In The Name of God



Faculty of Agriculture Department of Agronomy and plant breeding

PhD Thesis

Mapping QTLs related to drought tolerance in durum wheat (*Triticum turgidum* var durum)

By: Leila Zarei

Evaluated and approved by thesis committee:as Excellent

Dr. Ezatollah Farshadfar

Dr. Kianoosh Cheghamirza

Dr. Mohsen Farshadfar

External Examiner

Dr. Bahman Bahramnezhad

External Examiner

Dr. Sohbat Bahraminejad

Internal Examiner

Dr. Danial Kahrizi

Internal Examiner



Faculty of Agriculture Department of Agronomy and plant breeding

PhD Thesis

Mapping QTLs related to drought tolerance in durum wheat (Triticum turgidum var durum)

Supervisor: Dr. Ezatollah Farshadfar

Advisor: Dr. Kianoosh Cheghamirza

> By: Leila Zarei

March 2013

Abstract

Durum wheat (Triticum turgidum L. var durum) is a tetraploid constituted of A and B genomes (AABB) and is the main source of semolina for the production of pasta, spaghetti, and grain for burghul. Drought stress is the main constraint of the wheat production in many parts of the world. Identifying chromosomal regions associated with drought tolerance in wheat will improve understanding the genetic basis of drought tolerance. New genetic tools and more powerful statistical analyses provide an alternative approach to enhance genetic improvements through the identification of molecular markers linked to genomic regions or QTLs controlling quantitative traits. The main objective of this research was to identify genomic regions associated with drought tolerance in a F₆ population of durum wheat under two environmental conditions (rainfed and supplemental irrigation conditions). A population composed of 130 F5:6 recombinant inbred lines (RILs) was derived from the cross of Zardak × 249 (local variety and genotype of Kermanshah province, Iran, respectively). A total of 256 marker loci including 79 microsatellites, 11 EST-SSR, 123 AFLPs, 39 RAPDs and 4 ISSRs were scored. The preliminary genetic linkage map consists of 71 loci on 15 linkage groups. AFLPs and ISSRs markers remained unlinked to linkage groups or were eliminated because they span very large distances. The linkage map covers 913.5 cM with marker loci spaced at an averaged 13.16 cM. Under both environmental conditions, 27 morphological, phenological and physiological traits were evaluated. Interval mapping (IM) method identified 117 QTL peaks with LOD scores ≥ 2.0 under rainfed conditions and 96 QTL peaks with LOD scores > 2.0 under supplemental irrigation conditions. Stable QTLs were detected in two environmental conditions for plant height (PH), awn length (AL), flag leaf length (FL), number of seeds per spike (NSPS), chlorophyll florescence (Fv/Fm), peduncle length (PED), date to heading emergence (DHE), date to flowering emergence (DFE) and spikelet density (SpD), suggesting the presence of loci related to stability of these traits under drought stress conditions. Some markers (e.g. BF483631, Xcfd48, Xgwm499, and Xgwm495, Xbarc68) were consistently distinguished for multiple traits (e.g. number of seed per spike (NSPS), spike density (SpD), mean grain weight (MGW), flag leaf length (FL) and date to heading emergence (DHE) under rainfed and supplemental irrigation conditions, indicating broad adaptability and potential use of these markers in marker-assisted breeding. Among all traits, the two-locus QTL analysis detected a total of 12 QTLs with significant (P < 0.005) additive \times additive epistatic (aa) effects for spike length (aa=-0.195 and 0.506), awn length (aa=-1.30), harvest index (aa=-1.81), excised leaf water retention (aa=1.90) and chlorophyll florescence (aa=0.020). QTL × environment interaction (QE) effect was not significant for none of the traits. This is the first genetic map of a cross involving local genotypes of durum wheat from Kermanshah province of Iran using DNA markers and therefore, it could be used for further detection of OTLs controlling resistance to biotic and abiotic stresses. The results also support the use of identified QTLs to enhance the selection efficiency in plant breeding, especially those showing high explanation rates.

