis BP%	Potence ratio	Inbreeding depression %
Stripe rust resistance	1	-21.47**	-58.13**	-0.25	-4.43*
	2	-35.26**	-67.13**	-0.36	-46.51**
	3	-70.13**	-82.28**	1.02	-53.5**
	4	-79.55**	-87.01**	1.39	-154.27**
	5	-9.57**	-11.27**	5.00	-89.44**
Stem rust resistance	1	-43.45**	-70.86**	0.46	35.13**
	2	-62.81**	-80.67**	-0.68	-163.39**
	3	-92.27**	-96.03**	0.97	-959.5**
	4	-80.45**	-90.11**	0.82	-1.67**
	5	40.94**	-1.34**	-0.96	21.62**

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

With regard to potence ratio, values presented in Table 20, showed that the value of potence ratio was approximately equal unity with negative sign for the third cross (Shandweel 1 × Misr 1), indicating the presence of dominance inheritance of this trait. Meanwhile, the values of the first cross (Line 1 × Misr 1) was less than unity, indicating the presence of partial dominance controlling the inheritance of this trait for this cross. On the other hand, The values of potence ratio were more than unity with negative sign for fourth (Sakha 94 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses indicating the presence of over dominance

inheritance of this trait. **Said (2003) and Yasen (2008)** obtained similar results such they found partial dominance toward resistance, while **Ragab (2005)** obtained over- dominance.

With respect to inbreeding depression percent data in Table 20 showed that all the studied crosses exhibited significant or/and highly significant negative for strip rust disease. These results were in the same line with **Ragab (2005)** and **Yasen (2008).**

4.2.3.2.Stem rust disease resistance

Data in Table 20 showed that all crosses exhibited high significant negative heterotic effects relative to mid-parent and better parent except for the fifth one (Sakha 94 × Sakha 95) which had highly significant positive (undesirable) relative to mid-parent. These results were in the same line with **Aglan (2003) and Ragab (2005).**

For potence ratio, the values were less than unity with positive or negative sign in all crosses, indicating the presence of partial dominance in the inheritance of this trait. These results were in agreement with **Aglan (2003)** who found partial dominance.

With regard to the inbreeding depression percent data presented in Table 20 showed highly significant positive for the first cross (Line 1 × Misr 1) and the fifth cross (Sakha 94 × Sakha 95), while highly significant negative inbreeding depression were detected for remaining crosses.

4.2.4. Estimation of type of gene action.

4.2.4.1.Scalling test:

The scale tests for the stripe and stem rust diseases are presented in Table 21.

Most values of A, B, C and D were significant for all the studied crosses, indicating the presence of non-allelic interaction in these crosses. Regarding the adequacy of the six parameters model to explain the type of gene action controlling the traits in these crosses.

Table (21): Scaling test parameters A , B and C for days to heading, stripe and stem rusts resistance in the five studied crosses.

Traits	Crosses	Scaling test		
		A	B	C
Stripe rust resistance	1	45.61**	-6.94	-7.49
	2	72.71**	-1.9	14.98*
	3	-0.24	1.69*	-1.49*
	4	0.52	1.77*	-0.72
	5	0.62	0.42	2.83**
Stem rust resistance	1	-6.16**	12.56**	-26.48**
	2	-16.96**	6.92	18.04**
	3	12.1**	-7.16	22.81**
	4	-1.66	-27.91**	-32.65**
	5	-0.13	2.05**	-0.31

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

4.2.4.2.Gene action effects:

Type of gene action for stripe and stem rust diseases characters are shown in Table 22. The estimated mean effects (m), which reflected the contribution due to over-all mean plus the locus effects and interaction of the fixed loci was found to be highly significant for all the studied characters in all crosses, indicating that these characters were quantitatively inherited. These results are in harmony with those of **Aglan (2003), Ragab (2005)** and **Sharshar (2015).**

From the results illustrated in Table 22, it could be concluded that the additive (a) gene effects for stripe rust resistance was highly significant positive for the first

(Line 1 × Misr 1) and second (Line 2 × Sakha 95) crosses. Meanwhile, the third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses exhibited highly significant positive for stripe rust resistance. Whereas, the fifth cross (Sakha 94 × Sakha 95) was insignificant with positive sign. On the other side, all the studied crosses exhibited high significant negative values stem rust resistance except for the second cross (Line 2 × Sakha 95), reflecting that the additive effects play an important role in the genetic variation of these characters.

Table (22): Type of gene action for stripe rust resistance and stem rust resistance in the five studied crosses.

Traits	Crosses	Scaling test					
		(m)	(a)	(d)	(aa)	(ad)	(dd)
Stripe rust resistance	1	21.18**	48.89**	40.62**	46.16**	26.28**	-84.83**
	2	28.46**	66.41**	45.26**	55.84**	37.31**	-126.66**
	3	0.89**	-2.3**	1.58	2.94**	-0.96**	-4.4**
	4	1.13**	-1.88**	1.27	3.01**	-0.63	-5.3**
	5	1.59**	0.08	-1.87	-1.78	0.1	0.74
Stem rust resistance	1	5.84**	-24.33**	25.96**	32.88**	-9.36**	-39.28**
	2	15.05**	2.25	-37.73**	-28.08**	-11.94**	38.12**
	3	16.65**	-9.6**	-36.62**	-17.87*	9.63**	12.93
	4	4.07**	-6.86**	-13.37**	3.09	13.13**	26.47**
	5	0.84**	-1.42**	2.54*	2.23*	-1.09**	-4.15*

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

On the other hand, dominant gene effects (d) were significant or highly significant with positive or negative sign for the two characters, except for stripe rust resistance in the third (Shandweel 1 × Misr 1), the fourth (Sakha 94 × Misr1) and the fifth (Sakha 94 × Sakha 95) crosses. These results indicate the importance of dominance gene effects in the inheritance of these characters.

In some cases ,where the absence of significant (d) component implies no dominance genetic differences between the two parents and the dominant effects have no important role in the genetic control of these cases.

It could be observed that dominance effects are several times larger than additive one in most crosses. This might indicate that dominance gene effects play the major role in controlling the genetic variation of most studied characters. However, when additive effects are larger than non-additive ones, it is suggested that selection in early segregating generations would be effective. Meanwhile, if non-additive portion are larger than additive one, the improvement of the characters need intensive selection through later generations. These conclusion are in the same line with those found by **Shehab El-Din and Abd El-latif (1996), Aglan (2003), Ragab (2005), Sharshar (2015)** and **Hermas and El-Sawi (2015)**.

On the other side, positively significant or highly significant additive × additive effects (aa) were detected for; stripe rust resistance in all crosses except for , the fifth cross (Sakha 94 × Sakha 95) as well as stem rust resistance in the first (Line 1 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses . Meanwhile, negatively significant or highly significant additive × additive type was found for stem rust resistance in the second (Line 2 × Sakha 95) and third (Shandweel 1× Misr1) crosses. In addition, significant or highly significant with positive signs additive × dominance effects (ad) were found for stripe rust resistance in the first (Line 1 × Misr 1) and the second (Line 2 × Sakha 95) crosses as well as for stem rust resistance in the third (Shandweel 1 × Misr 1) and the fourth (Sakha 94 × Misr 1) crosses. On the other hand, significant or highly significant with negative signs additive × dominance types of epistasis were found for stripe rust resistance in the third cross (Shandweel 1 × Misr 1) as well as for stem rust in the first (Line 1 × Misr 1), second (Line 2 × Sakha 95) and fifth (Sakha 94 × Sakha 95) crosses. The

dominance × dominance types of effects (dd) were positively highly significantly for stem rust resistance in the second (Line 2 × Sakha 95) and fourth (Sakha 94 × Misr 1) crosses. On the other hand, negatively significant or highly significant dominance × dominance types of epistasis were found for stripe rust resistance in all crosses except for the fifth cross (Sakha 94 × Sakha 95) as well as for stem rust resistance in the first (Line 1 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses. These findings which recorded the presence of the additive, dominance and the epistasis (additive × additive, additive × dominance and dominance × dominance) were reported by **Mahgoub (2001)**, **Aglan (2003), Yasen (2008)** and **Hermas and El-Sawi (2015)**.

With regard to the negative values observed in most cases either with the main effects; (a) and (d) or the non-allelic interactions; (aa), (ad) and (dd), these might indicate that the alleles responsible for less value of traits were over dominant over the alleles controlling high value.

However, when epistatic effects were significant for a trait, the possibility of obtaining desirable segregates through inter-mating in early segregations by breaking undesirable linkage could be available or it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement. These results are in agreement with those of **Mahgoub (2001)** and **Ragab (2005).**

4.2.5. Components of variance, heritability and expected genetic advance.

4.2.5.1.Components of variances

The additive variance (1/2D), dominance variance (1/4H) and environmental variance (VE) for the stripe and stem rusts disease resistance for the five studied crosses are presented in Table 23.

Stripe rust disease resistance:

Additive and dominance variance estimates were highly significant in all crosses, indicating the importance of each additive and dominance variances in controlling this disease. Similar results were obtained by **Shehab El-Din and Abd El-Latif (1996)**, who demonstrated the presence of additive and non-additive in inheritance of stripe rust resistance disease.

Stem rust disease resistance:

Concerning, additive variance, highly significant were obtained for all crosses. Dominance variance estimates were highly significant in all crosses except for the fifth cross (Sakha 94 × Sakha 95). These results were in agreement with those obtained by **Shehab El-Din et al.,(1991)**, **Mahgoub (2001)** and **Aglan (2003)** came to the conclusion where the stated that, the genetic components (additive and dominance) exhibited equal magnitude in the inheritance of stem rust disease resistance.

Table(23): Additive V (1/2D), dominance V (1/4H) and environmental variance (VE) for stripe and stem rusts diseases resistance in the five studied crosses .

Traits	Crosses	V(1/2D)	V(1/4H)	VE
Stripe rust resistance	1	99.42**	454.24**	5.27
	2	99.41**	330.35**	4.86
	3	87.28**	3**	0.66
	4	94.52**	3.5**	0.43
	5	99.39**	4.62**	0.08
Stem rust resistance	1	90.5**	22.57**	4.24
	2	99.1**	104.53**	2.84
	3	99.47**	215.13**	2.18
	4	98.42**	23.98**	1.26
	5	94.02**	1.46	0.52

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

4.2.5.2.Heritability estimates and predicted genetic advance from selection.

Heritability estimates in both broad and narrow sense and expected genetic advanced for stripe and stem rust diseases resistance are presented in Table 24.

Stripe rust disease resistance:

Regarding to stripe rust disease resistance, heritability estimates in broad sense were high and ranged from 87.28 % for the third cross (Shandweel 1× Misr 1) to 99.42% for the first cross. These results were in good agreement with those obtained **by Abd EL Latif and Omyma (2000)** and **Said (2003)** who recorded, high heritability values in broad. On the other side, heritability in narrow sense were moderate with values ranged from 29.53% for the third cross (Shandweel 1× Misr 1) to 64.03 for the fifth cross (Sakha 94 × Sakha 95). **Shehab El-Din and Abd El-Latif (1996)** and **Zhang et al. (2001)** reported high values for broad sense heritability and moderate values of narrow sense heritability in this concern.

Estimates of predicted genetic advance from selection as percentage of F_2 mean ($\Delta g\%$) ranged from 122.87% for the second cross (Line 2 × Sakha 95) to 299.46% for the fifth cross (Sakha 94 × Sakha 95).

