FUNCTIONAL GENOMIC STUDIES TO IDENTIFY LEAF RUST RESISTANCE RELATED GENES IN BREAD WHEAT

By

MOHAMMED MOSTAFA ELMAHDY ABD ALLAH

B.Sc. Agric. Sc. (Genetics), Ain Shams University, 2010

A Thesis Submitted in Partial Fulfillment

Of

The Requirements for the Degree of

in
Agricultural Sciences
(Genetics)

Department of Genetics Faculty of Agriculture Ain Shams University

Approval Sheet

FUNCTIONAL GENOMIC STUDIES TO IDENTIFY LEAF RUST RESISTANCE RELATED GENES IN BREAD WHEAT

By

MOHAMMED MOSTAFA ELMAHDY ABD ALLAH

B.Sc. Agric. Sc. (Genetics), Ain Shams University, 2010

This thesis for M.Sc. degree has been approved by:	
Dr. Abdel-Wahab Mohamed Hassan Prof. Emeritus of Genetics, Faculty of Agriculture, Ber University.	
Dr. Mohamed Abdel-Salam Rashed Prof. Emeritus of Genetics, Faculty of Agriculture, Ain Sha University.	
Dr. Eman Mahmoud Fahmy Prof. Emeritus of Genetics, Faculty of Agriculture, Ain Sha University.	ms
Dr. Fatthy Mohamed Abdel-Tawab Prof. Emeritus of Genetics, Faculty of Agriculture, Ain Sha University.	 ms

Date of examination: 23 / 5 / 2017

FUNCTIONAL GENOMIC STUDIES TO IDENTIFY LEAF RUST RESISTANCE RELATED GENES IN BREAD WHEAT

By

MOHAMMED MOSTAFA ELMAHDY ABD ALLAH

B.Sc. Agric. Sc. (Genetics), Ain Shams University, 2010

(

Under the supervision of:

Dr. Fatthy Mohamed Abdel-Tawab

Prof. of Genetics, Department of Genetics, Faculty of Agriculture, Ain-Shams University (principle supervisor).

Dr. Eman Mahmoud Fahmy

Prof. of Genetics, Department of Genetics, Faculty of Agriculture, Ain-Shams University.

Dr. Sameh Elsayed Hassanain

Senior Researcher, Agricultural Genetic Engineering Research Institute, Agricultural Research Center.

ABSTRACT

Mohammed Mostafa El-mahdy Abd-Allah: Functional Genomic Studies to Identify Leaf Rust Resistance Related Genes in Bread Wheat. Unpublished M.Sc. Thesis, Department of Genetics, Faculty of Agriculture, Ain Shams University, 2017.

Wheat, one of three most important commercial crops around the world, is considered the first strategic food crop in Egypt. Wheat leaf rust caused by Puccinia triticina Eriks, reduces the yield and quality of the grain and yields. It cause yield loss between 20-50% if infection occurs very early. Differential display reverse transcription PCR (DDRT-PCR) was used to study the response of bread wheat to leaf rust infection at the molecular level. Three Egyption cultivars of bread wheat were used in this study; Shandwell 1, Gemmeiza 1 and Sids 1 representing resistant, moderately resistant and sensitive cultivars, respectively. Performance of non infected cultivars and after one and two weeks from infection was evaluated. Two hundred and forty eight differentially expressed fragments were observed as up-regulated, up- & down-regulated, down- & upregulated and Down-regulated EST. Sixty four fragments were selected, extracted from the gel, reamplified and sequenced. BLAST program from National Center for Biotechnology Information (NCBI), USA were used to determine similar sequences of these fragments. Results of the database sequence alignment identified fragments with significant homology to genes and/or proteins with known function, other fragments with homology to unknown or hypothetical ESTs with unknown functions, and some fragments revealed no homology in the databases. These results implicated that several pathways are involved in the plant's response to leaf rust infection which still needs to be elucidated further.

