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Identification of Candidate Microsatellite Markers Associated with Agronomic Traits in Rice (*Oryza sativa* L.)

M. Z. Mattar[1] ,Kh. F.M. Salem[2]* and A. B. El- Abd[3]

[1] Botany Department, Faculty of Science, Menoufia University,
[2]Plant Biotechnology Department, Genetic Engineering and Biotechnology Research Institute (GEBRI), Sadat City University, Sadat City and [3]Rice Research Department, Filed Crops Research Institute, Agriculture Research Center (ARC), Giza. Egypt.

A DIVERSE collection of Egyptian and exotic rice genotypes, were evaluated for agronomic traits. Subsequently in order to assess the allele diversity of quantitative trait loci *(QTLs)* attributed to agronomic traits. The genotypes were characterized using a set of 23 microsatellite markers. In total, 24 significant marker-trait associations *QTLs* were identified; 2 for heading date, 10 for plant height, 2 for panicle length, 4 for number of panicles per plant, 1 for number of filled grains per panicle, 1 for 1000-grain weight and 4 for grain yield per plant. More of these *QTLs* were located on chromosomes 2 and 7. Association analysis of SSR markers showed 4 markers *RM6, RM118, RM151* and *RM307* had significant association with most of agronomic traits. Detection of *QTLs* for agronomic traits at different chromosomes indicated that these characters are controlled by multiple loci. Higher R^2 values were obtained for most traits and ranged from -0.366* to 0.695** for grain yield per plant and plant height, respectively. Genetic analysis identified the best rice microsatellite markers attributed to agronomic traits and they can be informative for improvement of agronomic traits through marker-assisted selection. Breeders can use this information to design crosses that assemble new potentially durable combinations of genes/*QTLs* to improve rice genotypes.

Keywords: Agronomic traits, Allele size, Marker-trait associations, Microsatellite, *Oryza sativa*, *QTLs*, Rice

Rice (*Oryza sativa* L.) is the second most important staple food crop for more than half of world's population (Delseny *et al.*, 2001 and Feng *et al.*, 2013). Grain yield is one of the most important and complex traits in cereal crops that does not evolve independently but shows correlations with other yield components traits. Thus, breeders have to consider correlated traits in breeding

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salemcairo@yahoo.com*Author for correspondence *E-mail:*

programs. Grain yield and its related traits are quantitatively inherited and controlled by many genes with small effects subject to environmental effects (Inostroza *et al*., 2009 and Shi *et al*., 2009). Genetic improvement of yield remains a major breeding objective to meet the ever increasing demand for food. In rice, grain weight is one of the three main yield components, the other two being number of panicles per unit area and number of grains per panicle (Fan *et al*., 2009). Hence, estimation of the positions and effects of quantitative trait loci (*QTLs*) for agronomic traits related to yield is vitally important for marker-assisted selection for yield improvement (Li *et al.*, 2011). *QTLs* related to yield have been identified through classical linkage mapping approaches (Moncada *et al*., 200l, Jiang *et al*., 2004, and Suh *et al*., 2005). With a few exceptions, most of these *QTLs* have not been successfully validated or consistently used in crop improvement (Bernardo, 2008).

Classical approaches are too simplistic to effectively model most of the genetic variation for complex traits, because they are unable to reflect the genetic realities of these traits (Cooper *et al*., 2005 and Holland, 2007). In rice marker-assisted selection (MAS) is a promising technique to enhance traits with economic and agricultural value (Yamamoto *et al*., 2009). DNA markers for genes/*QTLs* determined agronomic traits allow breeders to precisely select plans with beneficial traits in breeding programs. Marker-assisted selection (MAS) enhanced the cropping potential of an elite cultivar by enabling the development of versions of the cultivar with diverse heading dates. Four *QTLs* for heading date *Hd6, Hd1, Hd4*, and *Hd5* were introgressed (Takcuchi *et al*., 2006). Association mapping, has been practiced a number of plant species (Agramma *et al*., 2007; Mazzucato *et al*., 2008, Zhu *et al*., 2008 and Xu *et al*., 2014). Association mapping has the potential of simultaneous discovery of gene lock responsible for multiple traits with no need to develop permanent segregating populations.