As previously shown, the fifth cross (Sakha 94 × Sakha 95) was considerable as the best cross and may be used in wheat breeding program to improving resistance to stripe rust disease.

Stem rust disease resistance

Regarding to stem rust disease resistance, heritability estimates in broad sense were high in all crosses. Similar results were reported by **Shehab El-Din, et al., (1991b)** who reported high values of heritability in one cross and intermediate in other one. Meanwhile, narrow sense heritability estimates were moderate in all

crosses. **Mahgoub (2001)** reported low narrow sense heritability and it was around 50%.

Predicted genetic advance from selection as percentage of F2 mean (Δg%) ranged from 94.04% for the first cross (Line 1 × Misr 1) to 554.11% the fifth cross (Sakha 94 × Sakha 95).

As previously shown, the fourth (Sakha 94 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses were the best crosses which can be used in wheat breeding program to improve stem rust disease resistance.

Table (24): Estimates of heritability percentage in broad (H) and narrow (h^2) senses and expected (Δg) genetic advance from selection in five bread wheat crosses.

Traits	Crosses	Heritability		Genetic advance	
		H%	h^2%	Δg	Δg %
Stripe rust resistance	1	99.42	49.59	30.84	145.58
	2	99.41	59.22	34.98	122.87
	3	87.28	29.53	1.39	155.07
	4	94.52	50.16	2.90	256.28
	5	99.39	64.03	4.77	299.46
Stem rust resistance	1	90.50	39.90	5.49	94.04
	2	99.10	65.90	24.09	160.05
	3	99.47	46.91	19.55	117.43
	4	98.42	68.34	12.57	309.11
	5	94.02	77.12	4.67	554.11

(*)and (**) significant at 0.05 and 0.01 levels of probability , respectively. (Cross1) Line 1 × Misr 1, (Cross 2) Line 2 × Sakha 95, (Cross 3) Shandweel 1 × Misr 1, (Cross 4) Sakha 94 × Misr 1, (Cross5) Sakha 94 × Sakha 95

Molecular analysis

Polymorphism based on SSR markers

To save the power of statistics by reducing the cost and simplifying analytical procedure, selective assess, such as selective genotyping, by which only individuals with highly extreme phenotypes (usually the two tails selected from a sample population also and Selective genotyping could be used, along with pooled DNA analysis, to change genotyping the entire population) were analyzed, has been proposed (Sun *et al*., 2010). A further significant cost reduction is to bulk all the individuals selected from each tail of the population and analyse as a pool. For example, pooled DNA analysis for marker identification was developed by two groups independently but named differently as bulked segregant analysis (Michelmore *et al*., 1991) Bulked segregant analysis was originally designed to target the traits controlled by major genes with large effect and less confounded by environments. Recent developments in BSA have increased the power of bulked segregant analysis in identifying minor causal alleles (Sun *et al*., 2010)

Over 10 pairs of SSR primers were used to identify the polymorphism between the stripe and stem rust resistant and the susceptible DNA bulks. Genetic diversity analysis of six populations (P1, P2, F_1, BC_1, BC_2 and F_2) resulted from crosses Line 2 × Sakha 95 for stripe rust and Sakha 94 × Misr 1 for stem rust based on molecular markers was an important aim for this study. Knowledge of the genetic similarity among the six population is very useful and successful for genetic improvement (**Ceron and Angel, 2001**). Understanding the genetic variability among wheat cultivars opens up a possibility for developing a molecular genetic map that will lead to the application of marker-assisted selection tools in genetic improvement of wheat for stripe rust resistance.

To measure the degree of genetic variability among the used wheat genotypes, SSR-PCR technique was applied. Calculating the genetic similarity among the studied genotypes and studying the genetic relationships among the results populations of wheat.

The main role of these markers were to detected the polymorphism which can be used for qualitative or quantitative trait loci, diversity, pedigree analysis, assess taxonomic and phylogenetic relationships, linkage mapping, etc.

SSR is polymerase chain reaction (PCR) based markers help us in detection of polymorphism at the molecular level from many individuals or pooled samples at a very fast rate. Also, it's preferred by many geneticists and plant breeders because of its higher repeatability, co-dominant nature, specificity and having multiple alleles (Cheng *et al.* 2009).

SSR markers associated with stem or stripe rust was used with bulk sergeant analysis (BSA) to be used in marker assisted selection (MAS) program and to develop a database which will enable the utilization of genetic markers as selection tools to improve wheat rust characterization. As Michelmore et al., (1991) described BSA, F_2 plants presented by at least 200 individuals will be classified into groups according to their behavior rust stress. The extreme groups will be detected, first one refer to the best growing F_2 plants under (most resistance) and the other group refers to the (most sensitive).

Stripe Rust

Polymorphism patterns were observed among the studied populations for cross Line 2 × Sakha 95. A total of five SSR primers were initially used to establish SSR fingerprints for this cross. Only three primers successfully generated reproducible polymorphic and scorable bands xgwm18, xgwm501 and xgwm382.

Moreover, using xgwm18 Fig 1 , most of the resistant F_2 plants presented the same DNA with 160 bp band as Sakha 95 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA band or presented the same DNA band as Line 2 or the susceptible DNA bulk did. Similarly, most of the susceptible F_2 plants presented the same DNA with 186 bp band as Line 2 or the susceptible DNA bulk did, and most of the resistant F_2 plants did not present these DNA band or presented the same DNA band as Sakha 95 or the resistant DNA bulk did.

With respect, primer Xgwm 501 Fig 2, most of the resistant F_2 plants presented the same DNA with 165 bp band as Sakha 95 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA band or presented the same DNA band as Line 2 or the susceptible DNA bulk did. Similarly, most of the susceptible F_2 plants presented the same DNA with 195 bp band as Line 2 or the susceptible DNA bulk did, and most of the resistant F_2 plants did not present these DNA band or presented the same DNA band as Sakha 95 or the resistant DNA bulk did.

With regard to, using xgwm382 Fig 3, most of the resistant F_2 plants presented the same DNA with 200 bp band as Sakha 95 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA band or presented the same DNA band as Line 2 or the susceptible DNA bulk did. On the other hand, most of the susceptible F_2 plants presented the same DNA with 230 bp band as Line 2 or the susceptible DNA bulk did, and most of the resistant F_2 plants did not present these DNA band or presented the same DNA band as Sakha 95 or the resistant DNA bulk did.

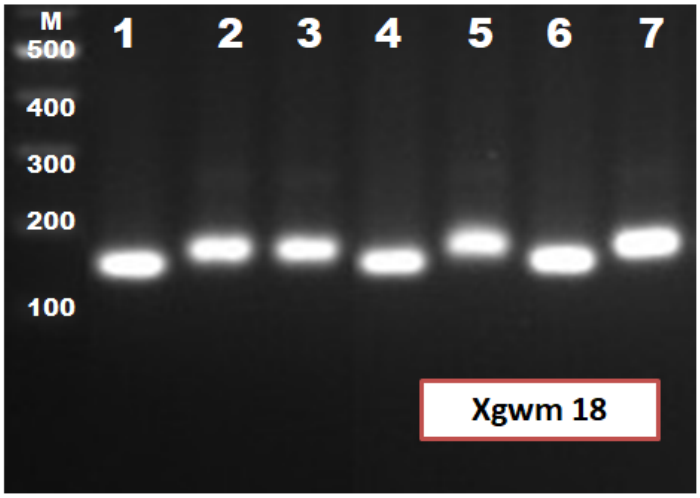

Figure 1: Agarose gel showing the allelic segregation of the Xgwm 18 SSR marker in the analyzed 1-(R) P, Sakha 95 2- (S)P, Line 2; 3- F_1; 4- (R)BC1; 5- (S)BC2; 6- Resistant DNA pool F_2 plants; 7- Susceptible DNA pool F_2 plants M: 100 bp DNA ladder.

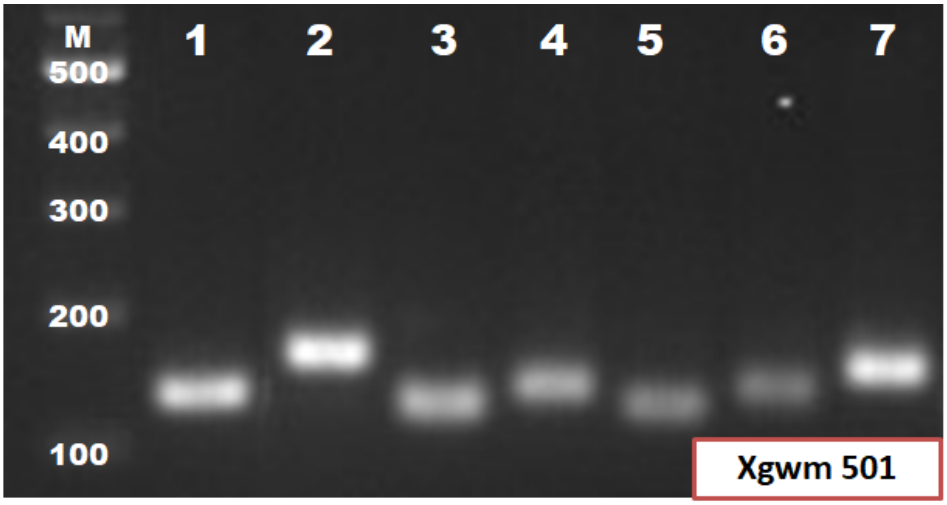

Figure 2: Agarose gel showing the allelic segregation of the Xgwm 501 SSR marker in the analyzed 1-(R) P, Sakha 95 2- (S)P, Line 2; 3- F_1; 4- (R)BC1; 5- (S)BC2; 6- Resistant DNA pool F_2 plants; 7- Susceptible DNA pool F_2 plants M: 100 bp DNA ladder.

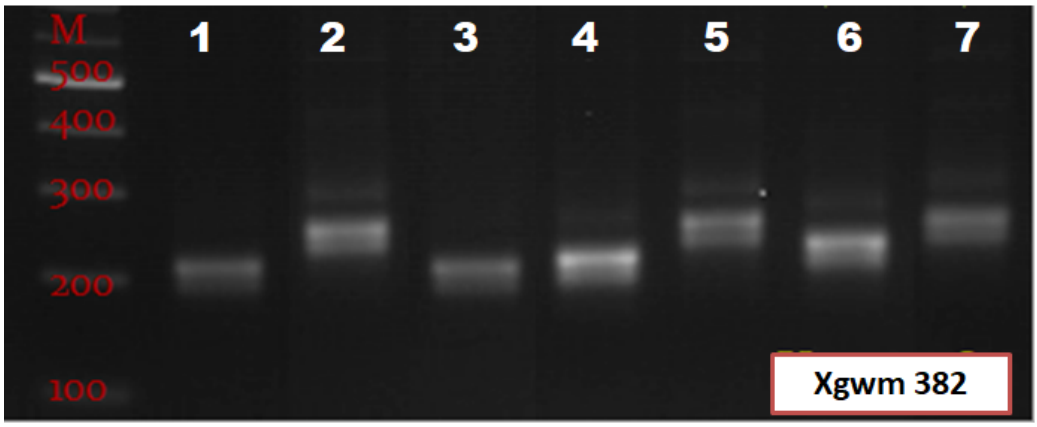

Figure 3: Agarose gel showing the allelic segregation of the Xgwm 382 SSR marker in the analyzed 1-(R) P, Sakha 95 2- (S)P, Line 2; 3- F_1; 4- (R)BC1; 5- (S)BC2; 6- Resistant DNA pool F_2 plants; 7- Susceptible DNA pool F_2 plants M: 100 bp DNA ladder.