Unlinked AFLP/ISSR/RAPD markers subjected to multiple regression to find association of markers with each of 27 traits under both conditions. Markers XMcaaEact350 (chlorophyll: florescence Fv/Fm), OPD20-760 (grain yield: GY), XMcccEcga290 and XMcaaEact200 (number of seeds per spike: NSPP), McaaEcga140 (plant height: PH), UBC51-850 (relative water loss: RWL2), XMcaaEgtc320 (chlorophyll index: SPAD) were found to be associated with an individual trait under both conditions.

Key Words: Drought stress, durum wheat, linkage map, QTL analysis

Table of Contents

Contents	page
Chapter 1	
1. Introduction	2
1-1- Durum wheat	3
1-1-1- Origin of durum wheat	3
1-1-2- Uses of durum wheat	4
1-1-3- Durum wheat production in Iran	4
1-2- Drought stress	4
1-2-1- Mechanism of drought tolerance	5
1-2-1-1- Drought escape	5
1-2-1-2- Dehydration avoidance	5
1-2-1-3- Dehydration tolerance	6
1-2-2- Morphological responses	6
1-2-2-1- Growth	6
1-2-2- Yield	6
1-2-3- Physiological responses	7
1-2-3-1- Root signaling under drought stress	7
1-2-3-2- Cell membrane stability	8
1-2-3-3- Photosynthesis	8
1-2-3-4- Chlorophyll contents	8
1-2-3-5- Water relations	8
1-2-3-6- Osmolyte accumulation	9
1-2-4- Biochemical responses	9
1-2-4-1- Reactive oxygen species (ROS)	9
1-2-4-2- Antioxidant enzymes	10
1-2-5- Estimation of drought tolerance	10
1-3- Genetic diversity of durum wheat	10
1-4- Molecular markers to assess genetic diversity	11
1-4-1- Types of molecular markers	11
1-4-1-1- Restriction Fragment Length Polymorphism (RFLPs)	11
1-4-1-2- Cleaved Amplified Polymorphic Sequences (CAPS)	12
1-4-1-3- Random Amplified Polymorphic DNAs (RAPDs)	13
1-4-1-4- Amplified Fragment Length Polymorphism (AFLP)	14
1-4-1-5- Microsatellites	16
1-4-1-6- Single Nucleotide Polymorphisms (SNPs)	18
1-4-1-7- Diversity Arrays Technology (DArT) as an alternative market	٠.
	18

1-4-1-8- Retrotransposons as molecular markers	20
1-4-1-9- ISSR markers	21
1-5- Genetic map and its importance to breeding	22
1-5-1- Linkage analysis and methods for linkage analysis	22
1-5-1-1- Two-Point Analysis	22
1-5-1-2- Three-Point Analysis	22
1-5-2- Genetic Models	23
1-5-3- Segregating population	23
1-5-4- Linkage analyses and map construction	25
1-5-5- Population size	25
1-5-6- Basic assumptions	25
1-5-7- Linkage groups and chromosomes	26
1-5-8- Segregation and recombination	26
1-5-9- Mapping functions	27
1-5-9-1- Mather's Formula	28
1-5-9-2- The Morgan Map Function	28
1-5-9-3- Haldane's Mapping Function	28
1-5-9-4- Interference	29
1-5-9-5- Kosambi's Mapping Function	30
1-5-10- Relationship between genetic and physical maps	31
1-5-11- Marker Segregation Analysis	32
1-5-12- Segregation distortion	33
1-5-13- Saturated maps	33
1-5-14- Construction of linkage maps in polyploids	33
1-5-15- Construction of linkage map in durum wheat	34
1-6- Quantitative traits	34
1-6-1- Quantitative Trait Loci Mapping	34
1-6-2- QTL mapping and marker association with plant traits	35
1-6-3- QTL mapping and linkage analysis in durum wheat	36
1-6-4- Methods for QTL analysis	38
1-6-4-1- Single-marker analysis	38
1-6-4-1-1- t-Tests	39
1-6-4-1-2- ANOVA analysis using single marker genotypes	39
1-6-4-1-2-1- The disadvantages of analysis of variance	40
1-6-4-1-3- Regression Methods	40
1-6-4-1-3-1- Problems with the regression approach	41

