BIOCHEMICAL AND MOLECULAR GENETIC STUDIES ON WHEAT RESISTANCE TO LEAF RUST

BY

ESSAM AHMAD HASSAN MOSTAFA
B.Sc. Agric. Sc. (Horticulture), Cairo University , 1991
M.Sc. Agric. Sc. (Botany), Cairo University , 1999

A thesis submitted in partial fulfillment
of
the requirements for the degree of

DOCTOR OF PHILOSOPHY
in
Agricultural Science
(Genetics)

Department of Genetics
Faculty of Agriculture -Ain Shams University

2006

Approval Sheet

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This thesis for Ph.D. degree has been approved by:

Prof. Dr. Mahmoud Imam Nasr ……………..
Prof. Emeritus of Genetics, Institute of Genetics Engineering and Biotechnology, El-Menoufia University

Prof. Dr. Alia Ahmed Mohamed El-Seoudy ……………..
Prof. Emeritus of Genetics, Faculty of Agriculture, Ain Shams University

Prof. Dr. Fotouh Mohamed A. El-Domyati ……………..
Prof. of Genetics, Faculty of Agriculture, Ain Shams University

Prof. Dr. Sayed Hassan Hassanien ……………..
Prof. Emeritus of Genetics, Faculty of Agriculture, Ain Shams University

Date of Examination 6 / 9 / 2006

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ESSAM AHMAD HASSAN MOSTAFA
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Under the supervision of:

Prof. Dr. Sayed Hassan Hassanien
Prof. Emeritus of Genetics, Dept. of Genetics, Faculty of Agriculture, Ain Shams University (Principal Supervisor)

Prof. Dr. Fotouh Mohamed A. El-Domyati
Prof. of Genetics, Dept. of Genetics, Faculty of Agriculture , Ain Shams University

Prof. Dr. Ibrahiem Mostafa Mahmoud
Prof. Emeritus of Genetics, Statistics and Plant Breeding, Dept. of Genetics & Cytology, Division of Genetics Engineering & Biotechnology, National Research Centre.

ABSTRACT

Essam Ahmad Hassan Mostafa. Biochemical and Molecular Genetic Studies on Wheat Resistance to Leaf Rust. Unpublished Doctor of Philosophy Dissertation. Ain Shams University, Faculty of Agriculture, Department of Genetics, 2006.

Diallel cross was made between five wheat varieties (Sakh61, Saka69, Giza164, Sids1 and Chinese spring (C.S)). Parents, F1's and F2's crosses were open field evaluated in split plot design with three blocks. The plants were infected in adult stage with leaf rust in the open field and greenhouse. Three characters, plant height, number of spikes per plants and grain weight per plant, exhibited highly significant differences between entries. Highly significant differences were noted between the genotypes with respect to all studied traits. Both general and specific combining ability variances were found to be significant for spike length, grain weight per spike and grain weight per plant for control and infected plants and their combined data. GCA/SCA ratios were found to be greater than unity for all studied traits except for number of spikelets per spike at the control and combined data. With respect to rust disease measurements, all measurements showed significant values in F1 and F2 generations. Highly significant differences were found among parents and among hybrids for these five studied measurements. The three parental varieties Sakha 69, Giza 164 and Sids 1 showed highly significant negative GCA effects for all measurements. SCA effects were also highly significant in all characters in all crosses, except receptivity in cross P_2 X P_4. The SDS-PAGE of water soluble proteins in three parents (Sakha 69, Sids1 and C.S) and two F1's (Sakha69 x Sids1 and C.S x Sids1) under control and infection conditions, showed one band with M.W of 59 kDa which may be used for distinguish between resistant and susceptible wheat genotypes. F2 plants from C.S x Sids1 cross showed 16 bands, two of which with M.W (59 and 7 kDa) may be considered as positive markers for resistant wheat genotypes. Peroxidase isozyme of F2 plants from cross C.S x Sids1 revealed one band (R.F: 0.09) which is present in resistant group and absent in susceptible one. Cross C.S x Sids1 showed two DNA-RAPD markers resulted from primer OP-B08 related with leaf rust resistance in wheat, whereas cross Sakha69 x Sids1 revealed one marker resulted from each of primer OP-B05 and OP-B14

Key words: Wheat, Leaf rust, Combining ability, SDS-PAGE, RAPD-PCR markers

ACKNOWLEDGEMENT

First and foremost, I'm indebted to ALLAH forever, the most beneficent and merciful.