Meanwhile, the rest primers xgwm 413 was monomorphic and primer xgwm 44 was polymorphic but without specific band to distinguished resistant or Susceptible parents and F_2. Out of polymorphic patterns of the scorable SSR primers among the used six populatins are shown in Tables (25). The fragment patterns of SSRs using primers exhibited a total of 12 amplified fragments for cross Line 2 × Sakha 95, with different sizes ranged from 160 to less than 186 bp.

Table (25): Numbers and types of the amplified DNA bands as well as the total polymorphism percentage generated by the five SSR primers for Stripe rust.

Primer	Total bands	Monomorphic bands	Polymorphic bands	Polymorphism percentage
Xgwm 44	3	0	3	100%
Xgwm 18	2	0	2	100%
Xgwm 501	3	0	3	100%
Xgwm 382	3	0	3	100%
Xgwm 413	1	1	0	0
Total	12	1	11	

Stem Rust

Polymorphism patterns were observed among the studied populations for cross Sakha 94 × Misr 1. A total of five SSR primers were initially used to

establish SSR fingerprints for this cross. Only two primers successfully generated reproducible polymorphic and scorable bands xwmc 453 and xgwm533.

Moreover, using xwmc 453 Fig 4 , most of the resistant F_2 plants presented the same DNA with 187 and 200 bp bands as Sakha 94 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA bands or presented the same DNA band as Misr 1 or the susceptible DNA bulk did. Similarly, most of the susceptible F_2 plants presented the same DNA with 195 and 205 bp bands as Misr 1 or the susceptible DNA bulk did, and most of the resistant F_2 plants did not present these DNA band or presented the same DNA band as Sakha 94 or the resistant DNA bulk did.

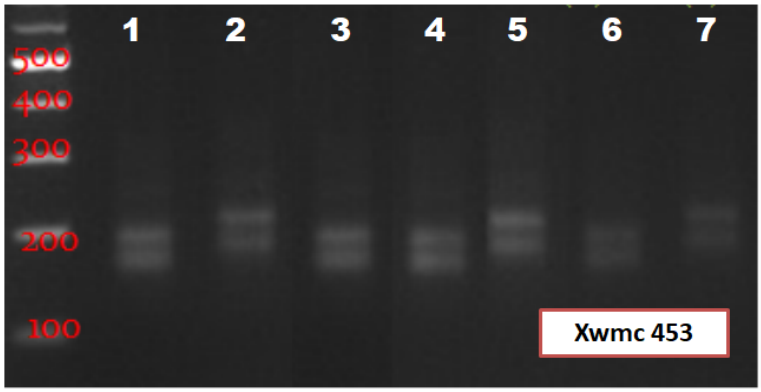

Figure 4: Agarose gel showing the allelic segregation of the Xwmc 453 SSR marker in the analyzed 1-(R) P, Sakha 94 2- (S)P, Misr1; 3- F_1; 4- (R)BC1; 5- (S)BC2; 6- Resistant DNA pool F_2 plants; 7- Susceptible DNA pool F_2 plants M: 100 bp DNA ladder.

With respect, primer Xgwm 533 Fig 5, most of the resistant F_2 plants presented the same DNA with 120 bp band as Sakha 94 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA band or presented the same DNA band as Misr 1 or the susceptible DNA bulk did. Similarly, most of the susceptible F_2 plants presented the same DNA with 150 bp band as Misr 1 or the susceptible DNA bulk did, and most of the resistant F_2 plants

did not present these DNA band or presented the same DNA band as Sakha 94 or the resistant DNA bulk did.

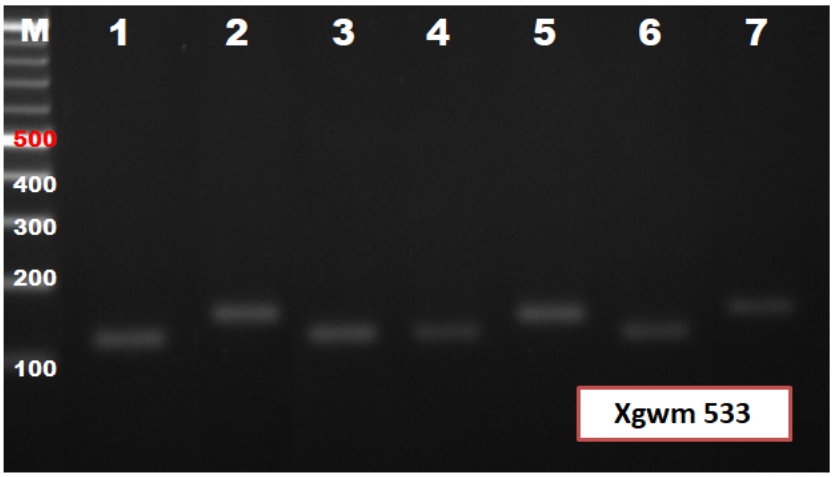

Figure 5: Agarose gel showing the allelic segregation of the Xgwm 533 SSR marker in the analyzed 1-(R) P, Sakha 94 2- (S)P, Misr1; 3- F_1; 4- (R)BC1; 5- (S)BC2; 6- Resistant DNA pool F_2 plants; 7- Susceptible DNA pool F_2 plants M: 100 bp DNA ladder.

Meanwhile, the primer xwmc 633 was monomorphic with band 150 bp **Fig 6**. Also, the rest two primers did not score any amplified bands even they were repeated twice.

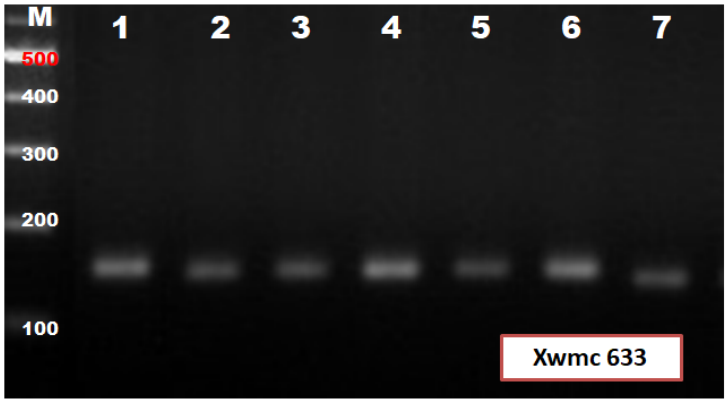

Figure 6: Agarose gel showing the allelic segregation of the Xwmc 633 SSR marker in the analyzed 1-(R) P, Sakha 94 2- (S)P, Misr1; 3- F_1; 4- (R)BC1; 5- (S)BC2; 6- Resistant DNA pool F_2 plants; 7- Susceptible DNA pool F_2 plants M: 100 bp DNA ladder.

The five discriminatory SSR primer pairs were used to evaluate the genetic diversity of stem rust resistance in six population for cross Sakha 94 × Misr1. These primer pairs revealed a total of 7 alleles ranging from one to four alleles per locus **(Table 26)**.

Table (26): Numbers and types of the amplified DNA bands as well as the total polymorphism percentage generated by the five SSR primers for stem rust.

Primer	Total bands	Monomorphic bands	Polymorphic bands	Polymorphism percentage
Xwmc 453	4	0	4	100%
Xgwm 533	2	0	2	100%
Xwmc 633	1	1	0	0
Xgwm 319	-	-	-	-
Xgwm 47	-	-	-	-
Total	7	1	6	

Many molecular markers used for MAS of the target genes and they have also been used to detect disease resistance genes, such as Sr26 for resistance to stem rust (Qureshi et al., 2018 a), Yr34 and Yr48 for resistance to stripe rust (Qureshi et al., 2018 b). Due to an importance of Sr2 for resistance against stem rust and providing durable resistance against all prevalent stem rust races including the Ug99 group of races, Sr2 has been widely deployed with other major genes in world (Singh et al. 2011). Here the data exploited Xgwm533 marker for the cross Sakha 94 × Misr 1 and screening F_2 and represented parents genotypes as well back crosse. The Xgwm533 marker perfectly discriminate them (Mago et al. 2011; Malik et al. 2013).

In conclusion, the results of this investigation provided some SSR based molecular markers associated either positively or negatively with wheat genotypes to rust resistance which could be used to enhance breeding programs aimed to improve their rusts resistance by pyramiding genes controlling this trait by the aid of marker assisted selection. It is feasible that more markers can be generated for

rusts resistance if more and extensive SSR primers were used. At least, the SSR markers developed from this study could be consequently be used in any further study to identify rusts resistance genotypes in wheat which could be used to enhance breeding programs aimed to improve their rusts resistance. This concept has been advocated by several investigators who stated that molecular markers have several advantages over the traditional phenotypic markers that were previously available to plant geneticists. They offer great scope for improving the efficiency of conventional plant breeding by carrying out selection not directly on the trait of interest but on molecular marker linked to that trait. In addition, this approach is more reliable, environment independent, reproducible, rapid and cost-effective which can reduce the required time for wheat breeding programs.

ENGLISH SUMMARY

5-SUMMARY

In the present study, the field work was conducted at the Experimental Farm of Sakha Agricultural Research Station during the period from 2014/2015 to 2016/ 2017. In addition, the molecular study was conducted at Genetic Engineering and Tissue Culture Lab., accredited based on ISO 17025:2005, Genetics Department, Faculty of Agriculture, Kafrelsheikh University.

The main objectives of this study can be defined in the following points: -

1. Studying the nature of inheritance of stripe and stem rusts disease resistance caused by *Puccinia striiformis* and *Puccinia gramenis f.sp. tritici*, respectively.
2. Studying the natural inheritance of some agronomic traits including grain yield and its components.
3. Detection of SSR markers associated with strip and/or stem rusts resistance in studied breed wheat crosses.

In 2014/2015 season, six parental wheat genotypes, i.e., Line 1, Line 2, Misr 1, Shandweel 1, Sakha 94 and Sakha 95 were sown to produce the following crosses, (Line 1 × Misr 1), (Line 2 × Sakha 95), (Shandweel 1 × Misr 1), (Sakha 94 × Misr 1) and (Sakha 94 × Sakha 95).

In 2015/2016 season, the parents and the five obtained F_1's were sown to produce F_2 seeds of the five crosses and two their backcrosses (BC_1 and BC_2).

In 2016/2017 season, all six generations of each cross [the two parents, F_1, F_2, BC_1 and BC_2] were sown in a randomized complete block design with three replications. All recommended culture practices were applied at the proper time.

The experiment was surrounded by highly susceptible wheat cultivars to rusts as a spreader.

The data were recorded for; stripe and stem rust diseases, days to heading, days to maturity, plant height, number of spikes/plant, number of kernels /spike, 100 kernels weight and grain yield/plant. The following statistical and genetical parameters were estimated for different traits: mean, variances, standard deviation, type of gene actions (by using generation mean and generation variance methods) heterosis, inbreeding depression, potency ratio, heritability estimates and predicted genetic advance from the selection. Finally, nature of inheritance of resistance to stripe and stem rust diseases were estimated by using chi-square (X^2) test.