1-6-4-1-4- ANOVA analysis using multiple marker genotypes (n regression analysis)	
1-6-4-1-5- Maximum Likelihood estimation	
1-6- 4-1-6- Simple interval mapping	
1-6- 4-1-6-1. Maximum Likelihood Analysis	
1-6- 4-1-6-2- Likelihood Ratio Test	
1-6- 4-1-6-3- The advantage of interval mapping	
1-6- 4-1-6-4- The limitation of interval mapping	
1-6- 4-1-6-5- LOD thresholds for interval mapping	
1-6-4-2- Bayesian Methods	
1-6-4-3- Multiple markers Methods	
1-6- 4-3-1- Composite interval mapping (CIM)	
1-6- 4-3-1-1- Likelihood Analysis	
1-6-4-3-1- 2- Advantages of CIM	51
1-6- 4-3-1- 3- Limitations of CIM	51
1-6- 4-3-2- Inclusive composite interval mapping (ICIM)	51
1-6-4-3-3- A mixed-model based composite interval mapping (MCIM)	53
1-6- 4-3-4- Multiple interval mapping (MIM)	53
1-6- 4-4- Multiple quantitative trait loci	54
1-6- 4-5- The genetic effects of QTL	55
1-6-4-6- Analysis of distorted markers	55
1-6- 4-7- Genomic Dissection of Genotype × Environment Interactions	56
1-6- 4-8- QTL Characterization and Validation	56
1-6- 4-9- Problems of QTL mapping	57
1-6- 4-10- Functional genomics and QTL cloning	57
1-6- 4-10-1- Cloning QTLs for traits affecting drought tolerance	57
1-6- 4-10-2- Positional Cloning	58
1-6-4-11- Postgenomics Approaches	59
1-6-4-12- Transcriptomics	59
1-6- 4-13- Association Mapping: Natural populations as a tool for gene mapp	oing59
Chapter 2	
2- Materials and methods	62
2-1- Sites description	62
2-2-1- Experimental design	62
2-2-3- Trait evaluation in advanced families of durum wheat $(F_5$ population)	62
2-2-4- Screening plant materials	62
2-2-5- Statistical analysis	63

2-2-5-1- Analysis of variance	63
2-2-5-2- Simple correlation	64
2-2-5-3- Path analysis	64
2-2-5-4- Factor analysis	64
2-2-5-5- Stepwise multiple linear regression	64
2-2-5-6- Principal component analysis	64
2-2-5-7- Cluster analysis	64
2-3- F ₆ mapping population	64
2-3-1- Drought test	65
2-3-2- Evaluation of phenotypic traits for mapping population (F ₆)	65
2-3-2-1- Phenological traits	65
2-3-2- Morphological traits	65
2-3-2-3- Physiological measurements	66
2.3.2.4. Drought stress indices	67
2-3-3- Genomic DNA extraction for mapping	68
2-3-3-1- Concentration measurement of DNA	68
2-3-3-2- UV quantification of DNA	68
2-3-3- 3- RAPD amplification	69
2-3-3-4- ISSR amplification	70
2-3-3-5- AFLP analysis	70
2-3-3-6- Microsatellite analysis	72
2-3-4- Statistical Analysis	74
2-3-4-1- Field data analysis	74
2-3-4-1-1- Analysis of variance	74
2-3-4-1-2- Heritability calculation	74
2-3-4-1-3- Statistical parameters	74
2-3-4-1-4- Phenotypic correlation	74
2-3-4-2- Linkage analysis and map construction	74
2-3-4-2-1- Quantitative trait loci analysis	75
2-3-4-2-2- MQM analysis	75
2-3-4-2-3- QTL network	75
2-3-4-2-4- Multiple Regression	76
Chapter 3 3-1 -Evaluation of F ₅ population	78
3-1-1 -Analysis of variance	78
3-1-2- Relationship between grain yield and the morpho-physiological through the correlation analysis	
3-1-3 -Modeling and predicting durum wheat yield using stepwise regression	n 83

