

MICROSATELLITES AS MARKERS FOR EGYPTIAN WHEAT GENOTYPING

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ABSTRACT

Microsatellite markers have been shown to be highly polymorphic and simple to use in hexaploid wheat. This study was undertaken with the following objectives: (1) to assess the level of polymorphism among 19 Egyptian wheat varieties and (2) to study the potential of microsatellite markers and specify microsatellite(s) in particular for Egyptian wheat genotype identifications. A total of 42 microsatellite primers were included which, were located on all 21 chromosome pairs with distribution of one microsatellite marker per chromosome-arm of A, B and D genomes. The total number of alleles detected was 172 and the number amplified by each locus ranged from 2 to 10 with an average of 4.10 alleles. Calculated polymorphic information content (PIC) values ranged from 0.11 to 0.86 with 30 loci (71.43%) scoring 0.50 or higher and the average was 0.57. In the present study, only seven primers of the 42 could discriminate the 19 Egyptian wheat genotypes. Therefore, the present set of the 42 microsatellite primers would be useful for detecting polymorphism and for DNA fingerprinting of Egyptian wheat genotypes. Finally, this set of microsatellite markers could act as a reference set of markers for a range of research application for Egyptian wheat.

INTRODUCTION

Wheat genotyping or DNA fingerprinting of wheat, is a technology that has very widespread practical application. It has application in the identification of wheat for commercial purposes, breeding and research. Commercial applications include the protection of plant breeders' rights, and patents, quality control in wheat production and processing and labeling of wheat-derived foods and other products. Wheat breeding applications range from marker-assist selection to the conformation of identity of parents and progeny in breeding populations. Research applications, also include the analysis of evolutionary relationships and population genetics.

Genomic polymorphism can arise between individuals through several different mechanisms. These mechanisms include single nucleotide changes, deletions and insertions and above all, through variable numbers of simple sequence repeats namely, microsatellites. Microsatellites are repetitive length of a simple sequence of DNA nucleotides where the repeat unit is usually 1-6 base pairs. Their relative abundance, co-dominant and highly polymorphic nature and ease of use made microsatellites valuable molecular markers for use in genetic studies (Li *et al.* 2002). The use of microsatellites in a range of crop species has been reported for applications such as varietal identification, genetic diversity, genetic map development and markers assisted selection. The development, assessment and application of microsatellites in hexaploid wheat is also well documented (Sourdille *et al.* 2004, Dreisigacker *et al.* 2004 and Varshney *et al.* 2005). Moreover, microsatellites show a much higher level of polymorphism and more informative in hexaploid wheat than any other marker systems (Huang *et al.* 2002 and Li *et al.* 2003).

In this communication, it has been reported the results of a study involving the screening of 19

wheat genotypes using 42 microsatellite primers. The study was undertaken with the following objectives: (1) to assess the level of polymorphism among 19 Egyptian wheat varieties and (2) to study the potential of microsatellite markers in general and specify microsatellite(s) in particular for Egyptian wheat genotype identifications.

MATERIALS AND METHODS

Plant materials

The plant materials used in this study consisted of 19 Egyptian wheat varieties (Table 1). These varieties were regarded as a representative of available wheat varieties adopted by breeders.

DNA extraction

Total genomic DNA was extracted from five plants of each variety according to the protocol of Riede and Anderson (1996) with some modifications.

Microsatellite marker analysis

Microsatellite analysis was carried out using 42 microsatellite markers for the 19 wheat varieties. PCR reactions were performed in a total volume of 10 μ l containing 100 nM of each primer, 0.2 mM of each deoxynucleotide, 1.5 mM $MgCl_2$, 0.5 unit Taq polymerase and 30-45 ng template DNA. After initial denaturation step for 10 min at 94 °C, 35 cycles were performed with 1 min at 94 °C, 1 min at 50, 55 or 60 °C (depending on the individual primer), 2 min at 72 °C, followed by a final extension step of 10 min at 72 °C. Products of PCR were run on polyacrylamide gels containing 32% (v/v) formamide as described by Litt *et al.* (1993) and were visualized by silver staining technique according to the protocol of Bassam *et al.* (1991). All steps of staining were performed in plastic containers. Silver nitrate was used three times, for each the time of treatment was increased 10 min. Developer solutions were prepared two to three hours before utilization and cooled to low temperature (4 °C before use).