Key words: Bread wheat, Biotic stresses, Leaf rust, *Puccinia triticinia*, Differential display reverse transcription (DDRT), PCR, cDNA, Gene expression and GenBank Database.

ACKNOWLEDGMENT

Firstly, all praises to **ALLAH** the most merciful and compassionate, for the strengths, support, help, generosity and blessing in my life and completing this thesis.

I wish to express my sincere appreciation and deep gratitude to **Prof. Dr. Fatthy M. Abd El-Tawab;** Prof. of Genetics, Genetics Dept., Fac. of Agric., Ain Shams University, **Prof. Dr. Eman Fahmy;** Prof. of Genetics, Genetics Dept., Fac. of Agric., Ain Shams University and **Dr. Sameh Elsayed Ibrahim;** Senior Researcher and Head of Bioinformatics Department, Agricultural Genetic Engineering Research Institute (AGERI), Agriculture Research Center (ARC) for their valuable supervision; suggesting the scientific problem, productive help, energetic guidance, conclusive instructions throughout the course of this investigation and in the writing and reviewing the thesis.

The pleasure of completion is to look over the journey and remember all the friends and family who have helped and give me support along this time, my family love provided my inspiration, moral support and positive energy, I owe them everything and wish I could show them just how much I love and appreciate them.

Sincere appreciation is due to **Dr. Rania Mahmoud**; Senior Researcher, (AGERI), **Dr. Mohamed Abdel Sattar**; Senior Researcher, (AGERI), **Dr. Omneia Osama**; Researcher, (AGERI), **Dr. Marwa Hanafy**; Assistant Researcher, (AGERI) and **Mr. Yasser Bahaa Eldin**; Assistant Researcher, (AGERI) for their encouragement and serving as a model to me as a junior member of the Academia. They have been strong and supportive advisors to me throughout my career.

Special and great thanks for **Dr. Reda Sallam**; Senior Researcher and **Dr. Walid El-Oraby**; Senior Researcher, Wheat Diseases Research Department (WDRD) for their valuable help, kind and supporting.

During this work I have been blessed with a friendly and cheerful group of junior scientists, Great and deep thanks to my dear staff

members: Mr. Kareem Ahmed, Mrs. Rasha Abdel Kader, Mrs. Warda Alaa, Mrs. Esraa Bassam and my friend Mrs. Marwa Ibrahim for their great help, assistance and encouragement, and many thanks to assistants Mrs. Lamiaa Ahmed, Mrs. Rabab Ibrahim and Mr. Adel Abdel Rady for their assistance.

Many thanks are also due to head and all staff members of Genetics Department, Fac. of Agric., Ain Shams University.

Extended grateful thanks for all members of Agricultural Genetic Engineering Research Institute (AGERI), Agriculture Research Center (ARC).

I wish to express my deepest thanks to my dear Mother, Father, Sisters, Friends and Relatives for their encouragement and spiritual support.

CONTENTS

Title	Page
I. INTRODUCTION	1
II. REVIEW OF LITERATURE	5
2.1. Wheat	5
2.2. Leaf Rust	6
2.3. Molecular genetics studies	11
2.4. Differential Display	13
III. MATERIALS AND METHODS	19
3.1. Materials	19
3.1.1. Plant materials	19
3.1.2. Leaf rust pathogen	19
3.2. Methods	19
3.2.1. Plant infection	19
3.2.2. RNA extraction	20
3.2.3. RNA Electrophoresis	21
3.2.4. Determination of RNA concentration	22
3.2.5. DNase treatment	23
3.2.6. Reverse transcription of mRNA	23
3.2.7. PCR amplification of cDNA	24
3.2.8. Differential display of amplified cDNA on sequencing	
gel	25
3.2.8.1. Preparation of a denaturing polyacrylamide gel	25
3.2.8.2. Gel electrophoresis	27
3.2.8.3. Gel staining	28
3.2.9. Extraction of cDNA fragments from the acrylamide urea	
gel	28