As association mapping exploits the historical recombination events that have occurred during establishment of the sample population, higher mapping resolution could be obtained than that possible in small bi-parental experimental crosses (Flint-Garcia *et al*., 2005). This strategy has an attractive advantage in the ability to detect the comparative effects of multiple alleles at each genetic locus that exists in crop germplasm. Association mapping is a powerful tool for identifying quantitative trait loci (*QTL*), because it takes advantage of accumulated historic recombination events in natural populations. Therefore, it should be promising for identifying causative polymorphisms of complex traits (Stich *et al*., 2008). In particular, this approach is superior when genotypes are selected from breeding populations or collections (Thornsberry *et al*., 2001 and Kraakman *et al*., 2004).

However, association mapping is complicated by population structure in most germplasm sets (Flint-Garcia *et al*., 2003). Blast resistance gene pi21 was found to be linked with gene(s) associated with inferior eating quality (Fukuoka *et al*., 2009). Zhang *et al*. (2005) successfully conducted whole-genome

association analysis between microsatellite markers and multiple agronomic traits using discriminant analysis (DA) in 218 inbred lines of rice. Iwata *et al.* (2007) associated RFLP markers with the width and length of milled rice grains in a set of 332 rice germplasm using Bayesian method. SSR markers and their allele diversity are useful to effectively distinguish rice genotypes. This approach is now being used to differentiate rice germplasm with different sources of mineral elemental contents and phenotypic traits (Zeng *et al.*, 2009). Also, this approach used to differentiate rice germplasm for grain weight *GW2* (Dixit *et al.*, 2013), through the use of microsatellite markers. *QTLs* mapping of many important agronomic traits, a major goal in plant breeding, requires informative markers in an intra-specific context. The objectives of this study were to i) detect chromosomes that control agronomic traits, ii) determine candidate rice microsatellite markers associated with agronomic traits on a diverse collections, iii) study genetic variation for agronomic traits, (iv) provide useful information for a study on possible SSR functions and (v) demonstrate the utility of MTAs for agronomic traits.

Materials and Methods

Plant materials and phenotypic variation

A diverse collection of 22 Egyptian and exotic rice (*Oryza sativa* L.) genotypes were randomly selected and used to establish the experimental materials for this investigation. The genotypes were supplied by Agricultural Research Center [(ARC), Giza, Egypt], International Rice Research Institute, (Los Banos, Philippines) and National small grain collection, (USDA, ARS, USA). Details of rice genotypes presented in Table 1.

Genomic DNA isolation

DNA was extracted from fresh seedling leaves for each genotype following a modified CTAB method (McCouch *et al.*, 1988). Based on the rice microsatellite genetic linkage map of Akagi *et al.* (1996) and Temnykh *et al.* (2000), 23 rice microsatellite (RM) markers were selected to represent the entire rice genome. The loci, chromosomal location, primer sequence, annealing temperature (°C) and fragment size are presented in Table 2.

Field experiment

This investigation was carried out at the Experimental Farm of the Rice research and Training Center (RRTC), Sakha, Kafer El-Sheikh, Egypt. Divers collections utilized in this study were grown during the two rice succession growing seasons, 2011 and 2012. The experiment was arranged in a randomized complete block design (RCBD), with three replicates. Each rice genotype was transplanted into a plot; each plot comprised two rows, 5 meters long and contained 25 hills. Ordinary cultural practices for rice production were applied.

TABLE 1. List of rice cultivars used in the study.

No	Genotype Name	Origin	Source of seed	Subspecies Group
1	IR 20	Philippines	IRRI	*Indica*
2	IR 22	Philippines	IRRI	*Indica*
3	IR 24	Philippines	IRRI	*Indica*
4	IR 50	Philippines	IRRI	*Indica*
5	IR 64	Philippines	IRRI	*Indica*
6	IR 74	Philippines	IRRI	*Indica*
7	Bala	India	IRRI	*Indica*
8	IET 1444	India	IRRI	*Indica*
9	Arabi	Egypt	USDA, USA	*Japonica*
10	Agamy M1	Egypt	USDA, USA	*Japonica*
11	Nahda	Egypt	USDA, USA	*Japonica*
12	Yabani M1	Egypt	USDA, USA	*Japonica*
13	Yabani M7	Egypt	USDA, USA	*Japonica*
14	Yabani 15	Egypt	USDA, USA	*Japonica*
15	Yabani lulu	Egypt	USDA, USA	*Japonica*
16	Giza 14	Egypt	USDA, USA	*Japonica*
17	Giza 171	Egypt	ARC, Egypt	*Japonica*
18	Giza 172	Egypt	ARC, Egypt	*Japonica*
19	Giza 177	Egypt	ARC, Egypt	*Japonica*
20	Giza 178	Egypt	ARC, Egypt	*Indica/ Japonica*
21	Giza 181	Egypt	ARC, Egypt	*Indica*
22	Gz 1386-5-4	Egypt	ARC, Egypt	*Indica*