Data analysis

Allele types at the 42 microsatellite marker loci were determined for each variety. Also, the polymorphic information content (PIC) value was calculated for each marker according to the simplified version of Anderson *et al.* (1993) formula:

$$PIC = 1 - \sum p_i^2$$

Where p_i is the frequency of the i th allele for each marker.

Finally, Duncan's Multiple Range Test (Snedecor and Cochran, 1976) was conducted for allele distribution of the 42 microsatellite marker loci values among the three genomes and also, among the seven homocologous chromosomes of the 19 hexaploid Egyptian wheat varieties used.

RESULTS DISCUSSION

The present study reinforces the utility of microsatellite primers for providing unique genetic identities or fingerprints of individual Egyptian wheat variety. The relatively high allele frequencies of the microsatellites combined with their even distribution throughout the whole genome made them most suitable for procuring such information.

In this work, a total of 42 microsatellite primer sets were used which were selected among primer pairs of Roder *et al.* (1998) and designated with the prefix "GWM". Also, two microsatellite markers were used; designated with the prefix "BARC"; and kindly provided by Q. J. Song and P. Cregan, USDA-ARS, Beltsville, MD, USA. For an even coverage of the total wheat genome one microsatellite was selected for each chromosome-arm. These microsatellites, in addition to their coverage of the wheat genomes (A, B and D), they were included in this investigation because of their reproducible amplification and clearly distinguishable fragments. They were located on all the 21 chromosome pairs with distribution of one microsatellite marker per chromosome-arm of A, B and D genomes (Table 2). Also, all varieties used in this study were adopted by Egyptian breeders. These varieties were regarded as a representative random sample of the available Egyptian wheat accessions.

The PCR results using primers for loci GWM 368 (A), GWM 140 (B) and GWM 155 (C) are shown in Figure (1). It can be seen that the amplicons exhibited a molecular mass in the range of 245- 250 bp for GWM 368, 200-250 bp for GWM140 and 140-150 bp for locus GWM 155, respectively. Estimation of the molecular weight was always based on the band displaying the highest mass because as a rule, amplification of repeats consisting of a few nucleotides generates an array of bands (Hayden and Sharp, 2001a and b; Brian *et al.*, 1997; and Rodriguez and Zapata, 2002). The polymorphisms observed in Figure (1) are fairly typical of the pattern obtained for most loci.

The amplification profiles obtained with 42 individual microsatellite primer pairs could be grouped into three categories: (1) those containing one prominent fragment (Figure 1a), (2) those containing two co-migrating prominent fragment with equal spacing (Figure 1b), and (3) those containing three fragments including the co-migrating prominent fragments with equal spacing (Figure 1c). While scoring the above amplification profiles, care was taken to exclude the possibility of stuttering effect, particularly in the case of two co-migrating prominent fragments. In each case of two co-migrating prominent fragments, it was considered they are belonging to one locus.

Number of alleles:

