Abstract

Developing crop cultivars with high grain yield has been the principal aim of durum wheat breeding programs worldwide. The potential yield is defined as the performance of an adapted genotype grown under optimal management and in the absence of biotic and abiotic factors. The grain yield of wheat can also be dissected into, spike characters (grain number/spike and grain weight/spike, number of spikelets/spike, spike fertility, number of grains/fertile spikelets and number of grains/total spikelets) and also it can be correlated with the agronomic traits (plant height, thousand-grain weight, test weight and harvest index) and morphological characters (peduncle length).

The objective of this thesis was to characterize the genetic nature of yield and its components in various environments and mapping genomic regions associated to these traits in a population of RILs of durum wheat derived from the cross Kofa x UC1113.

Based on this overall objective, the following three specific objectives were planned: 1. To quantify and evaluate the response of RILs in different environments of Argentina (location and year), 2. To estimate genetic parameters that permits the genetic-biometric characterization of the mentioned traits, 3. To map QTL associated with yield and its components, 4. To identify molecular markers linked to these traits, 5. To find correlations between yield and its components and in among components also, and 6. To determine pleiotropic regions for these traits.

To fullfil these objectives, the yield and its components were evaluated in a population of 93 RILs derived from the cross UC1113 x Kofa, parents and 8 commertial cultivars of Argentina. These materials were planted in four environments (CEI-Barrow 2006/07, INTA-Balcarce 2007/08, CEI-Barrow 2007/08 y ACA-Cabildo 2007/08).

Grain yield and its components evaluated in this thesis were expressed in the following units: grain yield (Kg/ha), thousand-grain weight (g), test weight (Kg/hl), plant height (cm), peduncle length (cm), grain weight/spike (g), harvest index (%), spike fertility (%) and in number for total spikelets/spike, grains/spike, grains/fertile spikelets and grains/total spikelets.

When growing in the field the RILs showed a particularity: the presence of white spikes in between the normal green ones. These white spikes were observed only in some of the spikes and with different magnitudes. The grain yield used for mapping was adjusted in the way mentioned by other authors (Khan et al. (2000) and uses in CIMMYT), to minimize or eliminate the effect of white spikes.

The phenotypic data of RILs showed a bi-directional transgressive inheritance for all the characters in all environments. According to Shapiro-Wilk test (α = 0.05) the distribution of frequencies of phenotypic values obtained (yield and its components for each environment) were normal in all the environments for most of the characters. The distribution was completely normal in all environments for the characters, plant height, total spikelts/spike and grain weight/spike, partially normal (from one to three environments) for the characters thousand-grain weight, test weight, peduncle length, number of grains/spike, number of grains/total spikelets, harvest index, spike fertility and number of grains/fertile spikelets. However, the character grain yield was not distributed normally in none of the environments considered.

The phenotypic variance for the characters number of grains/spike, grain weight/spike, thousand-grain weight, test weight, plant height, peduncle length, number of total spikelets/spike and number of grains/total spikelets, had a higher genetic component than the environmental one. This resulted in a high heritability for these characters. Spike fertility and number of grains/fertile spikelets showed the phenotypic variance more affected by the environment than from the genotype in two of the four environments. However, for grain yield, the phenotypic variance was highly influenced by the environment, higher than genotype one in majority of environments. The Genotype x Environment interaction resulted highly significant for all the characters, indicating that the differences in the characters among different genotypes are not the same in different environments.

The significant LOD threshold values for all the characters were calculated for each environment and on average of all by using the 1000 permutations test and was considered around 3 for all the characters. The threshold values for different characters ranged between 2.0 (spike fertility) and 3.4 (grain yield).

A total of 74 significant QTL and 36 probable QTLs were found for grain yield and its components. The significant QTL found in this thesis were: 5 for grain yield; 7 for number of grains/spike; 4 for grain weight/ spike; 8 for thousand-grain weight; 5 for test weight; 7 for plant height; 8 for peduncle length; 5 for harvest index; 6 for number of total spikelets/spike; 6 for spike fertility, 5 for number of grains/fertile spikelets and 8 for number of grains/total spikelets. The probable QTL were: 4 for grain yield; 3 for number of grains/spike; 5 for grain weight/ spike; 3 for thousand-grain weight; 4 for test weight; 2 for peduncle length; 5 for harvest index; one for number of total spikelets/spike; 2 for spike fertility, 6 for number of grains/fertile spikelets and one for number of grains/total spikelets.

In total, 80 new QTL (60 significant & 20 probable) were found for grain yield and its components. The new QTL were: 2 for grain yield; 7 for number of grains/spike; 5 for grain weight/ spike; 5 for thousand-grain weight; 7 for test weight; 3 for plant height; 10 for peduncle length; 8 for harvest index; 5 for number of total spikelets/spike; 8 for spike fertility; 11 for number of grains/fertile spikelets and 9 for number of grains/total spikelets. A less number of stable QTL were found for each character. The number of stable QTL for each character was: one for number of grains/spike; one for test weight; 5 for plant height; 4 for peduncle length; 3 for number of total spikelets/spike and one for number of grains/fertile spikelets. The number of probably stable QTL for each character was: one for grain yield; one for grain weight/ spike; 3 for thousand-grain weight; 2 for harvest index; 2 for spike fertility and one for number of grains/total spikelets.