3.2.10. Reamplifying the cDNA by PCR	29
3.2.11. Agarose gel extraction	30
3.2.12. Sequencing of the cDNA insert	31
3.2.13. Identification of the cDNA fragments and protein	
product(s) homologous to the cDNA using the NCBI	
database	32
IV. RESULTS AND DISCUSSION	33
4.1. Screening of plant infection	33
4.2. RNA isolation	35
4.3. Differential Display-PCR	36
4.4. Expression patterns of detected DD cDNAs	37
4.5. Analysis of differentially expressed patterns amplified DD-	
fragments	47
4.6. Re-amplification of cDNA fragments	54
4.7. Sequencing of selected DD cDNA fragments	58
4.8. Data analysis for sequenced fragments	75
V. SUMMARY	89
VI. REFERENCES	92
ARARIC SUMMARY	

LIST OF TABLES

Table no.		Page
Table (1)	Primers used in preparation of first and second strand cDNA	25
Table (2)	The number of spots on leaves of the three cultivars (Shandweel 1, Gemmeiza 1 and Sids 1)	34
Table (3)	The concentrations of RNAs samples Ng/ μ l	36
Table (4)	Differential expression of Shandweel 1 using T ₁₉ A with AP1 and AP2	48
Table (5)	Differential expression of Shandweel 1 using T ₁₉ A with AP3 and AP4.	49
Table (6)	Differential expression of Shandweel 1 using T ₁₉ A with AP5 and AP6.	50
Table (7)	Differential expression of Shandweel 1 using T ₁₉ A with AP7 and AP8.	50
Table (8)	Differential expression of Gemmeiza 1 using T ₁₉ A with AP1 and AP2.	51
Table (9)	Differential expression of Gemmeiza 1 using T ₁₉ A with AP3 and AP4.	51
Table (10)	Differential expression of Gemmeiza 1 using T ₁₉ A with AP5 and AP6.	52
Table (11)	Differential expression of Gemmeiza 1 using T ₁₉ A with AP7 and AP8.	52

Table (12)	Differential expression of Sids 1 using T ₁₉ A with AP1 and AP2.	53
Table (13)	Differential expression of Sids 1 using T ₁₉ A with AP3 and AP4.	53
Table (14)	Differential expression of Sids 1 using T ₁₉ A with AP5 and AP6.	54
Table (15)	Differential expression of Sids 1 using T ₁₉ A with AP7 and AP8.	54
Table (16)	Expression patterns of the obtained 64 DD fragments.	58
Table (17)	Up regulated fragments.	76
Table (18)	Up & down regulated fragments.	77
Table (19)	Down & up regulated fragments.	85
Table (20)	Down regulated fragments.	87

LIST OF FIGURES

Figure no.		Page
Fig. (1)	Spots of urediniospores (leaf rust symptoms) after two weeks of artificial infection.	34
Fig. (2)	Agarose gel electrophoresis (1%) of total RNA extraction from all cultivars seedling (Shandweel 1, Gemmeiza 1 and Sids 1). (C=Control, 1W=1week of infection, 2W=2weeks of infection).	35
Fig. (3)	positive control show smear bands, negative control show no bans.	37
Fig. (4)	Anchor primer T19A with arbitrary primers H-AP1.	39
Fig. (5)	Anchor primer T19A with arbitrary primers H-AP2.	40
Fig. (6)	Anchor primer T19A with arbitrary primers H-AP3.	41
Fig. (7)	Anchor primer T19A with arbitrary primers H-AP4.	42
Fig. (8)	Anchor primer T19A with arbitrary primers H-AP5.	43
Fig. (9)	Anchor primer T19A with arbitrary primers H-AP6.	44
Fig. (10)	Anchor primer T19A with arbitrary primers H-AP7.	45
Fig. (11)	Anchor primer T19A with arbitrary primers H-AP8.	46
Fig. (12)	Fragments from anchor primer T19A with arbitrary primers H-AP1.	55
Fig. (13)	Fragments from anchor primer T19A with arbitrary primers H-AP2.	55
Fig. (14)	Fragments from anchor primer T19A with arbitrary primers H-AP3.	56
Fig. (15)	Fragments from anchor primer T19A with arbitrary primers H-AP4.	56