Using the above criteria, the total number of alleles detected was 172 and the number amplified by each locus ranged from 2 to 10. The average, 4.10 alleles was detected per microsatellite primer pair. Other studies found that the average number of alleles per primer ranged from 3.6 to 18.1 (Prasad *et al.*, 2000; Ahmad, 2002; Christiansen *et al.*, 2002; Fahima *et al.*, 2002; Huang *et al.*, 2002; Kobiljaki *et al.*, 2002 and Dreisigacker *et al.*, 2004). The number of varieties or accessions used in previously mentioned references ranged from 13 to 998. Therefore, comparing these researchers data with this study, it can be concluded that the number of alleles detected is relatively adequate number. The most likely factor accounts for the differences in estimates of total number of alleles is the differences in sample sizes. Further evidence was detected from another study in our laboratory (Fahmi *et al.*, 2004) in which twenty seven microsatellite markers were used to measure genetic diversity among 11 Egyptian wheat varieties, where, only five these varieties were included in the present study. The total number of alleles detected was 91 among the 11 varieties and the number of alleles detected per locus ranged from 1 to 6 with a mean of 3.37 alleles per locus. The main difference with the previous study was in number of varieties used, where increasing number of varieties used increased number of detected alleles.

Polymorphism Information Content (PIC)

Polymorphism Information Content (PIC) values, as a measure of gene diversity at a locus, were calculated on allele sizes from the 19 varieties with a total of 42 PIC values being reported. The presence of null alleles was included in the calculation of the 42 scores. Calculated PIC values (excluding monomorphic microsatellites) ranged from 0.11 to 0.86 with 30 loci (71.43%) scoring 0.50 or higher with average 0.57. PIC value depends on the diversity among the used accessions and does not depend on the number of used accessions. For example, Huang *et al.* (2002) who used 998 accessions, obtained 0.77 PIC value, while Prasad *et al.* (2000) who used 55

accessions, obtained almost the same PIC value of 0.71. Consequently, our PIC value (0.57) reflects the diversity of the studied varieties. The other study in our laboratory of Fahmi *et al.* (2004) indicated that the average of PIC value of 0.626, which was in the same range of the present study considering the number of varieties used.

The correlation coefficient between PIC values and the number of alleles was high and significant; $r = 0.72$ ($P < 0.05$). The linear relationship between them is shown in Figure (2). This means that the value of PIC increased with the number of alleles at a given locus. Therefore, the number of alleles can be used for evaluation of genetic diversity in this study. These results did not agree with those Prasad *et al.* (2000) who reported that the PIC value was not correlated with the number of alleles. However, the results agreed with the study of Huang *et al.* (2002). This discrepancy among different studies may be due to the differences in the diversity between the varieties under study and the type of the microsatellites used.

Distribution of alleles at A, B and D genomes

Although the largest total number of alleles detected was found in the B genome, there were no significant differences were found among the three genomes in the allele number. Also, the numbers of alleles per locus were not significantly different among the three genomes, but the largest number was at the B genome too. These results indicated equal contributions of three genomes to genetic variation of the varieties under study.

The lowest number of alleles per locus among the seven homoeologous groups was observed in the homoeologous group 4 with the lowest PIC value. However, no significant differences among homoeologous groups were noticed in PIC value or in allele per locus. Similar results were reported by Huang *et al.* (2002), Byoko *et al.* (1999) and Ma *et al.* (2001). It is most likely that the chromosome structure of homoeologous group 4 is conserved or that some factors for important characters are located on these chromosomes. Therefore, any large variation or mutation occurring in these chromosomes might lead to the death of plants. It is known that one recessive gene and one dominant gene for male sterility were located on the short arm of chromosomes 4B and 4D of wheat, respectively (Barlow and Driscoll 1981; Liu and Deng 1986).

DNA polymorphism and genotype identification

Microsatellite primer pairs are locus-specific and are therefore, generally considered to be single locus makers as against other molecular markers like RFLP probes, AFLP and RAPD, which are multilocus in nature. In the present study 42 microsatellite loci were identified using the 42 primer pairs (a locus for each primer). The microsatellite loci are also multiallelic (2-10 alleles per locus with a mean of 4.1

alleles/locus in the present study) and the alleles co-dominant, thus suggesting their relative superiority in detecting DNA polymorphism over some other markers (e. g. RAPD and AFLP), which are biallelic and dominant with multilocus. The co-dominant nature of microsatellite primers is useful, as it also enables the detection of heterozygosity at specific loci. Another advantage of wheat microsatellites over other markers is their specificity, since microsatellite homoeoloci on three chromosomes of the same homoeologous group, if present, are generally not amplified with the same primer pair. In contrast to this, the same RFLP probe would generally identify the homoeoloci as RFLPs (Devos and Gale, 1992; Devos *et al.* 1993; and Xie *et al.* 1993).