The obtained results could be summarized as follows:

Agronomical experiments

A-Agronomic traits

1. The F_1 mean values exceeded the mid-parent for grain yield/plant for the first (Line 1 × Misr 1), third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses detecting the presence of dominance towards the better parent.
2. The variances of the non-segregating populations (P_1, P_2, and F_1) were the lowest than those of segregating populations (F_2, BC_1, and BC_2). This indicates that they were more homogeneous than the F_2 and both B.C populations which showed greater variances.
3. The fifth cross (Giza 171 × Misr 2) was the best for all the studied traits. Consequently, it would be interested in breeding programmes for improving traits for yield and its components,
4. Heterosis estimates relative to mid-parent and the better parent for grain

yield per plant were positive and highly significant for the first (Line 1 × Misr 1), third (Shandweel 1 × Misr 1) and fourth (Sakha 94 × Misr 1) crosses.

5. Highly significant negative heterosis (desirable) relative to mid-parent and a better parent for the first (Line 1 × Misr 1), second cross (Line 2 × Misr 1) and third (Shandweel 1 × Misr 1) crosses for days to maturity.
6. Some percentages of inbreeding depression of grain yield per plant were positive; this was logic since the expression of heterosis in F_1 will be followed by a considerable reduction in F_2 generation.
7. For grain yield per plant, potency ratio values were more than unity indicating the presence of over dominance for all the studied crosses except for the second (Line 2 × Sakha 95) and fifth (Sakha 94 × Sakha 95) crosses which had value less than unity, indicating the presence of partial dominance for this trait in these crosses.
8. Dominance effects are several times larger than additive one in most crosses, this might indicate that dominance gene effects play the major role in controlling the genetic variation of most studied characters. Also, genetic interaction components were important in the inheritance of grain yield and its components and the other studied traits.
9. Additive genetic variance (1/2D) was greater than that of dominance variance (1/4H) in all the studied crosses for days to heading, days to maturity, number of spikes per plant, 100- kernel weight as well as for plant height except the third cross (Shandweel 1 × Misr 1), indicating that the selection for these traits might be more effective in an early generation for improving such traits in our studied crosses.

10. Heritability estimates in a broad sense were high for all the studied traits in all crosses, ranged from 92.41% for plant height in the fourth cross (Sakha 94 × Misr 1) to 99.82% for number of kernels/spike in the first (Line 1× Misr 1) and second (Line 2× Sakha 95) crosses.
11. Heritability estimates in narrow sense were low to relatively high for all the studied traits in all crosses, the best cross was the fifth one (Sakha 94 × Sakha 95) where it showed high values of narrow sense heritability and predicted genetic advance under selection for grain yield and some of its component so using it in a breeding program will be useful.

B-Inheritance of resistance to stripe and stem rust diseases

1. All crosses exhibited highly significant negative heterotic effects relative to mid-parent and a better parent for the stripe and stem rusts except the fifth cross (Sakha 94 × Sakha 95) which had highly significant positive (undesirable) relative to the mid-parent.
2. highly significant negative inbreeding depression was found for stripe rust in five studied crosses. Moreover, highly significant negative inbreeding depression was found for stem rust in all studied crosses except for the first (Line 1 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses which had highly significant and positive values.
3. Moreover, over dominance and partial dominance ranges were found for most cases either in a stripe or stem rust diseases.
4. The additive genetic component was found to be greater in its magnitude than dominance effect in the inheritance of resistance to stripe rust disease. While the two genetic components (additive and dominance) exhibited equal

role and had considered magnitude in the inheritance of resistance to stem rust disease.

5. The estimates of heritability in broad sense were very high in all studied crosses, indicating that the phenotypic variability was mostly attributed to genetic effects. Narrow sense heritability estimates were ranged from high to moderate in all cases.
6. The high and desirable values of heritability in narrow sense for the two diseases resistance were obtained from the second (Line 2 × Sakha 95), fourth (Sakha 94 × Misr 1) and fifth (Sakha 94 × Sakha 95) crosses, referring the importance role of additive gene effects for the two rust diseases. Meanwhile, the first (Line 1 × Misr 1) and third (Shandweel 1 × Misr 1) crosses gave moderately desirable values of heritability in narrow sense.
7. Maximum predicted genetic advances as percent of F_2 mean (Δg) were achieved for stripe and stem rusts disease in the fourth cross (Sakha 94 × Misr 1) and fifth cross (Sakha 94 × Sakha 95).

C-Molecular analysis

- Over 10 pairs of SSR primers were used to identify the polymorphism between the stripe and stem rust resistant and the susceptible DNA bulks. Genetic diversity analysis of six populations (P1, P2, F_1, BC_1, BC_2 and F_2) resulted from crosses Line 2 × Sakha 95 for stripe rust and Sakha 94 × Misr 1 for stem rust based on molecular markers was an important aim for this study.
- Polymorphism patterns were observed among the studied populations for cross Line 2 × Sakha 95. A total of five SSR primers were initially used to establish SSR fingerprints for this cross. Only three primers successfully

generated reproducible polymorphic and scorable bands xgwm18, xgwm501 and xgwm382. Moreover, using xgwm18, xgwm501 and xgwm 382 most of the resistant F_2 plants presented the same DNA with bands size 160 bp, 165bp and 200bp, respectively. as Sakha 95 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA band or presented the same DNA band as Line 2 or the susceptible DNA bulk did. Meanwhile, the rest primers xgwm 413 was monomorphic and primer xgwm 44 was polymorphic but without specific band to distinguished resistant or Susceptible parents and F_2.

- Polymorphism patterns were observed among the studied populations for cross Sakha 94 × Misr 1. A total of five SSR primers were initially used to establish SSR fingerprints for this cross. Only two primers successfully generated reproducible polymorphic and scorable bands xwmc 453and xgwm533. Moreover, using xwmc 453 and xgwm533 , most of the resistant F_2 plants presented the same DNA with bands size 200 bp and 120bp, respectivily as Sakha 94 or the resistant DNA bulk did, and most of the susceptible F_2 plants did not present these DNA bands or presented the same DNA band as Misr 1 or the susceptible DNA bulk did. Meanwhile, the primer xwmc 633 was monomorphic with band 150 bp. Also, the rest two primers did not score any amplified bands even they were repeated twice.

REFERENCES

6. REFERENCES

Abd El-Aty, M. S. and Y. S. Katta (2002). Genetic analysis and heterosis of grain yield and related traits in bread wheat (*Triticum aestivum* L.) J. Agric. Res. Tanta Univ., 28(2): 287-300.

Abd El-Aty, M. S. M.; Y. S. Katta and **M. A. El-Hity. (2005).** Estimation of genetic parameters using six populations of different wheat crosses. Egypt.J. Plant Breed; 9 (1):17-30.

Abd El-Latif, A. H. and Omayma A. Alaa EL–Dein (2000). Quantitative studies on wheat resistance, to stripe rust caused by *Puccinia striiformis tritici*. J.Agric. Sci . Mansoura Univ., 25(4): 1901- 1908.

Abd El-Nour, Nadia A. R. (2006). Gene effect on yield and yield components for three bread wheat crosses (*Triticum aestivum* L.). Egypt. J. Agric. Res., 84(3): 1157-1170.

Abd El-Nour, Nadia A. R. (**2011).** Estimation of genetic parameters for grain yield and its components in three breed wheat crosses under low input of nitrogen fertilizer. Egypt. J. Agric. Res., 89 (3) 959-973.

Abd El-Nour, Nadia A. R. and M. Kh. Mosherf (2006). Gene effect and variances in three wheat crosses using the five parameters model. Egypt J. Plant Breed, 10(1): 305-318**.**

Abdel-Hafez, A.G.; M.E. Mosalem.; I.I. El-Essawy and M.S. Hathout (2003). Gene effects, variance components, heritability and genetic advance from selection for earliness in bread wheat. Proc.10th Conf. Agron., Suez Canal Univ., Fac., Environ. Sci., El-Arish, 1188-1200.

Aboshosha, A. M. and S.M. Hammad (2009). Estimation of parameters for yield and yield components and some agronomic characters in two crosses of bread wheat (*Triticum aestivum* L.). J. Agric. Sci.,

Mansoura Univ., 34(5): 4293-4300.

Afiah, S.A.N. (1999). Combining ability, association and path coefficient analysis of some wheat (*T. aestivum* L.) a diallel crosses under desert conditions Mansoura. J. Agric. Res. 24 (4): 1583-1596.

Aglan, M. A. (2003). Breeding studies on wheat resistance to leaf and stem rusts and its association with yield and its components. M.Sc. Thesis, Minufiya Univ., Egypt.

Ahmadi, J.; S. F. Orang; A. A. Zali; B. Yazdi–Samadi; M. R. Ghannadha and A. R. Taleei (2007). Study of yield and its components inheritance in wheat under drought and irrigated conditions. J. Sci. & Technol. Agric. & Natur. Resour., 11(1): 214-228.

Akfirat, S. F.; Y. Aydin; F. Ertugrul; S. Hasancebi; H. Budak; K. Akan; Z. Mert; N. Bolat and A. A. Uncuoglu, (2010). A microsatelite marker for yellow rust resistance in wheat. Ce-real Res. Commun. 38:203-210.

Al-Kaddoussi, A.R. 1996. Using genetic components for predicting new recombinant lines crosses of Egyptian wheat *(Triticum aestivum L.)*. Zagazig J. Agric. Res. 23:463 –475.

Al-Kaddoussi, A.R., and M.M. Eissa. 1990. Gene action and prediction of some yield attributes in four wheat crosses *(Triticum aestivum L.)*. Annals of Agric. Sci., Moshtohor, 28: 2013-2022.

Allard, R.W. (1960). Principles of plant breeding. New York: John Wiley & Sons, Inc. 485 pp.

Amin, K. P. **and R. F. Park**. **(2007).** Evaluation of seedling and adult plant resistance to stem rust in European wheat cultivars**.** Euphytica, 155(1): 87-105.

Anderson JA et al. (2001) DNA markers for Fusarium head blight resistance QTLs in two wheat populations Theoretical and Applied Genetics 102:1164-1168.

Ashoush, H. A.; A. A. Hamada and I. H. Darwish. (2001). Heterosis and combining ability in the F_1 and F_2 diallel crosses of wheat (*Triticum aestivum* L.). J. Agric. Sci., Mansoura Univ., 26(8): 2579-2592.

Awaad, H. A. (2002). Assessment of some genetic parameters using diallel cross fashion and their implications in breeding programs of bread wheat (*Triticum aestivum L.*). Zagazige. J. Agric. Res., 29 (4): 1125-1141.

Aykuttonk, F.; E. Ilker and M. Tosun.(2011). Quantitative inheritance of some wheat agronomic traits. Bulgarian J. of Agric. Sci., 17 (6): 783-788**.**

Babiker, E.; A. M.H Ibrahim; Y. Yen and J. Stein, (2009). Identification of a microsatellite marker associated with stem rust resistance gene Sr35 in wheat. Australian journal of crop science, (3);195-200.

Bahadur, P. and R. C. Mathuria (2008). Genetics of stem rust resistance in four bread wheat cvs. HD2733, HD2768, HD2781 and HD2784. Indian Phytopath, 61 (4): 445-448.

Bai, D.; R. Knott, and J. M. Zale (1997). The inheritance of leaf and stem rust resistance in *Triticum monococcum* L. Can. J. Plant Sci., 78(2): 223-226.

Bhardwaj. **S.C. (2013).** *Puccinia Triticum* interaction: an update. Indian Phytopath, 66 (1): 14-19**.**

Biffen, R. H. (1905). Mendel's laws of inheritance and wheat breeding. J. Agric. Sci., 1 : 4-48

Boyed, L.A. (2005) Centenary review: Can Robigus defeat an old enemy? – Yellow rust of wheat. J Agric Sci 143:1–11.