TABLE 2. SSR markers, chromosomal location, motive, annealing temperature (ºC), repeat category and expected fragment size.

No.	SSR markers	Chromosomal location	Motif	Annealing temperature (ºC)	Repeat category	Expected Fragment size (bp)
1	*RM 5*	1	(GA)14	55	di	84
2	*RM151*	1	(TA)23	55	di	197
3	*RM6*	2	(AG)16	55	di	163
4	*RM154*	2	(GA)21	60	di	106
5	*RM22*	3	(GA)22	55	-	194
6	*RM55*	3	(GA)17	55	di	213
7	*RM307*	4	(AT)14(GT)21	55	complex	104
8	*RM161*	5	(AG)20	60	di	116
9	*RM 413*	5	(AG)11	50	di	65
10	*RM133*	6	(CT)8	60	di	224
11	*RM162*	6	(AC)20	60	di	130
12	*RM11*	7	(GA)17	55	di	115
13	*RM118*	7	(GA)8	60	di	106
14	*RM408*	8	(CT)13	55	di	109
15	*RM433*	8	(AG)13	50	di	215
16	*RM215*	9	(CT)16	55	di	126
17	*RM285*	9	(GA)12	55	-	205
18	*RM271*	10	(GA)15	55	di	65
19	*RM 474*	10	(AT)13	55	di	195
20	*RM552*	11	(TAT)13	55	tri	153
21	*RM144*	11	(ATT)11	55	tri	208
22	*RM19*	12	(ATC)10	55	tri	195
23	*RM277*	12	(GA)11	55	di	108

Evaluation of agronomic traits

In total, 7 traits were scored for each genotype. The symbolization of *QTLs* follows the rules of MacIntosh *et al*. (2003) (Table 3). Ten guarded of each genotype from each replicate were selected randomly to determine characteristic phenotypes, including heading date (*Hd*), plant height (*Ht*), panicle length (*Pl*), number of panicles per plant (*NoP*), number of filled grains per panicle (*Nofg*), 1000-grain weight (*Tgw*) and grain yield per plant (*Gyp*).

Microsatellite markers analysis

A total of 23 rice microsatellite markers were selected for genotyping as given in Table 2. SSR markers were chosen on the basis of their proximity to genome specificity and according to information available in the Rice Genesdatabase (http:// www.gramene.org/microsat/Rmprimers. html) most of the marker positions within chromosomes were based on the published rice microsatellite from work map. Microsatellite amplifications, polymerase chain reaction and fragment analysis for SSR markers were performed according to Akagi *et al*. (1996) and Temnykh *et al*. (2000). Rice microsatellite (RM) designation, chromosomal location, motif, annealing temperature (**°C)** and fragment size location in 'IR 36' (bp) of the amplified loci were reported by Akagi *et al*. (1996) and Temnykh *et al*. (2000).

Statistical analysis

Data on each of the 7 agronomic traits were separately correlated t each of the 23 polymorphic rice microsatellite markers. When a genotype showed its heterozygosity at a certain SSR locus, the molecular weight for that SSR marker in that accession was represented by the mean of two allele size. Correlation was determined by applying Pearson's method. Statistical significance was defined at *P<0.05*. The coefficient of determination (R^2) was estimated for each of SSR markers using SPSS 10.5 software (SPSS, Inc., Chicago, USA).