	3-1-4 -Phenotypic path coefficient analysis for the determination of the nature of the trait association	
	3-1-5 -Exposing the interrelation between the traits using principal compone analysis	
	3-1-6 -Analysis of factors influencing the yields under drought stress conditions 8	66
	3-1-7 -Cluster analysis of morpho-physiological traits	7
	3-1-8 -Cluster analysis of F ₅ families for selection of mapping population8	8
3.	-2- Phenotyping of F6 population9	2
	3-2-1- Rainfed conditions9	2
	3-2-1-2 -Analysis of variance and Heritability9	5
	3-2-1-3 -Correlation analysis9	
	3-2-1-4- Drought tolerance indices	00
	3-2-1-5 -Distributions of traits	1
	3-2-1-6 -Parents comparison (Zardak and 249)10	6
	3-2-2 -Irrigated conditions	6
	3-2-2-2 -Comparison of blocks and check varieties under irrigated conditions10	9
	3-2-2-3 -Correlation analysis	0
	3-2-2-4 -Correlation between two environmental conditions	4
	3-2-2-5 -Distribution of traits	4
	3-2-2-6- Parents comparison (Zardak and 249)11	9
	3-2-3-Combined analysis of both condithions	0
	3.2.3.1. Combined analysis of variance and heritability	0
	3-2-3-2 -Relative reduction in rainfed conditions	2
3.	-3- Linkage mapping and QTL analysis12	:3
	3-3-1 -Segregation Distortion of the Molecular Markers	:3
	3-3-2 -The linkage map	6
3.	-4 -QTL analysis13	0
	3-4-1 -Plant height (PH)	0
	3-4-3 -Peduncle length (PED)	1
	3-4-4 -Awn length (AL)	3
	3-4-5 -Number of tiller per plant (NTPP)	5
	3-4-8 -Number of seeds per spike (NSPS)	7
	3-4-9 -Mean grain weight (MGW)	0
	3-4-10 -Spike seed weight (SSW)	-2
	3-4-11 -Spike weight (SW)	.3
	3-4-12 -Harvest index (HI)	4
	3-4-14 -Relative water loss (RWL2)14	-5
	3-4-15 -Excised leaf water retention (ELWR)	-6

	3-4-16 -Flag leaf (FL)	. 146
	3-4-17 -Peduncle/Plant height (PED/PH)	. 148
	3-4-18 -Spike density (SpD)	.149
	3-4-19 -Chlorophyll fluorescence (Fv/Fm)	.152
	3-4-20 -Kruskal Wallis test	.153
	3-4-21 -Chlorophyll fluorescence (Fv/Fm)	.153
	3-4-22 -Days to heading emergence (DHE)	.154
	3-4-23 -Days to flowering emergence (DFE)	.155
	3-4-25 -Days to maturity emergence (DME)	.157
3	-5- MQM mapping (Multiple QTL Mapping)	.158
3	-6- Evaluation of epistatic QTLs and QTL × environment interaction effects	.159
	3-6-1- Plant Height (PH)	.160
	3-6-2- Spike length (SL)	.161
	3-6-3- Awn length (AL)	.162
	3-6-4- Number of seeds per spike (NSPS)	.164
	3-6-5- Harvest index (HI)	.165
	3-6-6- Excised leaf water retention (ELWR)	.166
	3-6-7- Chlorophyll florescence (Fv/Fm)	.167
3	-7- Overall results from QTL mapping	.168
3	-8- Multiple regression analysis for unlinked markers	.170
	3-8-1- Awn length (AL)	.171
	3-8-2- Biomass (BIO)	.171
	3-8-3- Days to flowering emergence (DFE)	.172
	3-8-4- Days to heading emergence (DHE)	.172
	3-8-5- Days to maturity emergence (DME)	.173
	3-8-6- Excised leaf water retention (ELWR)	.173
	3-8-7- Spike seed weight (SSW)	.174
	3-8-8- Spike Weight (SW)	.174
	3-8-9- Flag leaf (FL)	.175
	3-8-10- Chlorophyll fluorescence (Fv/Fm)	.175
	3-8-11-Grain yield (GY)	.176
	3-8-12- Harvest index (HI)	.177
	3-8-13- Mean grain weight (MGW)	.177
	3-8-14- Number of spike per plant (NSPP)	.177
	3-8-15- Number of seeds per spike (NSPS)	.178
	3-8-16-Number of tiller per plant (NTPP)	.178
	3-8-17- Proline content (PC)	