Carmen D.; G. Vanegas; F.David; G. James and A. Kolmer. (2008). Genetics of stem rust resistance in the spring wheat cultivar Thatcher and the enhancement of stem rust resistance by Lr3**.** Euphytica 159(2): 391–401.

Ceron, A. and F. Angel (2001). Genetic diversity in sugarcane hybrids in Colombia measured using molecular markers. Proc. Int. Soc. Sugarcane Technol. 24:626-627.

Chandra, D.; M. A. Islam and N. C. D. Barma. (2004). Variability and interrelationship of nine quantitative characters in F_5 bulk of five wheat crosses. Pakistan J. of Biol. Sci., 7(2): 1040-1045.

Charan, R. and P. Bahadur (1997). Inheritance of resistance to stem rust in five bread wheat cultivars. Wheat Info. Serv., 84(4): 40-48.

Chen, X. m. and R.F. Line (1995). Gene action in wheat cultivars for durable; high temperature, adult plant resistance and interaction with race specific, seedling resistance to *puccinia striiformis.* Phytopathology, 85(5): 567 - 572.

Cheng, X. M.; J. S. Xu; S. Xia; J. X. Gu; Y. Yang; J. Fu; X. J. Qian; S. C. Zhang; J. S. Wu and K. D. Liu (2009). Development and genetic mapping of microsatellite markers from genome survey sequences in Brassica napus. Theor. Appl. Genet., 118:1121–1131.

Cheruiyot, D.; P. O. Ojwang; P. N. Njau; P. F. Arama; G K. Macharia (2014). Genetic analysis of adult plant resistance to stem rust (*Puccinia graminis* f. sp. tritici) and yield in wheat (*Triticum aestivum* L.). Acta Advances in Agricultural Sciences, 2(10): 49-63.

Chowdhry, M. A.; A. Ambreen and I. Khaliq (2002). Genetic control of some polygenic traits in *aestivum species*. Asian J. of Plant Sci., 1(3): 235-237.

Chowdhry, M. A.; M. Iqbal; G. M. Subhani and I. Khaliq (2001). Heterosis, Inbreeding depression and line performance in crosses of *Triticum aesitivum* .Pakistan J. of Biol. Sci., 4 (1) :56-58.

Cocherhan, C. C. (1961). Implication of genetic variance in hybrid breeding program. Crop Sci., 1: 52-74.

Darwish, I. H. and H. A. Ashoush (2003). Heterosis, gene effect, heritability and genetic advance in bread wheat. Minufiya J. Agric. Res., 28(2): 433 – 444.

Darwish, M. A. H. A. (2011). Genetical studies on some rusts in bread wheat. Ph.D. Thesis, Fac. of Agric, Tanta, Univ., Egypt.

Datta D.; S. K. Nayar; M. Prashar and S. C. Bhardwaj. **(2009)**. Inheritance of temperature-sensitive leaf rust resistance and adult plant stripe rust resistance in common wheat cultivar PBW343. Euphytica, 166 (2): 277-282.

Dixon, J.; H. J. Braun, P. Kosina and J. Crouch (2009). Wheat facts and futures 2009. Mexico, D.F.: CIMMYT.

Doyle, J.J. and J.L. Doyle (1990). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Focus, 12: 13-15.

El-Daoudi, Y.H.; Ikhlas S. Shenoda; Enayat, H. Ghaenm; S.A. Abu El-Naga; S.O. Sherif; M.O. Khalifa; R.A. Mitkees and A.A. Bassiouni (1996). Stripe rust occurrence in Egypt and assessment of grain yield loss in 1995. Proc. Du Symposium Regional Sur les Maladies des Cerales et des Legumineuses Alimentaries11-14 Nov.;Rabat, Maroc.,PP.341-351.

El-Fadly, G. A.; H. E. Galal, T. M. Shehab El-Din and A. H. Abd El-Latif (1991). Inheritance of wheat stem rust resistance at the adult stage under field conditions. J. Agric. Res. Tanta Univ., 17(2): 416-425.

El-Hawary, M.N.A. (2010). Breeding for stress tolerance in some bread wheat. Ph. D. Thesis, Fac. of Agric, Mansoura Univ., Egypt.

El-Hosary, A. A.; M.E. Riad; R.A. Nagwa and A.H. Manal (2000). Heterosis and combining ability in durum wheat. Proc. 6th Conf. Agron., Minufiya Univ. Sept., 2000: 101-117.

Ellis J.G.; E.S. Lagudah; W. Spielmeyer and P.N. Dodds. (2014). The past, present and future of breeding rust resistant wheat. Frontiers in Plant Science **5**: 641.

El-Refaey, R. A.; A. A. El-Gammaal; M. A. El-Moselhy and A. A. El-Naggar (2015). Quantitative inheritance of some barley agronomic traits under water stress conditions. J. Agric. Res. Kafr El-Sheikh Univ., 41(3): 885-901.

El-Sayed, E. A. M. and G. A. El-Shaarawy. (2006). Genetical studies on yield and some agronomic characters in some bread wheat (*Triticum aestivum* L.) crosses. J. Agric. Sci., Mansoura Univ., 31(8): 4901-4914.

Esmail, R. M. and S. A. Khattab (2002). Genetic behavior of yield and its components in three bread wheat crosses. Minufiya j. agric. Res., 27(2): 215 -224.

Falconer, D. S. (1989). Introduction to Quantitative Genetics .3rd ed., John Wiley&Sons, Inc., 650 Third Avenue, New York,Ny 10158.

Farooq, J. and I. Khaliq (2004). Estimates of heterosis and heterobeltiosis of some quantitative characters in bread wheat crosses. Asian j. of Plant Sci., 28(3): 508-511.

Feuillet, C.; M. Messmer; G. Schachermayr and B. Keller (1995). Genetic and physical characterisation of the Lr1 leaf rust resistance locus on wheat (*Triticum aestivum* L.). Mol. Gen .Genet., 248: 553-562.

Fida, H.; M. Ashraf; S. S. Mehdi and M. T. Ahmad (2004). Estimation of heterosis for grain yield and its related traits in wheat (*Triticum aestivum* L.) under leaf rust conditions. J. of Bio. Sci., 5 (4): 637-644.

Flor, H. H. (1955a). Host-parasite interaction in flax rust – its genetics and other implications. Phytopath. , 45(4): 680-685.

Flor, H. H. (1955b). Inheritance of reaction to rust in flax. J. Agric. Res., 74(2): 241-262.

Flor, H. H. (1956). The complementary genetic system in flax and flax rust. Adv. Genet., 8(2): 29-54.

Flor, H. H. (1971). Current status of gene-for-gene concept. Annu. Rev. Phytopath. 9(2): 275-296**.**

Gamble, E. E. (1962). Gene effects in corn (*Zea mays* L.). I-Separtion and relative importance of gene effects for yield. Can. J. Plant Sci., 42:339-348.

Ganeva, G.; M. Todorova and H. Kurzhin, (2001). Inheritance of the resistance to the causative agent of the brown rust in wheat varieties and lines. Rasteniev" dni Nauki38 181-185. (C.F. Review of Plant Pathol) 81: 9352.

Ghimiray, T.S. and K.K. Sarkar, 2000. Estimations of genetic parameters for some quantitative traits in wheat (*Triticum aestivum* L.) grown in Terai soils of West Bengal. Environment and Ecology 18:338-340 (C.F. CAB abst. 2000/2002).

Hamada, A. A. (2003). Gene effects for some agronomic traits in three bread wheat crosses. Annals Agric Sci., Ainshams Univ. Cairo, 48 (1): 131-146.

Hamam, **K .A. (2013).** Estimation of genetic parameters using five populations model in three bread wheat crosses under normal irrigation and drought stress. j. Plant bread. 17(2): 63-79.

Hammad, S. M. and M. S. M. Abd El-Aty (2007). Diallel analysis of genetic variation for earliness and yield and its components in bread wheat. J. Agric. Res., Kaferel-Sheikh Univ., 33(2): 88-100.

Hassan, M. S.; R. A. El-Said and S. H. Abd-El-Haleem (2013). Estimation of heritability and variance components for some quantitative traits in bread wheat (*Triticum aestivum* L.) World Appl. Sci. J., 27 (8): 944-949.

Hayman, B. I. (1954). The theory and analysis of diallel crosses. Genetics. 39:789-809.

Hayman, B. I. and K. Mather. (1955). The description of genetic interaction in continuous variation. Biometrics, 11:69-82.

Hendawy, F. A.; H. A. Dawwam; M. A. Abo Shereif and E. L. El-Massry (2009). Detection of epistasis in the inheritance of grain yield and its components in bread wheat. Minufiya J. Agric. Res., 34(2):625-640.

Hendawy, H. I. (1998). Combining ability and genetics of specific characters in certain diallel wheat crosses. Ph.D. Thesis, Faculty of Agric., Menofiya Univ. Egypt.

Hendawy, H. I. and S.A. Seleem. (2007). Studies genetic behavior for yield and its components in some bread wheat crosses . J. Agric. sci. Mansoura Univ., 32(3): 1659-1670.

Hermas, **Gamalat, A. and S. A. El-Sawi (2015).** Inheritance of stem rust resistance and some yield components in crosses from five egyptian wheat cultivars. Egypt. J. Plant Breed, 19(1):71 – 87.

Hitta, L.; S. Manni and M. Foolad (1995). Development of PCR-based markers to identify rice blast resistance gene Pi-2lt in a segregating population. Theor. Appl. Genet., 91: 9-14.

Jan M.; G. Hassan, and K. Raziuddin (**2005).** Estimates of heterosis and heterobeltiosis for morphological traits in wheat (*Triticum aestivum L*.) Pakistan J. Bio. Sci., 9(8): 1261-1264.

Jin Y, Szabo and L.M. Carson (2010). Century-old mystery of *Puccinia striiformis* f. sp. tritici life history solved with the identification of Berberis as an alternate host. Phytopathology 100:432-435.

Johnson R. (1992). Past, present and future opportunities in breeding for disease resistance, with examples from wheat. Euphytica, 63:3-22.

Johnson, H. W.; H. F. Robinson and R. E. Comstock (1955). Estimation of genetic and environmental variability in soybeans. Agron. J., 47:314-322.

Kaur, J. and H. S. Bariana (2010). Inheritance of adult plant stripe rust resistance in wheat cultivars Kukri and Sunco. J. of Plant Pathology, 92 (2): 391-394.

Kearsey, M. J. and H. S. Pooni (1996). The genetical analysis of quantitative traits. Chapman and Hall, 1st edition, London, p 46.

Khan, M. I.; G. S. Khattak; A. J. Khan; and S. J. Khan (2014). Genetic response of grain yield in wheat (*Triticum aestivum* L.) crosses. Songklanakarin J. Sci. Technol, 36 (4): 397-406.

Khattab, A. B. (2009). Genetic behavior of some traits of bread wheat (*Triticum aestivum* L.). J. Agric. Res. Kafr El-Sheikh Univ., 35(2): 446-479.

Khattab, S. A. M.; R. M. Esmail and A. M. F. Al-Ansary (2010). Genetical analysis of some quantitative traits in bread wheat (*Triticum aestivum* L.). New York Sci. J. 3(11):152-157.

Kolmer J.A. (2005). Tracking wheat rust on a continental scale. Curr Opin Plant Biol 8: 441-449.

Kolmer, J.A. (1966). Genetics of resistance to wheat leaf rust Ann. Rev of Phytopathology, 34:435-455.