I wish to express my deepest gratitude and appreciation to **Prof. Dr. S.H. Hassanien,** Prof. Emeritus of Genetics, Department of Genetics, Faculty of Agriculture, Ain Shams University, for his valuable advice, helpful criticism and fruitful suggestions throughout the progress of study and during preparation of the manuscript.

I would like to express my deepest thankfulness to **Prof. Dr. F.M. A. El-Domyati** Professor of genetics, Department of Genetics, Faculty of Agriculture, Ain Shams University for his helpful criticism and his advice during this study.

I would also like to express my gratitude and heartfelt thanks to **Prof. Dr. I. M. Mahmoud,** Prof. Emeritus of Plant Breeding, Department of Genetics and Cytology, Division of Genetic Engineering and Biotechnology, National Research Centre, for his help to solve problems and his encouragement throughout this study.

Thanks to all staff members of Department of Genetics, Faculty of Agriculture, Ain Shams University, for their sincere help and advice during the progress of this work.

All thanks are also due to Colleagues of Genetics and Cytology Department, Division of Genetic Engineering and Biotechnology, National Research Centre.

I express my sincere love for my family, my wife and my son, for their patience and encouragement.

CONTENTS

Page

LIST Of TABLES iii

LIST Of F[GURES vii

I INTRODUCTION 1

II REVIEW OF LITRATURE 3

1 Combining ability, heterosis and type of gene action 3

1.a Yield and yield components. 3

1.b leaf rust resistance 9

2 Biochemical and molecular marker 14

III MATERIALS AND METHODS 26

1 Materials 26

2 Methods 28

2.1 Statistical Analysis 28

2.1.a Mean performance 29

2.1.b Heterosis 29

2.1.c Estimation of Combining Ability Effects 30

2.1.d Estimation of Genetic Behavior (mode of gene action) 33

2.1.d 1 Estimation of genetic variance components 33

2.1.d 2 Estimation of genetic ratios 34

2.2 Biochemical genetic studies 35

2.2.1 SDS-protein electrophoresis 35

2.2.2 Isozymes electrophoresis 39

2.2.3 RAPD-PCR technique 42

IV RESULTS AND DISCUSSION 47

a Yield and yield components, Selection Index and Heterosis 47

a.1 Yield and yield components 47

a.2 Selection Index 48

a.3 Heterosis 53

b Combining ability and Mode of gene actions 62
    b.1 Combining ability analysis 62
    b.2 Mode of gene action 87
c Inheritance of rust symptoms measurements 98
    c. 1 Rust disease measurements, Selection index and Heterosis 98
    c. 2 Combining ability analysis 104
    c. 3 Genetic components of variance 110
d Molecular studies: 115
    d. 1 SDS- protein markers 115
    d. 2 Isozymes markers 121
    d. 3 RAPD-PCR markers 129
    d. 4 The importance of molecular markers in breeding 140
V Summary 144
VI References 148
VII Arabic summary

LIST OF TABLES

Table		Page
1	Split plots analysis for 7 studied characters in F1 generation	49
2	split plots analysis for 7 studied characters in F2 generation	49
3	Total means performance of uninfected plants and infected ones for 7 studied traits in F1 generation.	50
4	Total means performance of uninfected plants and infected ones for 7 studied traits in F2generation.	50
5	Selection index ranking of studied traits, simultaneously for entries in F_1 diallel cross of control treatment	51
6	Selection index ranking of studied traits, simultaneously for entries in F_1 diallel cross under infection treatment	52
7	Selection index ranking of studied traits, simultaneously for entries in F_2 diallel cross of control treatment	57
8	Selection index ranking of studied traits, simultaneously for entries in F_2 diallel cross of infection treatment	58
9	Percentage of heterosis over mid and better parent for all studied traits in the F1 generation	59
9	Cont.	60
9	Cont.	61
10	Mean squares of general and specific combining abilities from diallel cross (Parents and F1) analysis for all traits	64
10	Cont.	65
11	Mean squares of general and specific combining abilities from diallel crosses (Parents and F2) analysis for all traits	71
11	Cont.	72
12	Estimates of general combining ability effects for studied parents in F1 for all traits	73
12	Cont.	74
13	Estimates of general combining ability effects for studied parents in F2 for all traits	75