3-8-18- Peduncle length (PED)	179
3-8-19- Peduncle/Plant height ratio (PED/PH)	180
3-8-20- Plant height (PH)	180
3-8-21- Relative water content (RWC)	181
3-8-22- Relative water loss (RWL)	181
3-8-23- Relative water loss (RWL2)	182
3-8-24- Spike length (SL)	182
3-8-25- SPAD	183
3-8-26- Spike density (SpD)	183
3-9- Conclusion	187
3-10-Outlooks	188
References	189

Table of Figures

Contents page
Figure 1- 1. Principles of RFLP markers. This figure illustrates an RFLP marker which utilizes a site for the restriction enzyme (E) which is present in line A and not in line B (Huguet <i>et al.</i> , 2002)
Figure 1- 2. Principles of CAPS markers. This figure illustrates a CAPS marker which utilizes a restriction enzyme (E) that cleaves the amplified fragment at one site in line A and not at all in line B (Huguet <i>et al.</i> , 2002)
Figure 1- 3. Principle of AFLP markers (Huguet et al., 2002)
Figure 1- 4. Principle of SSR markers. This figure illustrates an SSR marker which utilises the fact that the number of (GA) repeat units is higher in line B than in line A
(Huguet <i>et al.</i> , 2002)
Figure 1- 6. Retrotransposon-based molecular marker methods (Schulman <i>et al.</i> , 2007).
Figure 1- 7. Expected frequencies of gametes and genotypes in a backcross breeding scheme with the parents in coupling phase. The recombination value "r" can take values between 0 and 0.5, with 0 = complete linkage and 0.5 = free recombination
Figure 3-2. Principal component analysis (PCA) projections on axes 1 and 2, accounting for 0.4931 of total variance, for 410 RILs of durum wheat
Figure 3-3. Dendrogram of cluster analysis of 13 quantitative traits of durum wheat using Wards' method.
Figure 3-4. Cluster analysis of F ₅ families based on measured traits under rainfed conditions
Figure 3-5. Frequency distributions of measured traits of recombinant inbred lines
(RILs) under rainfed conditions