Koumber, R. M. and A. A. El-Gammaal (2012). Inheritance and gene action for yield and its attributes in three bread wheat crosses (*Triticum aestivum* L.) World J. of Agric. Sci., 8 (2): 156-162.

Laghari, K. A.; M. A. Sial; M. A. Arain; A. A. Mirbahari; A. J. Pirzada; M.U. Dahot and S.M. Mangrio. (2010). Heritability studies of yield and yield associated traits in bread wheat. Pak. J. Bot., 42 (1): 111-115.

Liu, C.F., and S.M. Ma. (1994). A study of the heritability, genetic advance and correlation of the main agronomic characters in spring wheat. Ningxia J.Agric. and Forestry Sci. and Techn.6:7-9 (C.F. CAB . Abstracts 1995).

Ljubicic, N.; S. Petrovic; M. Kostic; M. Dimitrijevic; N. Hristov; A. Kondic-spika and R. Jevtic (2016). Diallel analysis of some important grain yield traits in bread wheat crosses. Turk J Field Crops, 22(1): 1-7.

Loegering, W. Q. (1984). Genetics of the pathogen – host association. Pages 165-192 in the cereal rusts, Vol. 1. Origins , Specificity, Structure and physiology. W. R. bushnell and A. P. Roelfs, eds. Academic press, New York. 546 pp.

Long, L.; F. Yao; C. Yu; X. Ye; Y. Cheng;Y. Wang;Y. Wu1; J. Li; J. Wang; Q. Jiang; W. Li; J. Ma; Y. Liu; M. Deng; Y. Wei; Y. Zheng and G. Chen,(2019). Genome-Wide Association Study for

Adult-Plant Resistance to Stripe Rust in Chinese Wheat Landraces (*Triticum aestivum* L.) From the Yellow and Huai River Valleys. Front Plant Sci. 16;10:596.

Lowe I.; L. Jankuloski; S. Chao; X. Chen; D. See and J. Dubcovsky (2011). Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat. Theor Appl Genet. 2011 Jun;123(1):143-57.

Ma, J.X.; R.H. Zhou; Y.C. Dong; L.F. Wang; X.M. Wang and J.Z. Jia (2001). Molecular mapping and detection of the yellow rust resistance gene Yr26 in wheat transferred from (*Triticum Turgidum*) L. using microsatellite. Euphytica, 120: 219-226.

Mago R.; G. Brown-Guedira and S. Dreisigacker (2011). An accurate DNA marker assay for stem rust resistance gene Sr2 in wheat. Theor. Appl. Genet. 122: 735-744

Mahgoub, Hayam S. (2001). Quantitative determination of the gene action of stripe, stem and leaf rust resistance in A 6- parent diallel cross of wheat. J. Agric Sci. Mansoura Univ., 26 (1): 147-155.

Mahgoub, Hayam, S. (2006) . Qualitative and quantitative studies on the inheritance of wheat resistance to the three rusts . Egypt. J.plant breed 10(2): 299- 315.

Malik, R.; S. Parveen and MS. Saharan (2013). Characterization of stem rust resistance gene Sr2 in Indian wheat varieties using polymerase chain reaction (PCR) based molecular markers. Afr. J. Biotechnol. 12: 2353.

Mather, K. (1949). Biometrical genetics. Dover Publications, Inc., London.

Mather, K. and J. L. Jinks (1971). Biometrical genetics 2nd ed. Chapman and Hall Ltd., London, pp.382.

Mather, K. and J. L. Jinks (1982). Biometrical genetics 3nd ed. Chapman and Hall., London.

McIntosh, R.A.; J. Silk and T.T. The (1996). Cytogenetic studies in wheat XVII Monosomic analysis and linkage relationships of gene Yr15 for resistance to stripe rust. Euphytica, 89: 395-399.

Menon, U., and S. N. Sharma. (1995). Inheritance studies for yield and yield component traits in bread wheat over the environments. Wheat Info. Ser.80: 1-5.

Menshawy, A. M. and M. Najeeb. (2004). Genetical and pathological studies on certain Egyptian wheat genotypes as effected by both leaf and stripe rusts. J. Agric. Sc. Mansoura Univ. 29(4):2041-2051.

Menshawy, A. M. and W. A. Youssef (2004). Inheritance of resistance to stripe and leaf rusts in spring wheat. Egypt J. Agric. Res., 82 (3):1199 -1211.

Michelmore, R. W.; I. Paran, and R. V. Kesseli. (1991). Identification of markers linked to disease-resistance genes by bulked segregant analysis: A rapid method to detect markers in specific genomic regions by using segregating populations. Proc. natl. Acad Sci. USA 88:9828-9832.

Mohamed, A. I. (2013). Genetic system controlling the yield and its components in three bread wheat (*Triticum aestivum, L.*) crosses. Egypt. J. Agric. Res., 91(2).

Monir, M.; M. A. Chowdhry and M. Ahsan (2007). Generation mean studies in bread wheat under drought condition. Int. J. Agric & Biology. 9 (2):282-286.

Nzuve, F. M.; G. Tusiime; S. Bhavani; P. N. Njau and R. Wanyera (2013). Studies of the genetics of inheritance of stem rust resistance in bread wheat. Afr. J. of Biotechnology, 12(4): 3153-3159.

Olivera, P.; M. Newcomb; L. J. Szabo; M. N. Rouse; J. Johnson; S. Gale; D. G. Luster; D. Hodson; J. A. Cox; L. Burgin; M. Hort; C. A. Gilligan; M. Patpour; A. F. Justesen; M. S. Hovmoller; G. Woldeab; E. Hailu; B. Hundie; K. Tadesse; M. Pumphrey; R. P. Singh, and Y. Jin (2015). Phenotypic and genotypic characterization of race TKTTF of *Puccinia graminis* f. sp. *Triticithat* caused a wheat stem rust epidemic in southern Ethiopia in 2013/14. Phytopathology 105:917-928.

Olson E. L.; G. Brown-Guedira; D. Marshall; E. Stack; R. L. Bowden; Y. Jin; M. Rouse, and M. O. Pumphrey, (2010). Development of Wheat Lines Having a Small Introgressed Segment Carrying Stem Rust Resistance Gene Sr22. Crop science, 50:1823-1830.

Ozkan, H.; T. Yagbasanlar, and I. Genc, (1997). Genetic analyses of yield components, harvest index and biological yield in bread wheat under Mediterranean climatic conditions. Rachis 16:49-52.

Patil, J. V.; A. B. Deokar and R. B. Deshmukh (2000). Genetic analysis of three wheat cultivars for reaction to stem rust of wheat. Indian J. Agric. Res., 34(4): 275-277.

Peng, J.H.; T. Fahima; M.S. Röder and Y.C. Li (1999). Microsatellite tagging of the stripe-rust resistance gene YrH52 derived from wild emmer wheat, *Triticum dicoccoides*, and suggestive negative cross over interference on chromosome 1B. Theor. Appl. Genet., 98: 862-872.

Plaschke, J.; M.W. Ganal and M.S. Röder, (1995). Detection of genetic diversity in closely related bread wheat using microsatellite markers. Theoretical and Applied Genetics 91(6-7):1001-1007.

Priyamvada, S.; M. S. Saharan and R. Tiwari (2011). Durable resistance in wheat. Inter. J. of Gen. and Molec. Biol., 3(8): 108-114.

Qureshi, N.; H.S.Bariana; P. Zhang; R. McIntosh; U.K. Bansal; D. Wong; M.J. Hayden; J. Dubcovsky and M. Shankar (2018b). Genetic relationship of stripe rust resistance genes Yr34 and Yr48 in wheat and identification of linked KASP markers. Plant Dis., 102, 413–420.

Qureshi, N.; P. Kandiah; M.K. Gessese; V. Nsabiyera; V. Wells; P. Babu; D. Wong; M.J. Hayden; H. Bariana and U. Bansal, (2018a). Development of co-dominant KASP markers co-segregating with Ug99 effective stem rust resistance gene Sr26 in wheat. Mol. Breed. 38, 97.

Rathi M.; M. Kumar; V. Singh; V. Kumar S; R.N. Sheokand and L. Chaudhary (2020). Marker assisted screening of breeding population of wheat segregating for stripe rust resistance using SSR markers. International Journal of Chemical Studies. 8(2): 1288-1292.

Ragab, K. E. (2005). Utilization of modern genetic techniques in studying resistance of wheat to some wheat rusts. M.Sc. Thesis, Minufiya Univ., Egypt.

Ragab, K. E. I. (2010). Breeding and genetical studies on resistance to leaf rust disease in wheat. Ph. D. thesis, Minufiya Univ. Egypt.

Randhawa, M. S.; N. S. Bains.; V. S. Sohu.; P. Chhuneja.; R. M. Trethowan.; H. S. Bariana and U. Bansal, (2019). Marker

Assisted Transfer of Stripe Rust and Stem Rust Resistance Genes into Four Wheat Cultivars. Agronomy, 9(9), 497.

Rehman, A. U.; M. Sajjad; S. H. Khan and N. Ahmad (2013). Prospects of wheat breeding for durable resistance against brown, yellow and black rust fungi. J. Agric. Biol., 15(4): 1209–1220.

Robinson, H. F., R. E. Comstock and P. H. Harvey (1951). Genetic and phenotypic correlations in corn and their implications in selection. *Agron. J*., 43: 283-287.

Roder MS et al. (1998) A microsatellite map of wheat Genetics 149:2007-2023.

Said, M. H. (2003). Traditional and molecular breeding of wheat in relation to rust resistance. Ph.D Thesis, Fac. Agric. Kafr El-sheikh, Tanta Univ., Egypt.

Salama, S. M., (2002). Genetic analysis of yield and some yield attributes in some Egyptian wheat cultivars. Zagazig J. Agric. Res. 29 : 1395 –1410.

Salem, A. H., S. A. Nigem , M. M. Eissa, and H. F. Oraby., (2000). Type and magnitude of gene action for some quantitative characters and their implication in applied wheat breeding. Zagazig J. Agric. Res. 27:805 –818.

Salem, A.H.; S.A. Nigem; M.M. Eissa and H.F. Oraby (2000). Type and magnitude of gene action for some quantitative characters and their implication in applied wheat breeding. Zagazig J. Agric. Res., 27:805 –818.

Salgotra, R. K.; K. S. Thakur; G. S. Sethi; and J. K. Sarma (2002). Heterosis in winter X spring wheat crosses. Indian J. Gen., 62(2): 104-106.

Senapati, N.; S.K. Swain and M.C. Patnaik, (1994). Genetics of yield and its components in wheat. Madras Agric. J., 81: 502-504.

Serpoush, M.; M. Khodarahmi and F. Afshari, (2018). Inheritance of Resistance to Stripe Rust (*Puccinia Striiformis* f.sp. *Tritici*) Race 198E154A+ In Wheat cv. Morvarid. Acta Scientific Agriculture 2(7): 27-31.

Shahin, A. A. and Kh. E. Ragab (2015). Inheritance of adult plant stripe rust resistance in wheat cultivars Giza160 and Giza168. J. Plant Prot. and Path., Mansoura Univ., 6 (4): 587 – 596.

Sharma, S. N. and R. S. Sain (2003). Genetic architecture of grain weight in durum wheat under normal and late sown environments. Wheat Information Service, 96: 28-32.