13 Cont. 76

14 Estimates of specific combining ability effects for F1 crosses 81

14 Cont 82

14 Cont 83

15 Estimates of specific combining ability effects for F2 crosses 84

15 Cont 85

15 Cont 86

16 Estimates of genetic components of variation in diallel crosses (Parents and F_1) for all traits 90

16 Cont 91

16 Cont 92

17 Estimates of genetic components of variation in diallel crosses (Parents and F_2) for all traits 95

17 Cont 96

17 Cont 97

18 Mean square estimates of ordinary analysis for rust disease measurements in parents and F1's crosses. 101

19 Mean square estimates of ordinary analysis for rust disease measurements in parents and F2's crosses 101

20 Selection index ranking of studied disease measurements, simultaneously for entries in F_1 diallel cross 102

21 Selection index ranking of studied disease measurements, simultaneously for entries in F_1 diallel cross 102

22 Percentage of heterosis over mid and better parent for all studied disease measurements in the F1 generation 103

23 Observed mean squares from general and specific abilities from diallel cross (Parents and F1) analysis for all traits 107

24 Observed mean squares from general and specific abilities from diallel cross (Parents and F_2) analysis for all traits 107

25 Estimates of general combining ability effects for parents studied in F1 for all disease measurements 108

26 Estimates of general combining ability effects for parents studied in F2 for all disease measurements 108

27 Estimates of specific combining ability effects for F1 crosses 109

28 Estimates of specific combining ability effects for F2 crosses 109

29 Estimates of genetic components of variation in diallel crosses (Parents and F_1) for all traits 113

30 Estimates of genetic components of variation in diallel crosses (Parents and F_2) for all traits 114

31 Densitometric profile for water-soluble protein profiles of the susceptible parent (Chinese spring (P_5)), the moderately susceptible parents (Sakha 69 (P_2) & Sids1 (P_4)), Chinese spring x Sids1 and Sakha 69 x Sids1 crosses under control and infection. 118

32 Densitometric profile for water-soluble protein profiles of the F2 susceptible and resistant groups of Sakha 69 x Sids1 cross under infection with leaf rust disease 119

33 Densitometric profile for water-soluble protein profiles of the F2 susceptible and resistant groups of Chinese spring x Sids1 under infection with leaf rust disease 120

34 The presence of peroxidase isozymes bands in parents and F1's crosses under control and infection condition. 122

35 The presence of peroxidase isozymes bands in F2 plants of Sids1 x Sakha 69 cross. 123

36 The presence of peroxidase isozymes bands in F2 plants of Sids1 x Chinese spring cross 124

37 The presence of esterase isozymes bands in parents and F1's under control and infection condition. 126

38 The presence of esterase isozymes bands in F2 plants of Sids1 x Sakha 69 cross. 127

39 The presence of esterase isozymes bands in F2 plants of Sids1 x Chinese spring cross 128

40 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 131

x Chinese spring) against primer OP-B05
41 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B08 132
42 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B11 133
43 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B14 134
44 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B05 136
45 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B08 137
46 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B11 138
47 The densitometric analysis of RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B14 139