Fig. (16)	Fragments from anchor primer T19A with arbitrary primers H-AP5.	56
Fig. (17)	Fragments from anchor primer T19A with arbitrary primers H-AP6.	57
Fig. (18)	Fragments from anchor primer T19A with arbitrary primers H-AP7.	57
Fig. (19)	Fragments from anchor primer T19A with arbitrary primers H-AP8.	57
Fig. (20)	The cDNA sequences of the 58 fragments.	59

LIST OF ABBREVIATIONS

Abbreviation Full Name

Arbitrary primer 1 Ap1 Arbitrary primer 2 Ap2 Arbitrary primer 3 Ap3 Arbitrary primer 4 Ap4 Arbitrary primer 5 Ap5 Ap6 Arbitrary primer 6 Arbitrary primer 7 Ap7 Ap8 Arbitrary primer 8

AFLP Amplified Fragment Length Polymorphism

ATP Adenosine triphosphate

BLAST

Basic Local Alignment Search Tool

BLASTn

Nucleotide blast (Search a nucleotide

database using a nucleotide query)

cDNA Complementary DNA

CTAB Cetyltrimethyl Ammonium Bromide

DD Differential display

ddH2O Double-distilled water

DDRT- PCR Differential display reverse transcription-

PCR

DNase Deoxyribonuclease

dNTP Deoxynucleotide

EDTA Ethylenediaminetetraacetic acid

ESTs Expressed Sequencing Tags

EtBr Ethidium bromide stain

MgCl₂ Magnesium chloride

mRNA messenger RNA

Na₂So₃ Sodium sulfite

NaCl Sodium chloride

NaI Sodium iodide

NCBI National Center for Biotechnology

Information

PCR Polymerase Chain Reaction

Re-PCR Reamplified-PCR

rRNA Ribosomal RNA

rpm Round per minute

SAM S Adenosylmethionine

T19A Anchored Primer A

TAE Tris-acetate-EDTA

TBE Tris Borate EDTA

INTRODUCTION

Wheat is one of three most important commercial cereal crops around the world, It ranks first as the largest cultivated area which surpasses any other commercial crop. Wheat contains protein higher than the other major; cereals, maize or rice. It providing more than 20% of all calories consumed by the people worldwide. **FAO**'s latest forecast for 2015 global wheat production stands at 719 million tonnes (**FAO**, 2015). In 2016, total Egyptian cereal harvest is 22.1 million tonnes, including nine million tonnes wheat production, this means that wheat represents 40.7 % of the total Egyptian cereal production (**FAO**, 2016). Bread making is a basic staple food for both urban and rural areas. It is the main source of plant protein in the human nutrition.

World population is increasing at an alarming rate and is expected to reach about nine billions by the end of year 2050. On the other hand, food productivity is decreasing due to the effect of various abiotic and biotic stresses. Therefore minimizing these losses is a major area of concern for all nations to cope with the increasing food requirements (Waraich et al., 2012). Nature including plants always encounter many changes, that lead to various stress whether abiotic stress (temperature changes, drought and salinity) or biotic stresses (viruses, bacteria and fungus). On the other hand, researches and tecnology always develop new solutions. In order to find suitable solutions, different situations, reasons and conditions must be studied, here is the important role of the molecular biologists, because natural changes lead to changes on physiological responses of cells at the molecular level (Harb 2010).

Globally important fungal diseases of wheat, caused by biotrophs (obligate parasites) include the three rusts (leaf rust *Puccinia triticinia*, stem rust *Puccinia graminis tritici* and yellow rust *Puccinia striiformis*), powdery mildew, and the bunts and smuts, whereas, those caused by hemibiotrophs (facultative parasites) include *Septoria tritici* leaf blotch, *Septoria nodorum* blotch, spot blotch, tan spot, and *Fusarium* head blight.