Sharshar, A. M. and Samar M. Esmail (2019). Estimation of Genetic Parameters for some Agronomic Traits, and Resistance to Stripe and Stem Rusts using Six Parameters Model in Three Bread Wheat Crosses. J. of Plant Production, Mansoura Univ.,Vol 10 (12):1139 - 1147.

Sharsher, A. M. (2015). Breeding bread wheat for resistance to some rusts. Ph. D. thesis, Fac. of Agric., Kafer EL Shikh , Univ., Egypt.

Shehab El-Deen, M. T. (2008). Genetic studies on earliness and drought tolerance in bread wheat. M.Sc. Thesis, Fac. of Agric., Cairo, Univ., Egypt.

Shehab El-Din, T. M. and A. H. Abd El-latif. (1996). Quantitative determination of the Gene action of stripe rust resistance in a 6-parent Diallel cross of wheat. J. Agric. Sci. Mansoura Univ., 21 (10): 3461-3467.

Shehab El-Din, T. M.; M. A. Gouda; S. Abouel-Naga and M. M. EL-Shami (1991a). Quantitative study on wheat resistance to stem rust

caused by *puccinia graminis tritici* .J. Agric. Sci. Mansoura Univ., 16 (8): 1298 –1303.

Shehab El-Din, T.M. (1997). Three methods for studying the genetic behavior of heading date and plant height in several wheat crosses. J. Agric. Sci. Mansoura University. 22:1297-1306.

Shehab El-Din. T. M.; M. A. Gouda; S. Abouel-Naga; and M.M. EL-Shami.(**1991b).** Genetic behavior of slow rusting in Sakha 61 against *puccinia graminis tritici* .J. Agric. Sci. Mansoura Univ. 16(8): 1304 –1309.

Sial, M. A; J. Akhter; A. A. Mirbahar; K. D. Jamali; N. Ahmed and H. Bux. (2013). Genetic studies of some yield contributing traits of F2 segregating generation of bread wheat. Pak. J. Bot., 45(5): 1841-1846.

Singh, P. and S. S. Narayanan (1993). Biometrical techniques in plant breeding. First ed. Kalyani Publishers, New Delhi, India.

Singh, R. P.; D. P. Hodson; J. Huerta-Espino; Y. Jin; P. Njau; R. Wanyera; S. A. Herrera-Foessel and R. W. Ward (2008). Will stem rust destroy the world's wheat crop? Advanced Agronomy 98: pp 271-309.

Singh, R. P.; D. P. Hodson; J. Huerta-Espino; Y. Jin; S. Bhavani; P. Njau; S. Herrera-Foessel; P. K. Singh; S. Singh; and V. Govindan (2011). The Emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. Annu. Rev. Phytopathol 49: pp 465–482 .

Singh, R. P.; D. P. Hodson; Y. Jin, J. Huerta-Espino; M. G. Kinyua; R. Wanyera; P. Njau and R.W. Ward (2006). Current status, likely migration and strategies to migrate the threat to wheat production from race Ug99 (TTKS) of stem rust pathogen. CAB

Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources 1: pp, 1-13.

Smith, H. H. (1952). Fixing transgressive vigor in nicotiana rustica. In gowen heterosis, Iowa state College Press. Ames , Ia, U. S. A.

Somers, D.J. and P. Isaac (2004) SSRs from the Wheat Microsatellite Consortium

Stakman, E. C.; D. M. Stewart; and W. Q. Loegering. (1962). Identification of physiologic races of Puccinia graminis var. tritici. ARS, USDA., Agr. Res. Serv. Bull. E6/7. 53pp.

Steel, R. G. D. and T. H. Torrie (1960). Principles and procedures of statistics. Mc-Grow Hill, N. Y.; U.S.A.

Stubbes, R. W.; J. M. Prescott; E. E. Saari and H. J. Dubin. (1986). Cereal disease methodology manual.(CIMMYT) .Mexico PP.222.

Stubbs, R.W. (1985). Stripe rust. In A.P. Roelfs & W.R. Bushnell, eds. The cereal rusts, vol. 2, Diseases, distribution, epidemiology, and control, p. 61-101. Orlando, FL, USA, Academic Press.

Sun Q.; Y. Wei; C. Ni; C. Xie and T. Yang, (2002). Microsatellite marker for yellow rust resistance gene Yr5 introgressed from spelt wheat. Plant Breed. 121:539–541.

Sun, Y.; J. Wang; J.H. Crouch, and Y. Xu, (2010) Efficiency of selective genotyping for genetic analysis of complex traits and potential applications in crop improvement. Mol. Breed, 26, 493–511.

Talbert, L. E.; S. P. Lanning; R. L. Murphy and J. M. Martin (2001). Grain filling duration in Twelve hard red spring wheat crosses: Genetical variation and association with other agronomic traits. Crop Sci., 41: 1390-1395.

Tammam, A. M. (2005). Generation mean analysis in bread wheat under different environmental conditions. Minufiya J. Agric. Res. 30(3): 937-956.

Tervet, I. and R. C. Cassell. (1951). The use of cyclone separation in race identification of cereal rusts. Pytopath., 41: 282-285

Tsilo T.J.; Y. Jin, and J.A. Anderson (2008) Diagnostic microsatellite markersfor the detection of stem rust resistance gene Sr36 in diverse ge-netic backgrounds of wheat. Crop Sci 48:253–261

Ullah, N.; N. Ali.; M. Iqba.; A. Din.; A. H. Shah.; I. Ur Rahman.; H. Ahmad.; Inamullah and G. M. Ali, (2016). Markers assisted selection for multiple stripe rust resistance genes in spring bread wheat lines. Vol. (8) 3:63-74.

Vander Plank, J. E. (1963). Plant disease. epidemics and control. New York: Academis. 349 pp.

Wang C.; Y. Zhang; D. Han; Z. Kang; G. Li; A. Cao and P. Chen,(2008). SSR and STS markers for wheat stripe rust resistance gene Yr26. Euphytica. 159:359–366.

Wang L. F.; J. X. Ma.; R.H. Zhou.; X.M. Wang and J.Z. Jia, (2002). Molecular tagging of the yellow rust resistance gene (Yr10) in common wheat, PI178383 (*Triticum aestivum* L.) Euphytica. 124:71–73.

Wellings, C.R. (2011). Global status of stripe rust: a review of historical and current threats. Euphytica, 179, 129:141.

Xianming, C. and F. L. Roland (1993). Inheritance of stripe rust (yellow rust) resistance in the wheat cultivar, "Carstens V" .Euphtica 71 :107-113.

Xu, H., J. Zhang; P. Zhang, et al., (2014). Development and validation of molecular markers closely linked to the wheat stripe rust

resistance gene YrC591 for marker-assisted selection. Euphytica (198):317–323.

Yadav, R. K. and V. G. Narsinghani. (2000). Heterosis and inbreeding depression in wheat (*Triticum aestivum* L. and *T. durum* Desf.) Ind. J. Gen., 60(4):381-382.

Yadava P. S.; V.K. Mishraa; B. Aruna; R. Chandb; M.K. Vishwakarmaa; N.K. Vasisthaa; A.N. Mishrac; I.K. Kalappanavar and Arun K. Joshi, (2015). Enhanced resistance in wheat against stem rust achieved by marker assisted backcrossing involving three independent Sr genes. Current Plant Biology 2 : 25–33.

Yao, Q.; M. M. He; L. Hou; J. H. Yan; Q. Y. Guo and J. X. Jing, (2017). Genetic analysis and molecular mapping of stripe rust resistance genes in Chinesenative wheat (Triticum aestivum) Lankao 5. Aust. Plant Pathol. 46, 213–221.

Yasen, M. M. M. (2008). Genetical studies on rusts in wheat. M.Sc. Thesis, Fac. of Agric, Mansoura Univ., Egypt.

Youssef, I. A. and M. S. Hamada (2012). Inheritance of stripe rust resistance in five egyptian bread wheat cultivars crossed to four yr,s. j.agric.chem. and biotech.,Mansoura Univ., 3 (11): 425 – 438.

Zaazaa, E. I.; M. A. Hager and E. F. El-Hashash (2012). Genetical analysis of some quantitative traits in wheat using six parameters genetic model. American-Eurasian J. Agric. & Environ. Sci., 12 (4): 456-462.

Zakari, A.; R.A. McIntosh; M.S. Hovmoller; C.R. Wellings; M.R. Shariflou; M. Hayden and H.S. Bariana (2003). Recombination of Yr15 and Yr24 in chromosome 1BS. In: Pogna, N.E., Romano, N., Pogna, E.A., Galterio,G. (eds.), Proc. 10th Int. Wheat Genet.

Symp. Instituto Sperimentale per la Cerealcoltura, Rome 1: 417-420.

Zakeri, A.; F. Afshari; M. Yasaie; A. R. Nikzad and S. Rajaei (2016). Genetic analysis of resistance to stripe rust in some Iranian bread wheat cultivars and elite lines. Crop Br. J. 6 (2): 1-8.

Zennah, K.; J. O. Owuoche; M. A. Okiror and P. N. Njau (2015). Inheritance of stem rust (*Puccinia graminis* Pers. F. Sp. *Tritici ericks* and *E. Hen*) resistance in bread wheat (*Triticum aestivum* L.) lines to TTKST race. Int. J. Agri. & Agri. R., 7(4): 1-13.

Zhang, Z. J.; G. H. Li; S. L. Jin and X. B. Yang (2001). Transgressive segregation, heritability and number of genes controlling durable resistance to stripe rust in one Chinese and two Italian wheat cultivars. Phytopath. 91(4): 680-686.

ARABIC SUMMARY

الملخص العربي

أجريت هذه الدراسة بمزرعة محطة البحوث الزراعية بسخا – مركز البحوث الزراعية فى الفترة من ٢٠١٤/٢٠١٥ الى ٢٠١٦/٢٠١٧، في حين أجريت الدراسات الجزيئية بعمل الهندسة الوراثية وزراعة الأنسجة معتمد على اساس ايزو ١٧٠٢٥ – كلية الزراعة كفر الشيخ – جامعة كفر الشيخ.

وقد كانت الأهداف الرئيسية لهذا البحث هي :-

١. دراسة وراثة مقاومة مرض الصدأ المخطط وصدا الساق الذي يسببه فطر *Puccinia striformis*, *Puccinia graminis f.sp. tritici* على الترتيب.

٢. دراسة وراثة بعض الصفات المحصولية متضمنة المحصول ومكوناته.

٣. تحديد بعض المعلمات لل SSR المرتبطة بصفة المقاومة للصدأ الاصفر وصدا الساق فى بعض الهجن تحت الدراسة.

في الموسم الاول ٢٠١٤/٢٠١٥ تمت زراعة الستة آباء (سلالة ١، سلالة ٢، مصر ١، شندويل ١، سخا ٩٤، سخا ٩٥) وذلك لإنتاج الخمسة هجن الآتية. الهجين الأول (سلالة ١ × مصر ١)، الهجين الثاني (سلالة ٢ × سخا ٩٥)، الهجين الثالث (شندويل ١ × مصر ١)، الهجين الرابع (سخا ٩٤ × مصر ١) والهجين الخامس (سخا ٩٤ × سخا ٩٥).

في الموسم الثانى ٢٠١٥/٢٠١٦ تم زراعة الستة آباء والهجن الخمسة الناتجة منها وذلك للحصول على بذور الجيل الاول، الجيل الثاني والهجن الرجعية لكلا الأبوين لكل هجين.