Results

Association analysis

Significant association was observed for 17 of the 23 polymorphic microsatellite markers with at least one of the 7 agronomic traits and the 23 markers identified with R^2 >10 % for traits (explained more than 10% of the phenotypic variation for each trait) (Table 3). In total, 24 marker-trait associations, significant *QTLs* for agronomic traits were identified. More *QTLs* were located on 2 and 7 chromosomes. The *QTLs* were distributed across 12 chromosomes, ranging from 1 *QTL* on chromosomes 6, 8, 9, 10 and 12 to 4 *QTls* located on chromosomes 2 and 7, respectively. In this study, the microsatellite markers *RM6, RM118, RM151* and *RM307* were appropriate MTAs to improve agronomic traits because most of agronomic related traits such as *Hd*, *Ht*, *Pl*, *NoP*, *Nofg, Tgw* and *Gyp* were significant with these

microsatellite markers. A higher R^2 values were obtained for most agronomic traits and ranged from -0.366* to 0.695** for grain yield per plant and plant height, respectively. In total, 24 detected *QTLs*, 14 *QTLs* for *Hd, Ht, Pl, Nop, Nofg, Tgw* and *Gyp* might be the same as that obtained in earlier studies.

TABLE 3. Association of microsatellite markers with agronomic traits.

Trait	*QTL* symbol	Chromosome	Marker	R-value
Heading date (*Hd*)	*QHd.RRTC.1.1*	1	*RM151*	-0.471*
	QHd.RRTC.2.2	2	*RM006*	-0.387*
Plant height (*Ht*)	*QHt.RRTC.2.1*	2	*RM006*	-0.512**
	QHt.RRTC.2.2	2	*RM154*	0.427*
	QHt.RRTC.3.3	3	*RM022*	-0.506**
	QHt.RRTC.3.4	3	*RM055*	-0.362*
	QHt.RRTC.5.5	5	*RM161*	0.694**
	QHt.RRTC.5.6	5	*RM413*	-0.440*
	QHt.RRTC.6.7	6	*RM162*	0.695**
	QHt.RRTC.7.8	7	*RM011*	-0.645**
	QHt.RRTC.8.9	8	*RM433*	-0.632**
	QHt.RRTC.12.10	12	*RM019*	-0.610**
Panicle length (*Pl*)	*QPl.RRTC.4.1*	4	*RM307*	-0.426*
	QPl.RRTC.7.2	7	*RM118*	-0.600**
Number of panicles per plant (*Nop*)	*QNop.RRTC.1.1*	1	*RM005*	-0.409*
	QNop.RRTC.2.2	2	*RM006*	0.436*
	QNop.RRTC.7.3	7	*RM118*	-0.470*
	QNop.RRTC.11.4	11	*RM552*	-0.420
Number of filled grains per panicle (*Nofg*)	*QNofg RRTC.1.1*	1	*RM151*	0.506**
1000-grain weight (*Tgw*)	*QTgw.RRTC.10.1*	10	*RM271*	-0.412*
Grain yield per plant (*Gyp*)	*QGyp.RRTC.4.1*	4	*RM307*	-0.373*
	QGyp RRTC.7.2	7	*RM118*	-0.366*
	QGyp RRTC.9.3	9	*RM215*	-0.491*
	QGyp.RRTC.11.4	11	*RM552*	-0.73*

The statistics shown refer to the coefficient of determination (R^2), Only SSR markers with significant marker-trait association are given.
*, ** Indicate significance at the probability levels of 0.05 and 0.01, respectively.
(*Hd*) heading date, (*Ht*) plant height, (*Pl*), panicle length, (*NoP*), number of panicles, (*Nofg*), number of filled grains (*Tgw*) 1000-grain weight and (*Gyp*) grain yield per plant.

Marker-traits associations (MTAs) analysis
   Heading date (Hd)
   Correlation analysis indicated that there was a significant correlation in two *QTLs* (r = - 0.387* to -0.471*) of the 23 traits pairs between microsatellite allele size and *Hd* (Table 3). These two *QTLs* were designated as *QHd.RRTC.1.1* and *QHd.RRTC.2.2. Hd* showed a significant correlation with the allele size of *RM6* and *RM151* on chromosomes 2 and 1, respectively.