Figure 3-7. Example of AFLP pattern of RILs population of durum wheatError!
Bookmark not defined.
Figure 3-8. Example of ISSR pattern of RILs population of durum wheatError!
Bookmark not defined.
Figure 3-9. Sample electropherogram of SSR markers obtained with GeneMapper v4
Figure 3-10. Example of RAPD pattern of RILs population of durum wheatError!
Bookmark not defined.
Figure 3- 11. Linkage groups for the Zardak/249 F ₆ population for chromosomes129
Figure 3-12. QTL position on the chromosomes and LOD scores for the markers linked
to PH under rainfed conditions (A) and irrigated conditions (B), represented as the peaks
in the graph Error! Bookmark not defined.
Figure 3-13. QTL positions on the chromosomes and LOD scores for the marker linked
to PED under rainfed (A) and irrigated conditions (B), represented as the peaks in the
graph
Figure 3-14. QTL positions on the chromosomes and LOD scores for the marker linked
to AL under rainfed (A) and irrigated conditions (B), represented as the peaks in the
graph
Figure 3-15. QTL positions on the chromosomes and LOD scores for the marker linked
to NTPP under rainfed conditions, represented as the peaks in the graph137
Figure 3-16.QTL positions on the chromosomes and LOD scores for the marker linked
to NSPS under rainfed (A) and irrigated (B) conditions, represented as the peaks in the
graph
Figure 3-17. QTL positions on the chromosomes and LOD scores for the marker linked
to MGW under rainfed (A) and irrigated (B) conditions, represented as the peaks in the
graph142
Figure 3-18. QTL positions on the chromosomes and LOD scores for the marker linked
to SSW under irrigated conditions (B), represented as the peaks in the graph143
Figure 3-19. QTL positions on the chromosomes and LOD scores for the marker linked
to SW under irrigated conditions (B), represented as the peaks in the graph144
Figure 3-20. QTL positions on the chromosomes and LOD scores for the marker linked
to HI under irrigated conditions (B), represented as the peaks in the graph145
Figure 3-21. QTL position on the chromosome and LOD score for the marker linked to
RWL under rainfed conditions (A), represented as the peaks in the graph145
Figure 3-22. QTL position on the chromosome and LOD score for the marker linked to
ELWR under rainfed conditions (A), represented as the peaks in the graph146
Figure 3-23. QTL position on the chromosome and LOD score for the marker linked to
FL under rainfed (A) and irrigated (B) conditions, represented as the peaks in the
grap
Figure 3-24. QTL position on the chromosome and LOD score for the marker linked to
PED/PH under rainfed (A) and irrigated (B) conditions, represented as the peak in the
graph149

Figure 3-25. QTL positions on the chromosomes and LOD scores for the markers linked
to SpD under rainfed (A) and irrigated (B) conditions, represented as the peaks in the
graph
Figure 3- 27. The predicted genetic architecture of PH in RILs population of durum
wheat under two environmental conditions. The red ball represents QTL with main
additive effect. Chromosome region in yellow indicts the support interval of a QTL161
Figure 3-28. F-statistic plots from 1D genome scan for QTLs with individual effects.
One peak exceeds the threshold F-value
Figure 3-29. The predicted genetic architecture of SL in RILs population of durum
wheat under two environmental conditions. The red ball represents QTL with main
additive effect. The black ball represents epistatic QTL without individual effect. The
red line shows the epistatic interaction between two loci. Chromosome region in yellow
indicts the support interval of a QTL
Figure 3-30. 2D genome scan was performed for epistasis interaction for SL. Two
peacks has been detected exceeding the threshold F-value
Figure 3-31. The predicted genetic architecture of AL in RILs population of durum wheat under two environmental conditions. The red ball represents QTL with main
additive effect. The black ball represents epistatic QTL without individual effect.
Chromosome region in yellow indicts the support interval of a QTL. The red line shows
the epistatic interaction between two loci
Figure 3-32. F-statistic plots from 1D genome scan for QTLs with individual effects.
One peak exceeds the threshold F-value.
Figure 3-33. 2D genome scan is performed between the regions for epistasis interaction
for AL. One has been detected exceeding the threshold F-value
Figure 3-34. The predicted genetic architecture of NSPS in RILs population of durum
wheat under two environmental conditions. The red ball represents QTL with main
additive effect. Chromosome region in yellow indicts the support interval of a QTL164
Figure 3-35. F-statistic plots from 1D genome scan for QTLs with individual effects.
One peak exceeds the threshold F-value.
Figure 3-36. The predicted genetic architecture of HI in RILs population of durum
wheat under two environmental conditions. The black ball represents epistatic QTL
without individual effect. Chromosome region in yellow indicts the support interval of a
QTL. The red line shows the epistatic interaction between two loci165
Figure 3-37. 2D genome scan is performed between the regions for epistasis interaction
for HI. One has been detected exceeding the threshold F-value
Figure 3-38. The predicted genetic architecture of ELWR in RILs population of durum
wheat under two environmental conditions. The black ball represents epistatic QTL
without individual effect. Chromosome region in yellow indicts the support interval of a
QTL. The red line shows the epistatic interaction between two loci166
Figure 3-39. 2D genome scan is performed between the regions for epistasis interaction
for ELWR. One has been detected exceeding the threshold F-value167
Figure 3-40. The predicted genetic architecture of Fv/Fm in RILs population of durum
wheat under two environmental conditions. The red ball represents QTL with main
additive effect. The black ball represents epistatic QTL without individual effect.