Keeping in mind their relative superiority in detecting DNA polymorphism as mentioned above, the utility of 42 specific microsatellites markers was also assessed for their power to uniquely discriminate the 19 wheat genotypes that were included in the present study. The results showed that a single microsatellite marker, GWM582, was sufficient to discriminate six genotypes; the two microsatellites (GWM582 and GWM140) discriminated nine genotypes and three microsatellites (GWM582, GWM140 and GWM301) discriminated 12 genotypes. A further addition, as many as, four more markers (GWM155, GWM135, GWM369 and GWM261), thus making a set of seven microsatellite markers, which were successful to discriminate all the 19 genotypes. However, the rest of the markers did not increase the discriminating ability of the genotypes. Since, in the present study, only seven primers from the 42 could discriminate as many as 19 Egyptian wheat genotypes. Then, the present set of the 42 microsatellite primers would be useful for detecting polymorphism and for DNA fingerprinting of a large number of Egyptian wheat genotypes. This discriminating ability of this set may be due to its uniform distribution across the three genomes.

In conclusion, the present study in Egyptian bread wheat has demonstrated that the microsatellite-based marker system can be effectively and efficiently utilized for variety of studies involving the DNA polymorphism, where, during the present study, it was possible to assess the relative superiority of microsatellites in detecting DNA polymorphism in Egyptian wheat varieties. Also, the super discriminating ability of the microsatellite markers in Egyptian wheat has been proven. Since only seven primers out of 42 were able to discriminate the 19 varieties under study. Also, this set of microsatellite markers could act as a reference set of markers for a range of research application for Egyptian wheat. Finally, this research should contribute to complete the efficiency of Egyptian wheat breeding programs.

Table 1. Pedigree of Egyptian wheat varieties used in microsatellite analysis.

Varieties	Pedigree
Giza 155	Rgent/2* Giza139//Mida-Cadet/2*Hindi62
Giza 157	Giza155//Pit62/LR6413/Tzpp/Knot
Giza 160	Chenab70/Giza155
Giza162	Vcni//Cno 67/7C/3/Kal/Bb CM8399-D-4M-3Y-1M-1Y-1M-0Y
Giza163	<i>T. aestivum</i> /Bon/Cno/7C CM33009-F-15M-4Y-2M-1M-1M-1Y-0Y
Giza 164	KVZ/Buha "s" //Kal/Bb CM33027-F-15M-500y-0M
Giza 165	0Mcno/Mfd//Mon "s" CM43339-C-1Y-1M-2Y-1M-2Y-0B
Giza 167	Au/UP301//G11/SX/Pew "s"/4/May "s" //Pew "s" CM67245-C-1M-2Y-1M-7Y-1M-0Y
Gemmeiza 1	Maya74/On//1160.147/3/Bb/1991 Gall/4/Chat "s" CM58924-1 GM- 0GM
Gemmeiza 3	Bb/7C*2//Y50/Kal*3//Sakha8/4/Prv/WW/5/3/Bg "s" //OnCGM 4024-1GM-13GM-2GM-0GM
Sakha8	Indus 66 X Norteno "S"-Pk 348
Sakha61	Inia/RL 4220//7C/Yr "S" CM 15430-25-55-0S-0S
Sakha 69	Inia/RL4220//7C/Yr "s" CM 15430-25-65-0S-0S
Sakha 92	Napo 63 x Inia 66 - Wren
Sids 6	Maya "s" /Mon "s" /CMH74.A592/3/Sakha8*2 SD10002-4SD-3SD-1SD-0SD
Sids 7	Maya "s" /Mon "s" /CMH74.A592/3/Sakha8*2 SD10002-8SD-1SD-1SD-0SD
Sids 8	Maya "s" /Mon "s" /CMH74.A592/3/Sakha8*2 SD10002-14SD-3SD-1SD-0SD
Sids9	Maya"s" / Mon"s" /4/ CMH 72.428 / MRC // Jup /3/ CMH 74a582 /5/Giza 157*2 SD10003
Sahel1	N.S 732 /PIMA / Veery "S" sD 735-4 sD-iSD-OSD