   Plant height (Ht)
   For *Ht*, the correlation analysis indicated that there was a significant correlation in ten *QTLs* (r = - 0.440* to 0.695**) of 23 pair traits between microsatellite allele size and *Ht* (Table 3). These ten *QTLs* were designated as *QHt.RRTC.2.1*, *QHt.RRTC.2.2*, *QHt.RRTC.3.3*, *QHt.RRTC.3.4*, *QHt.RRTC.5.5*, *QHt.RRTC.5.6*, *QHt.RRTC.6.7*, *QHt.RRTC.7.8*, *QHt.RRTC.8.9* and *QHt.RRTC.12.10*. *Ht* showed a significant correlation with the allele size of *RM6, RM154, RM22, RM55, RM161, RM413, RM162, RM11, RM433* and *RM19* on chromosomes 2, 3, 5, 6, 7, 8 and 12, respectively.

   Panicle length (Pl)
   From MTAs, there was a significant association with two *QTLs* (r = -0.426* to -0.600**) of 23 pair traits between microsatellite allele size and *Pl* (Table 3). These two *QTLs* were designated as *QPl.RRTC.4.1* and *QPl.RRTC.7.2. Pl* had a significant association with allele size of *RM307* and *RM118* on chromosomes 4 and 7, respectively.

   Number of panicles per plant (Nop): As for *Nop*, there was a significant correlation in four *QTLs* (r = -0.409* to 0.436*) of 23 pair traits between microsatellites allele size and *Nop* (Table 3). These four *QTLs* were designated as *QNop.RRTC.1.1*, *QNop.RRTC.2.2*, *QNop.RRTC.7.3*, and *QNop.RRTC.11.4*. *Nop* showed a significant correlation with some allele size of *RM5, RM6, RM552* and *RM118* on chromosomes 1, 2, 11 and 7, respectively.

Number of filled grains per panicle (Nofg): A significant MTAs only in one *QTL* (r = 0.506**) of 23 pair traits was obtained between microsatellites allele size and *Nofg* (Table 3). These *QTL* was designated as *QNofg.RRTC.1.1. Nofg* showed a significant correlation with the allele size of *RM151* on chromosome 1.

1000-grain weight (Tgw) : Concerning the *Tgw,* there was a significant correlation in one *QTL* (r = -0.412*) of 23 pair traits between microsatellites allele size and *Tgw* (Table 3). These *QTL* was designated as *QTgw.RRTC.10.1. Tgw* showed a significant correlation with allele size of *RM291* on chromosome 10.

Grain yield per plant (Gyp): There was a significant correlation in four *QTLs* (r = -0.366* to 0.491*) of 23 pair traits between microsatellites allele size and *Gyp* (Table 3). These four *QTLs* were designated as *QGyp.RRTC.4.1, QGyp.RRTC.7.2, QGyp.RRTC.9.3,* and *QGyp.RRTC.11.4. Gyp* showed a significant correlation with allele size of *RM215, RM307, RM552* and *RM118* on chromosomes 9, 4, 11 and 7, respectively.

Discussion

Yield is the most important and complex trait for genetic improvement in cereal crops, and marker-assisted selection enhances the improvement of efficiency. Marker-trait associations (MTAs) offers a very good tool for rice breeders to obtained high yield. Selection can be done on the markers associated with the targeted traits by using DNA-markers. Once, the phenotypic traits are fixed, breeders can evaluate large numbers of progenies for yield performance in a conventional way. A combination of MTAs and conventional evaluation could significantly improve the breeding program efficiency, its process and new released cultivars (Collard and Mckill, 2008).