The phenotypic variation for each character was in the following ranges: grain yield (9.67% to 27.51%). thousand-grain weight (9% to 42.01%). test weight (7.95% to 34.53%), plant height (8.41% to 45%), peduncle length (6.12% to 40.6%), harvest index (7.9% to 28%), number of total spikelets/spike (8% to 32.5%), number of grains/spike (8.35% to 24.6%), grain weight/ spike (8.54% to 22.4%), spike fertility (7.33% to 15.4%), number of grains/fertile spikelets (8.2% to 27.75) y number of grains/total spikelets (7.15% to 23%).

The additive effect for each character was in the following ranges: grain yield (109.9Kg/ha a 335.4Kg/ha), thousand-grain weight (0.60g to 1.46g), test weight (0.24Kg/hl to 0.56Kg/hl), plant height (1.55cm to 3.73cm), peduncle length (0.62cm to 1.63cm), harvest index (0.005% to 0.014%), number of total spikelets/spike (0.20 to 0.41), number of grains/spike (0.63 to 1.43), grain weight/ spike (0.03g to 0.07g), spike fertility (0.009% to 0.025%), number of grains/fertile spikelets (0.03 to 0.07) y number of grains/total spikelets (0.03 to 0.08).

For the character white spikes 7 significant and 4 probable QTLs were found. This character severely affected the grain yield and its components. There were 4 stable QTL for this character. This character showed a high heritability, ranging from 90-98% with an average of 94%. The phenotypic variance was found in a range of 3.03% to 24.45%. The additive effect ranged from 1.13% to 3.63%. Both the parents contributed favorable alleles for this character. The variety Kofa affected on the chromosomes 1B, 2B, 3A and 5A. The line UC1113 provided alleles over the chromosomes 3B, 5B and 7A.

UC1113 carried positive alleles for most of the characters like grain yield, number of grains/spike, grain weight/spike, thousand-grain weight, test weight, harvest index and number of grains/total spikelets. Those characters where both parents contributed with

favorable alleles were, plant height, peduncle length, number of total spikelets/spike, spike fertility y number of grains/fertile spikelets. As mentioned earlier, for the majority of QTL found, the favorable allele was inherited from UC1113 being the favorable parent for grain yield.

Pleiotropic regions or co-localization of various characters were found in different environments and in average of the environments. The chromosomes showing pleiotropic regions for most of the characters were: 2B associated with the marker *wmc361*, 3A associated with the marker *ksm28*, 3B associated with the markers *gwm493*, *barc147* y *cfd79*, 4A associated with the markers *gwm265* y *wmc258*, 4B associated with the marker *ksm62* y 5A associated with the marker *gwm126*. The plant height and peduncle length showed a stable association between them.

The correlation analyses showed highly significant correlations between different components of grain yield. Number of grains/spike and grain weight/spike showed a high positive correlation with grain yield, and also, they were correlated with all the other yield components. In addition, the characters correlated with some of the yield components in all environments, were: grain yield with grain number/spike, grain weight/spike y number of grains/total spikelets; 1000-grain weight with grain weight/spike; plant height with peduncle length, grain weight/spike y spike fertility; peduncle length with plant height y grain weight/spike; harvest index with grain number/spike, grain weight/spike, spike fertility, number of grains/fertile spikelets y number of grains/total spikelets; number of total spikelets/spike with grain number/spike y grain weight/spike; grain number/spike with grain yield, harvest index, number of total spikelets/spike, grain weight/spike, spike fertility, number of grains/fertile spikelets y number of grains/total spikelets; grain weight/spike with grain yield, 1000-grain weight, plant height, peduncle length, harvest index, number of total spikelets/spike, grain number/spike, spike fertility, number of grains/fertile spikelets y number of grains/total spikelets; spike fertility with plant height, harvest index, grain number/spike, grain weight/spike y number of grains/total spikelets; number of grains/fertile spikelets with IC, grain number/spike y grain weight/spike y number of grains/total spikelets with grain yield, grain number/spike, grain weight/spike, spike fertility y number of grains/fertile spikelets.

The direct or indirect selection for these components can increase the potential yield in durum wheat. The character white spikes showed negative correlations with all the yield components, and therefore the affected RILs should not be included in breeding programs.

In this thesis, various QTL were found throughout the chromosomes of durum wheat for the grain yield and its components. Those QTL and their associated markers can be used in durum wheat breeding programmes to obtain higher yields. This work was conducted in close collaboration with the Asociación de Cooperativas Argentinas and other national breeding companies of wheat and the breeding program of INTA through PAE 37108 (ANPCyT). The QTL found can be used for: introgression of favorable genes and QTLs into interesting plant materials, marker-assisted selection of plants in breeding programs and germplasm screening for the evaluated traits.

We can also conclude that all hypotheses were fulfilled:

Genomic regions were identified which are associated with yield and its components.

The response of different genotypes to environment was studied and differed in different levels for the different characters and the different environments.

The genetic map based on molecular markers allowed us to map QTLs and identify markers linked to QTL for the evaluated characters.