وفي موسم ٢٠١٦/٢٠١٧ تم زراعة الأجيال الستة لكل هجين (الأبوين والجيل الأول والجيل الثاني والهجين الرجعي الأول والهجين الرجعي الثاني) في تكرارات باستخدام تصميم القطاعات كاملة العشوائية . وتم تطبيق حزمة التوصيات الخاصة بالمعاملات الزراعية وتم إحاطة التجربة بداير من خليط من السلالات والأصناف الحساسة للصدأ المخطط وصدأ الساق لتوفير العدوى الطبيعية. وتم تجميع البيانات آلاتية:-

عدد الأيام حتى طرد السنابل، عدد الأيام حتى النضج الفسيولوجي، طول النبات، عدد السنابل/النبات، عدد حبوب السنبلة، وزن المائة حبة ومحصول الحبوب للنبات، الصدأ المخطط وصدأ الساق. وقدرت الثوابت الوراثية الآتية لكل صفة، المتوسط الحسابى، التباين، الانحراف القياسي، معامل الاختلاف النسبي، نوع الفعل الجيني باستخدام طريقتين الأولى متوسطات الأجيال (Gamble 1962) والثانية تباينات

الأجيال (Mather 1949) ، قوة الهجين، الانخفاض الناتج عن التربية الداخلية، درجة السيادة، درجة التوريث، التحسين الوراثي المتوقع نتيجة الانتخاب بالإضافة إلى دراسة وراثة المقاومة للأصداء باستخدام مربع كاى. كما تم إجراء تجارب معملية لمحاولة تعريف معلمات جزيئية DNA markers مرتبطة بمقاومة مرض الصدأ المخطط وصدأ الساق.

ويمكن تلخيص النتائج كالأتي:-

أولا: التجربة الحقلية:

أ- وراثه الصفات المحصولية:

١. زادت قيم الجيل الاول علي قيم متوسط الاباء لصفة محصول الحبوب للنبات لكل من الهجين الاول (سلالة ١ × مصر ١)، الثالث (شندويل ١ × مصر ١) والرابع (سخا ٩٤ × مصر ١) مما يشير الي وجود السيادة تجاه افضل الاباء.

٢. تباين العشائر غير الانعزالية (الاباء و الجيل الاول) وجد اقل من تباين العشائر للأجيال الانعزالية (الجيل الثاني والهجين الرجعى الاول والثاني) مما يوكد وجود تجانس وراثي اعلى في هذه العشائر.

٣. أظهرت قوه الهجين لصفه محصول الحبوب للنبات بالنسبة لمتوسط الابوين وافضل الابوين قيماً موجبه وعالية المعنوية لكل من الهجين الاول (سلالة ١ × مصر ١) والهجين الثالث (شندويل ١ × مصر ١) وكذلك الهجين الرابع (سخا ٩٤ × مصر ١) بالنسبة لمتوسط الابوين.

٤. أظهرت الهجن الاول (سلالة ١ × مصر ١)، الثاني (سلالة ٢ × سخا ٩٥) والثالث (شندويل ١ × مصر ١) قوة هجين سالبه (مرغوبه) وعالية المعنوية بالنسبة لمتوسط الابوين وافضل الابوين لصفة عدد الايام حتى النضج الفسيولوجي.

٥. كانت درجه السيادة اقل من الوحدة لكل الهجن المدروسة لصفه محصول الحبوب ماعدا الهجينين الاول والثالث مما يشير الي وجود السيادة الجزئية لصفه محصول الحبوب للنبات.

٦. كان الفعل الجيني السيادي اكبر من الفعل الجيني المضيف لمعظم الصفات المدروسة لغالبيه الهجن وهذا يدل علي أن الفعل الجيني المضيف كان أقل أهميه في وراثه هذه الصفات.

٧. التباين الوراثي المضيف كان له الأثر الأكبر في وراثة كل الصفات المدروسة فيما عدا صفتي عدد حبوب السنبلة ومحصول الحبوب للنبات حيث لعب التباين السيادي الدور الأكبر في وراثة هذه الصفة وهذا يشير الي أن الانتخاب لهذه الصفات سيكون أكثر فاعليه في الاجيال المبكرة.

٨. كانت التأثيرات الناتجة عن التفاعل بين العوامل غير الاليلية ذات أهمية فى وراثة محصول الحبوب للنبات ومعظم مكوناته وكذلك الصفات الأخرى.

٩. أظهرت درجه التوريث علي النطاق الواسع قيما عالية في كل الهجن المدروسة في كل الصفات حيث تراوحت من ٩٢,٤١% لصفه طول النبات في الهجين الرابع الي ٩٩,٨٤% لصفة عدد حبوب السنبلة في الهجين الاول.

١٠. أظهرت درجه التوريث علي النطاق الضيق قيما منخفضه الي عالية نسبيا في كل الصفات المدروسة لكل الهجن واظهرت النتائج أن الهجين الرابع كان افضل الهجن، حيث اعطي اعلي قيم لدرجه التوريث علي النطاق الضيق وكذلك للتحسين الوراثي المتوقع وذلك لصفه محصول الحبوب للنبات وبعض مكوناته ولذلك فان استخدام هذا الهجين سيفيد في برنامج تربيه القمح.

ب-وراثه مقاومه الصدأ المخطط وصدأ الساق:

١. اظهرت قوه الهجين بالنسبه لمتوسط الابوين وافضل الابوين لصفتي الصدأ المخطط وصدا الساق قيما سالبه وعاليه المعنويه (مرغوبه) في جميع الهجن المدروسة فيما عدا الهجين الخامس والذي أعطي قوه هجين موجبه وعاليه المعنويه بالنسبه لمتوسط الابوين لصفة صدأ الساق وبالتالي يمكن استخدام هذه الهجن في برنامج تربيه القمح لتحسين صفتي المقاومه لصدأ المخطط و صدأ الساق.

٢. اعطى الانخفاض الناتج عن التربية الداخليه قيما سالبه وعاليه المعنويه بالنسبه لصفة الصدأ المخطط. أيضا كانت قيم الانخفاض الناتج عن التربية الداخلية سالبة وعالية المعنوية لصفة صدا الساق في جميع الهجن المدروسة فيما عدا الهجين الاول والخامس.

٣. لوحظ وجود سياده فائقه، سياده جزئيه في كل من صفة صدأ الساق أو صدأ الاوراق للهجن المدروسه.

٤. كان الفعل الجيني المضيف اكبر من حيث أهميته عن الفعل الجيني السيادي في وراثة صفة المقاومة لمرض الصدأ المخطط . في حين تساوت أهمية كل من الفعل الجيني المضيف والسيادي في وراثة المقاومة لمرض صدأ الساق.

٥. دلت القيم العالية للكفاءة الوراثية بمعناها الواسع في جميع الهجن على القيمة الكبيرة التي يساهم بها التباين الوراثي بالنسبة للتباين الكلي. كما أن قيم الكفاءة الوراثية بمعناها الضيق كانت عالية الى متوسطة مما يعطي مؤشرا بأهمية الدور الذي يلعبه التباين المضيف في وراثة مقاومة الصدأ المخطط وصدأ الساق.

٦. أعطت الثلاثة هجن الثانى (سلالة ٢ × سخا ٩٥) والهجين الرابع (سخا ٩٤ × مصر ١) والهجين الخامس (سخا ٩٤ × سخا ٩٥) قيم عالية مرغوبة لكل من الكفاءة الوراثية بمعناها الواسع والضيق للمقاومة للصدأ المخطط وصدأ الساق . في حين أعطى الهجن الأول (سلالة ١ × مصر ١) والهجين الثالث (شندويل ١ × مصر ١) قيم مرغوبة متوسطة بالنسبة للتحسين الوراثي الراجع للانتخاب. في نفس الوقت فان الهجن السابقة أعطت قيم متوسطات مرغوبة لمكونات التباين الوراثي.

التحليل الجزيئى

- تم استخدام اكثر من ١٠ بوادىء لل SSR فى هذه الدراسة لتحديد الاختلافات الوراثية بين التراكيب الوراثية المستخدمة وهى عباره عن (الاب الاول، الاب الثانى، الجيل الاول، الجيل الثانى، الهجين الرجعى للاب الاول والهجين الرجعى للاب الثانى) والناتجه من هجينين الاول عباره عن (سلاله ٢ × سخا ٩٥) لدراسة صفة المقاومة للصدأ الاصفر والهجين الثانى (سخا ٩٤ × مصر ١) لدراسة صفة المقاومة لصدأ الساق.
- أظهرت النتائج وجود اختلافات خلال الست عشائر الناتجة من الهجين (سلاله ٢ × سخا ٩٥) وذلك من خلال ثلاث بوادىء فقط وهى xgwm18، xgwm 501 و xgwm 382 حيث اعطت هذه البوادىء حزم بحجم جزئى ١٦٠، ١٦٥ و٢٠٠ على التوالى. هذه الحزم ظهرت فى التراكيب الوراثية المقاومة فقط (نباتات الجيل الثاني المجمعة او الاب المقاوم) فى حين غابت فى التراكيب الوراثية الحساسة (نباتات الجيل الثاني المجمعة او الاب الحساس).
- بالنسبة لصفة المقاومة لصدأ الساق تم استخدام خمس بوادىء لل SSR للتفرقة بين الست عشائر الناتجة من الهجين (سخا ٩٤ × مصر ١). حيث أظهرت النتائج ان بادئين فقط نجحا فى اظهار اختلافات بين الست عشائر وهما xgwm 453 وxgwm 533 حيث أعطت حزم بحجم جزئى ٢٠٠ و ١٢٠ على التوالى. هذه الحزم ظهرت فى التراكيب الوراثية المقاومة فقط (نباتات الجيل الثاني المجمعة و الاب المقاوم) فى حين غابت فى التراكيب الوراثية الحساسة (نباتات الجيل الثاني المجمعة او الاب الحساس).

جامعة كفر الشيخ
كلية الزراعة
قسم الوراثة

دراسات وراثية وجزيئية على بعض التراكيب الوراثية من القمح لمقاومة الاصدأ

رسالة مقدمة من

محمود عبداللطيف حسين عبداللطيف

بكالوريوس العلوم الزراعية (وراثة)-كلية الزراعة - جامعة كفر الشيخ ٢٠١٠

ماجستير العلوم الزراعية (وراثة) -كلية الزراعة - جامعة كفر الشيخ ٢٠١٤

للحصول على درجة

الدكتوراه في العلـوم الزراعيـة

قسم الوراثة

كلية الزراعة

جامعة كفر الشيخ

٢٠٢١

جامعة كفر الشيخ
كلية الزراعة
قسم الوراثة

دراسات وراثية وجزيئية على بعض التراكيب الوراثية من القمح لمقاومة الاصدأ

رسالة مقدمة من

محمود عبداللطيف حسين عبداللطيف

بكالوريوس العلوم الزراعية (وراثة)–كلية الزراعة – جامعة كفر الشيخ ٢٠١٠

ماجستير العلوم الزراعية (وراثة) –كلية الزراعة – جامعة كفر الشيخ ٢٠١٤

للحصول على درجة

الدكتوراه في العلوم الزراعية

قسم الوراثة- كلية الزراعة- جامعة كفر الشيخ

لجنة الإشراف

أ.د / على أحمد أبو شوشة
أستاذ الوراثة– كلية الزراعة - جامعة كفر الشيخ

أ.د / اسماعيل عبدالحافظ خطاب

أستاذ الوراثة– كلية الزراعة – جامعة كفر الشيخ

أ.د / أسعد أحمد حماده
رئيس بحوث – قسم بحوث القمح- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية

٢٠٢١