The association between markers and genes/*QTLs* controlling the targeted traits must be first established prior the marker associated selection (MAS) process. This study was conducted to identify *QTLs* correlated with agronomic traits in rice. Microsatellite markers used were well distributed amongst the 12 chromosomes, (Cho *et al*., 2000 and Temnykh *et al*., 2000). Heading date (*Hd*) is a major determinant of the regional and seasonal adaptation of rice varieties. Data presented in this study clearly identified two *QTLs* for *Hd* associated with two microsatellite markers *RM6* and *RM151* on chromosomes 1 and 2, respectively. Yamamoto *et al*. (2000), have a putative *QTL* for heading date (*Hd*) on chromosomes 2 and 3. For heading date, the *QTL* associated with *Hd* (*QHd.RRTC*.2.2) on chromosome 2, might be the same as that found recently (Yamamoto *et al*., 2000). Plant height (*Ht*) is one of the most important traits related to plant status and yield potential. In the current study, a total of ten *QTLs* were identified for plant height on chromosomes 2, 3, 5, 6, 7, 8 and 12. There were several reported molecular marker based genetic analyses of plant height in rice, which detected a number of *QTLs* on chromosomes 1, 2, 4, 5, 6, 9 and 11 (Lin *et al*., 2011), Huang *et al*. (1996) analyzed *QTLs* for plant height in five rice populations and identified 13 major dwarfing genes were located in close proximity to these *QTLs*. Moreover, Yu *et al*. (2002) detected four *QTLs* for *Ht* on chromosomes 1, 5, 7, and 11. More recently, a gene for *Ht* on chromosome 5 was cloned using a map based cloning strategy (Ashikari *et al*., 1999) and on chromosomes 1, 3 and 7 (Hittalmani *et al.*, 2003). With regard to *Ht*, 7 *QTLs* (*QHt.RRTC.1.1, QHt.RRTC.2.2, QHt.RRTC.3.3, QHt.RRTC.3.4, QHt.RRTC.5.5, QHt.RRTC.5.6* and *QHt.RRTC.7.8*) from 10 detected were located on chromosomes 2, 3, 5, 6, 7, 8 and 12, respectively. The *QTLs* on chromosomes 2, 3, 5, 6 and 7 respectively, might be the same as that found by Ashikari *et al*. (1999), Yu *et al*. (2002), Hittalmani *et al*. (2003) and Lin *et al*. (2011).

For *Pl*, two *QTLs* were associated with two rice microsatellite markers *RM307* and *RM118* on chromosomes 4 and 7. Ahamadi *et al*. (2008) found *QTLs* for *Pl* on chromosomes 2, 4, 11, and 12. In previous studies, the *QTL* (*QPl.RRTC*.4.1) for *Pl* on chromosome 4 might be the same as that found by Ahamadi et al. (2008). Concerning the *Nop*, four *QTLs* were associated with microsatellite markers *RM5 RM5 RM6 RM118* and *RM552* on chromosomes 1, 2, 7 and 11. Hittalmani *et al*. (2003) reported one *QTL* was detected for *Nop* on chromosomes 1, 4 and 12. Also, Zhu *et al*. (2011) detected *QTL* for *Nop* on chromosome 1. In this case, the *QTL* (*QNop.RRTC*.1.1) for *Nop* on chromosome 1 might be the same as that found recently by Hittalmani *et al*. (2003) and Zhu *et al*. (2011). Large number of well-filled grains per panicle (*Nofg*) is an important yield component trait in rice. In this study, *QTL* for *Nofg* was identified by SSR marker *RM151* on chromosome 1. Ahamadi *et al*. (2008) detected a total of three *QTLs* for panicle grain number was on chromosomes 1 and 12. In this case, the *QTL* (*QNofg.RRTC*.1.1) for the number of filled grains on chromosome 1 might be the same as that found earlier by Ahamadi *et al*. (2008). 1000-grain weight (*Tgw*) is an important factor affecting grain yield as well as grain quality in rice. In the present study, *QTL* for 1000-grain weight was associated with SSR marker RM271 on chromosome 10. Tang *et al*. (2013) found a number of *QTLs* for 1000-grain weight on chromosomes 2, 3, 5, 6, 8 and 10. In this case, the *QTL* (*QTgw.RRTC*.10.1) for 1000-grain weight on chromosome 10 might be the same as that found recently by Tang *et al*. (2013). (*Gyp*) is a complex trait consisting of several yield components. It is of great importance to reveal the genetic relationships between *Gyp* and its yield components at the *QTL* level for multi-trait improvement in rice. In the present study, four *QTLs* for *Gyp* were associated with microsatellite markers *RM307, RM118, RM215* and *RM552* on chromosomes 4, 7, 9 and 11. Liu *et al*. (2008) detected 10 *QTLs* for *Gyp* on chromosomes 1, 2, 3, 4, 7, 8, and 12. The *QTLs* (*QGyp.RRTC*.4.1 and *QGyp.RRTC*.7.2) for *Gyp* on chromosomes 4 and 7 might be as that found by Liu *et al*. (2008).