the epistatic interaction between two loci		
Figure 3-41. 2D genome scan is performed for epistatic interactions for Fv/Fm. One has been detected exceeding the threshold F-value		
been detected exceeding the threshold 1-value.		
Table of Tables		
Table of Tables Contents page		
rog		
Table 1-1. Area, yields and production of durum wheat in the world during 2004 and 2005		
Table 1- 2. Durum use and quality requirements in different part of the world (Nachit <i>et al.</i> , 1992)		
Table 1-3. Expected trait values for a marker linked to a QTL in a DH population41		
Table 1- 4. Expected class frequencies for a QTL, Q, flanked by markers A and B, with		
recombination frequencies θAQ, θBQ and θAB between A and Q, B and Q, A and B respectively		
Table 2- 1. The list of the traits and abbrevaitons of the morphological traits65		
Table 2- 2. Name and characteristics of RAPD primers used for screening of parents of		
durum wheat population69		
Table 2- 3. The names and charecteristics of ISSR primers used for screening of parents		
of durum wheat population70		
Table 2- 4. Names and charecteristics of AFLP primer combination used for screening		
of parents of durum wheat population72		
Table 2- 5. Silver staining procedure of AFLP amplification products		
Table 2- 6. Names and reference of used SSR primers for screening of the parents of		
durum wheat population		
Table 3-1. ANOVA for the traits, showing the effects of blocks and check varieties79		
Table 3-2. Basis statistics (arithmetic mean, maximum and minimum values, standard		
deviation (SD) for the measured traits of durum wheat, and coefficient of variation		
(CV%) for analysis variance of checks		
durum wheat		
Table 3-4. Relative contribution in predicting wheat grain yield of durum wheat (model		
R ² , standard deviation and probability) by stepwise procedure analysis83		
Table 3-5. Regression coefficient (b), standard error (SE), t-value and probability (sig.)		
of the accepted variables that can be used to predict durum wheat grain yield by the		
stepwise procedure83		
Table 3-6. Path coefficient (direct and indirect effects) of the estimated yield attributes		
on grain yield variation in durum wheat85		
Table 3-7. Factor analysis for the estimated variables of durum wheat using principal		
component procedure		
Table 3-8. Number of selected F ₅ families through cluster analysis to form F ₆ poulation		
of durum wheat91		