LIST OF FIGURES

Figure		Page
1	SDS-PAGE of wheat leaf protein (water-soluble protein) of **1**:the susceptible parent (Chinese spring), **2**: the moderately susceptible parents Sakha 69, **3**: the moderately susceptible parents Sids 1, **4:** F1 cross Chinese spring x Sids 1 and **5**: cross Sakha 69 x Sids 1 under control and infection	118
2	SDS-PAGE of wheat leaf protein (water-soluble protein) of the F2 susceptible and resistant groups of Sakha 69 x Sids1 cross under infection with leaf rust disease.	119
3	SDS-PAGE of wheat leaf protein (water-soluble protein) of the F2 susceptible and resistant groups of Chinese spring x Sids1 under infection with leaf rust disease	120
4	Electrophoretic patterns of peroxidase Isozymes for wheat genotypes: **1**: susceptible parent (Chinese spring), **2**: moderately susceptible parent (Sakha 61), **3**: moderately susceptible parent (Sids 1), and the two F1 hybrids **4**: Sakha 61 x Sids 1 , **5**: Sids 1 x Chinese spring) under control and infection condition	122
5	Electrophoretic patterns of peroxidase isozyme for the resistant group (1:5) and the susceptible group (6:10) of cross Sakha 61 X Sids1 under infection with leaf rust disease.	123
6	Electrophoretic patterns of peroxidase isozyme for the resistant group (1:5) and the susceptible group (6:10) of cross Chinese spring X Sids1 under infection with leaf rust disease	124
7	Electrophoretic patterns of esterase isozymes for: **1**: susceptible parent (Chinese spring), **2**: moderately susceptible parent (Sakha 61), **3**: moderately susceptible parent (Sids 1), and the two F1 hybrids **4:** Sakha 61 x Sids 1, **5**: Sids 1 x Chinese spring) under control and infection condition.	126
8	Electrophoretic patterns of esterase isozyme for the F2 resistant group (1:5) and the susceptible group (6:10) of cross Sakha 61 x	127

Sids1 under infection with leaf rust disease.
9 Electrophoretic patterns of peroxidase isozyme for the F2 resistant group (1:5) and the susceptible group (6:10) of cross Chinese spring X Sids1 under infection with leaf rust disease 128
10 RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B05 131
11 RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B08 132
12 RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B11 133
13 RAPD-PCR products of hybrid (Sids1 x Chinese spring) against primer OP-B14 134
14 RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B05 136
15 RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B08 137
16 RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B11 138
17 RAPD-PCR products of hybrid (Sids1 x Sakha 69) against primer OP-B14 139

I. Introduction

Wheat (*Triticum aestivum* L.) is one of the major cereal crops grown in Egypt. It is a stable food for the Egyptians; therefore, it is grown on 2.5 million feddans in different agroecological regions to meet the ever increasing domestic requirements. **(Abdel-Sattar *et al* (2005))**

Leaf rust of wheat caused by the fungus *puccinia* is one of the most destructive and widely distributed diseases in diverse wheat growing area of the world. Losses caused by this disease can be quite high under favorable conditions. **Nazim *et al* (1996)** and **Mousa (2001)** demonstrated that under the favorable environmental conditions, leaf rust prevailing in the Delta region causes considerable losses in grain yield production of most wheat cultivars. The susceptible varieties cause yield loss up to 5-15% or grater depending on the stage of the crop when the initial rust infection occurs **(Kolmer, 1996)**

Many investigators confirmed that plant reaction for leaf rust is controlled by one, two or a few number of major genes. However, recently several studies indicated that it's a quantitative character controlled by many genes **(Milus and line 1987, Griffey and Allan, 1988, Kolmer 1996, Shehab El-Din and Abdel-Latif, 1996 and Boulot and El-Sayed 2001).**

Genetic resistance is the most economical method of reducing yield losses, caused by wheat leaf rust (*Puccinia recondita*). The identification and knowledge of the leaf rust resistance genes, in commonly used parental germplasm and released cultivars, became very important for utilizing the genetic resistance to wheat leaf rust fully. To date, approximately 90 leaf rust resistant genes have been found, 51 of which have been located and mapped to specific chromosomes, and 56 have been officially designated according to the standards set forth in the Catalogue of Gene Symbols for wheat. Twenty four wheat leaf rust resistance genes have been developed for molecular markers. It is very important to continuously isolate, characterize and map leaf rust resistance genes due to the resistance losses of the genes caused by the pathogen. **Yang and Liu (2004)**

Plant breeders require more information regarding to genetic components of leaf rust in order to breed new disease resistant cultivars to replace these that succumb to diseases.

This study was undertaken to identify some biochemical and molecular markers concerning leaf rust disease that will be of considerable value in breeding programmes for rust resistance. To achieve this principle goal, detailed studies concerning plant genotypes will be carried out. Helpful genetic studies on plant materials need designing proper field and greenhouse experiments to determine the suitable plant materials that will be used in molecular studies. These assisted experiments include:

1. Studying the inheritance of leaf rust resistance in some bread wheat cultivars regarding to combining ability, heterosis and mode of gene action.
2. Identifying and selecting the most resistant genotypes according to yield potential and degree of infection type.