Marker trait association (MTA) is new approach in cereal genetics and particularly in rice. In contrast to conventional bi-parental mapping, which can only analyze allelic differences between two parents, association mapping attempts to scan genetic variation across a wide spectrum of genotypes. The present study underlines the value of genetic basis of agronomic traits even with a relatively small collection of genotypes. A substantial number of MTAs for the whole set of agronomic traits were detected. Many loci were detected that coincide with known major genes/*QTLs* for agronomic traits, indicating the power of association mapping. Additionally, potential novel loci were identified that may help to better understand the architecture of complex genetic traits. Based on marker approach, the novel loci provide opportunities for further improvement of rice. Breeders can use this information to design crosses that

assemble new, potentially durable combinations of agronomic traits genes/*QTLs* to improve rice genotypes.

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تحديد المعلمات الجزيئية المرتبطة بالصفات المحصولية فى الأرز (*Oryza sativa* **L.**)

مجدي زكى مطر * ، **خالد فتحى محمود سالم** ** **و عبد المعطى العبد** ***

* قسم النبات – كلية العلوم– جامعة المنوفية و ** قسم البيوتكنولوجيا النباتية – معهد الهندسة الوراثية والتكنولوجيا الحيوية– جامعة مدينة السادات– مدينة السادات و ***قسم بحوث الأرز – معهد بحوث المحاصيل – مركز البحوث الزراعية – الجيزة – مصر .

يُعد استخدام المعلم الجزيئى الميكروستاليت (microsatellite) هام لتحديد الأليلات المرتبطة بالصفات المحصولية فى الأرز. ولقد أجريت هذه الدراسة بهدف:

تحديد الكروموسومات التى تتحكم في وراثة الصفات المحصولية.

تحديد المعلمات الجزيئية الميكروستاليت المرتبطة بالصفات المحصولية باستخدام مجموعة متنوعة من أصناف الأرز المصرية والأجنبية.

دراسة التباين الوراثي للصفات المحصولية.

توفير المعلومات الهامة للأستفادة من الأهمية الوظيفية للمعلم الجزيئي الميكروستاليت.

اثبات فائدة استخدام الأنتخاب باستخدام المعلمات الجزيئية للصفات المحصولية.

استخدم فى هذه الدراسة ثلاثة وعشرون بادئاً بالإضافة إلى سبعة صفات مورفولوجية هى ميعاد التزهير، طول النبات، طول السنبلة ، عدد السنيبلات لكل نبات ، عدد الحبوب بكل سنبلة ، وزن الألف حبة، محصول النبات الفردي وذلك لتحديد الأليلات المرتبطة بالصفات المحصولية. وفيما يلي ملخص لأهم النتائج :

تم تحديد ٢٤ موقعاً للصفات الكمية (*QTLs*) ، وكانت موزعة على الصفات المحصولية كما يلى : موقعين لصفة ميعاد التزهير، عشرة مواقع لصفة طول النبات ، موقعين لصفة طول السنبلة ، أربعة مواقع لصفة عدد السنيبلات على النبات ، وموقع واحد لصفة عدد الحبوب بكل السنبلة ، موقع واحد لصفه وزن الألف حبة ، واربعة مواقع لصفه محصول النبات الفردي. ووجد أن معظم هذه المواقع موجود على الكروموسومين ٢، ٧.

أظهرت النتائج باستخدام بادئات التكرارات المتسلسلة البسيطة ، أن أكثر المعلمات الجزيئية ارتباطا بمعظم الصفات المحصولية هى *RM6*، *RM118*، *RM151* ، *RM307*. كما أن وجود مواقع الـ*QTLs* المرتبطة بالصفات المحصولية على كروموسومات مختلفة مما يدل على أنه قد يتحكم في وراثه عديد من المواقع الوراثية.

أوضحت النتائج أن أعلى قيمة لمعامل الارتباط (R^2) لمعظم الصفات وتراوحت ما بين (*٠,٣٦٦-) الى (**٠,٦٩٥) لصفة محصول النبات الفردي وطول النبات على التوالى.

حدد التحليل أفضل معلم جزيئى للأرز نسبة إلى الصفات المحصولية ، وأنه يمكن لمربي الأرز تحسين الصفات المحصولية من خلال الانتخاب بمساعدة تلك المعلمات الجزيئية ، كما يمكن لمربي النبات استخدام هذه المعلومات لتحديد الهجن التي تجمع تراكيب جينية *QTLs* جديدة ، لتحسين التراكيب الوراثية في الأرز.