Table 3-9. Statical parameters for the measured traits of the RIL population and parents
(P ₁ :Zardak, P ₂ : 249) under rainfed conditions93
Table 3- 10. ANOVA for the traits, showing the effects of blocks and check varieties
under rainfed conditions96
Table 3-11. Matrix of simple correlation coefficients for the traits under rainfed
conditions99
Table 3- 12. Correlation coefficients of drought indices
Table 3-13. Mean value and significant level of the parents (Zardak and 249) under
rainfed conditions (n=3).
Table 3-14. Statistical parameters for the measured traits of RIL population and parents
(P ₁ :Zardak, P ₂ :249) under irrigated conditions
Table 3-15. ANOVA for the traits, showing the effects of blocks and check varieties
under irrigated coditions
Table 3-16. Matrix of simple correlation coefficients fot the traits under irrigated
conditions
Table 3-17. Spearman rank correlation coefficient between agronomic traits for RILs
population of durum wheat under in two different environmental conditions (n=130).114
Table 3- 18. Mean value and significant level of the traits of the parents (Zardak and
249) under irrigated conditions (n=3)
Table 3-19. A summary of combined ANOVA over two different environmental
conditions
Table 3- 20. Relative loss (%) of traits in rainfed conditions compared to irrigated
conditions (P ₁ :Zardak, P ₂ :249).
Table 3- 21. Marker loci information on a linkage map of the Zardak \times 249 F_6
poulation
Table 3-22. Genetic characterization of QTL linked to PH under rainfed and irrigated
conditions
-
conditions 132
Table 3-24. Genetic characterization of QTL linked to AL under rainfed and irrigated conditions
Table 3-25. Genetic characterization of QTL linked to NTPP under rainfed
conditions 136
Table 3-26. Genetic characterization of QTL linked to NSPS under rainfed and irrigated
conditions
Table 3-27. Genetic characterization of QTL linked to MGW under rainfed and irrigated
conditions
Table 3-28. Genetic characterization of QTL linked to SSW under irrigated
conditions
Table 3-29. Genetic characterization of QTL linked to SW under rainfed and irrigated
conditions
Table 3-30. Genetic characterization of QTL linked to HI under rainfed and irrigated
conditions

Table 3-31. Genetic characterization of QTL linked to RWL2 under rainfed
conditions
Table 3-32. Genetic characterization of QTL linked to ELWR under rainfed
conditions
Table 3-33. Genetic characterization of QTL linked to FL under rainfed and irrigated
conditions147
Table 3-34. Genetic characterization of QTL linked to PED/PH under irrigated
conditions
Table 3-35. Genetic characterization of QTL linked to SpD under rainfed and irrigated
conditions
Table 3-36. Genetic characterization of QTLs linked to Fv/Fm under irrigated
conditions
Table 3-37. Kruskal-Wallis test showing the association between markers and Fv/Fm
under rainfed conditions
Table 3-38. Kruskal-Wallis test shows association between markers and DHE under
rainfed conditions
Table 3-39. Kruskal-Wallis test shows association between markers and DHE under
Irrigated conditions
Table 3-40. Kruskal–Wallis test shows association between markers and DFE under
rainfed conditions
Table 3-41. Kruskal-Wallis test shows association between markers and DFE under
Irrigated conditions
Table 3-42. Kruskal–Wallis test shows association between markers and DME under
rainfed conditions
Table 3-43. Kruskal-Wallis test shows association between markers and DME under
irrigated conditions
Table 3-44. MQM analysis for the traits under rainfed conditions for RILs population of
durum wheat
Table 3-45. MQM analysis for the traits under irrigated conditions for RILs population
of durum wheat
Table 3-46. QTLs and epistasis for the traits in RILs population of durum wheat160
Table 3- 47. Summarized results for mapping QTLs with individual effects in RILs
population of durum wheat
Table 3-48. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for AL
Table 3-49. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for BIO
Table 3-50. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for DFE. 172
Table 3-51. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for DHE
Table 3-52. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for DME. 173

Table 3-53. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for ELWR
Table 3-54. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for SSW
Table 3-55. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for SW
Table 3-56. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for FL
Table 3-57. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for Fv/Fm
Table 3-58. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for GY176
Table 3-59. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for HI
Table 3-60. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for MGW
Table 3-61. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for NSPP
Table 3-62. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for NSPS
Table 3-63. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for NTPP179
Table 3-64. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for PC
Table 3-65. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for PED
Table 3-66. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for PED/PH. 180
Table 3-67. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for PH
Table 3-68. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for RWC
Table 3-69. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for RWL182
Table 3-70. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for RWL2.
Table 3-71. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for SL
Table 3-72. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for SPAD
Table 3-73. Details of multiple linear regression analysis using ISSR, AFLP and RAPD
markers for SpD
Table 3-74. Informative markers affecting more than one traits under rainfecting
conditions

Table	3-75.	Informative	markers	affecting	more	tha	one	traits	under	irrigated
conditions										