Table (2): Microsatellites identified based on Chromosome-arm Location, range of fragment size, number of alleles and polymorphic information content (PIC) value in Egyptian wheat.

Microsatellite	Chromosome-arm Location	Range of fragment size	No of alleles	PIC
GWM 136	1AS	120	2	0.47
GWM 135	1AL	240-330	6	0.81
GWM 582	1BS	130-210	10	0.86
GWM 140	1BL	200-250	10	0.79
GWM 458	1DL	115-125	3	0.66
GWM 33	1DS	110-130	3	0.23
GWM 95	2AS	110-125	2	0.11
GWM 294	2AL	85-115	5	0.59
GWM 429	2BS	210-330	4	0.38
GWM 120	2BL	140-170	4	0.71
GWM 261	2DS	165-190	3	0.54
GWM 301	2DL	160-270	9	0.80
GWM 369	3AS	150-310	6	0.68
GWM 155	3AL	140-150	3	0.54
GWM 376	3BS	145	2	0.19
GWM 247	3BL	160-190	5	0.73
GWM 161	3DS	150-155	3	0.65
GWM 3	3DL	80-90	3	0.64
GWM 165	4AS	180-270	2	0.49
GWM 397	4AL	160-220	5	0.62
GWM 368	4BS	245-250	2	0.27
GWM 149	4BL	140-170	5	0.74
Xbarc98	4DS	150-155	2	0.27
GWM 194	4DL	130-150	3	0.54
GWM 129	5AS	200-240	2	0.39
GWM 126	5AL	200	2	0.27
GWM 234	5BS	200-250	3	0.63
GWM 371	5BL	180-310	5	0.72
GWM 190	5DS	200-210	4	0.64
GWM 174	5DL	180-270	4	0.68
GWM 334	6AS	110-130	5	0.66
GWM 169	6AL	170-230	5	0.68
GWM 361	6BS	140	2	0.50
GWM 219	6BL	155-200	5	0.71
GWM 325	6DS	140-150	4	0.69
Xbarc23	6DL	220-225	2	0.49
GWM 471	7AS	140-180	3	0.60
GWM 332	7AL	200-290	4	0.68
GWM 46	7BS	145-180	4	0.50
GWM 577	7BL	140-180	4	0.48
GWM 295	7DS	210-250	5	0.72
GWM 437	7DL	110-130	7	0.76
Total			172	
Average		80-350	4.10	0.57

Table (3): Statistics of allele distributions at 42 microsatellite loci in the three genomes and homologous chromosomes of the 19 hexaploid Egyptian wheat varieties used.

	Number of alleles	Number of alleles per locus	Polymorphic information content
Genome			
A	52 ^a	3.71 ^o	0.54 ^o
B	65 ^a	4.64 ^o	0.59 ^o
D	55 ^a	3.93 ^o	0.59 ^o
Chromosome			
1	34 ^b	4.86 ^d	0.55 ^t
2	27 ^b	3.86 ^d	0.45 ^t
3	22 ^b	3.41 ^d	0.49 ^t
4	19 ^b	2.71 ^d	0.42 ^t
5	20 ^b	2.86 ^d	0.48 ^t
6	23 ^b	3.29 ^d	0.53 ^t
7	27 ^b	3.86 ^d	0.53 ^t
Total	172	4.10	0.57

Values within a column followed by the same letter(s) are not significantly different at the $P = 0.05$.

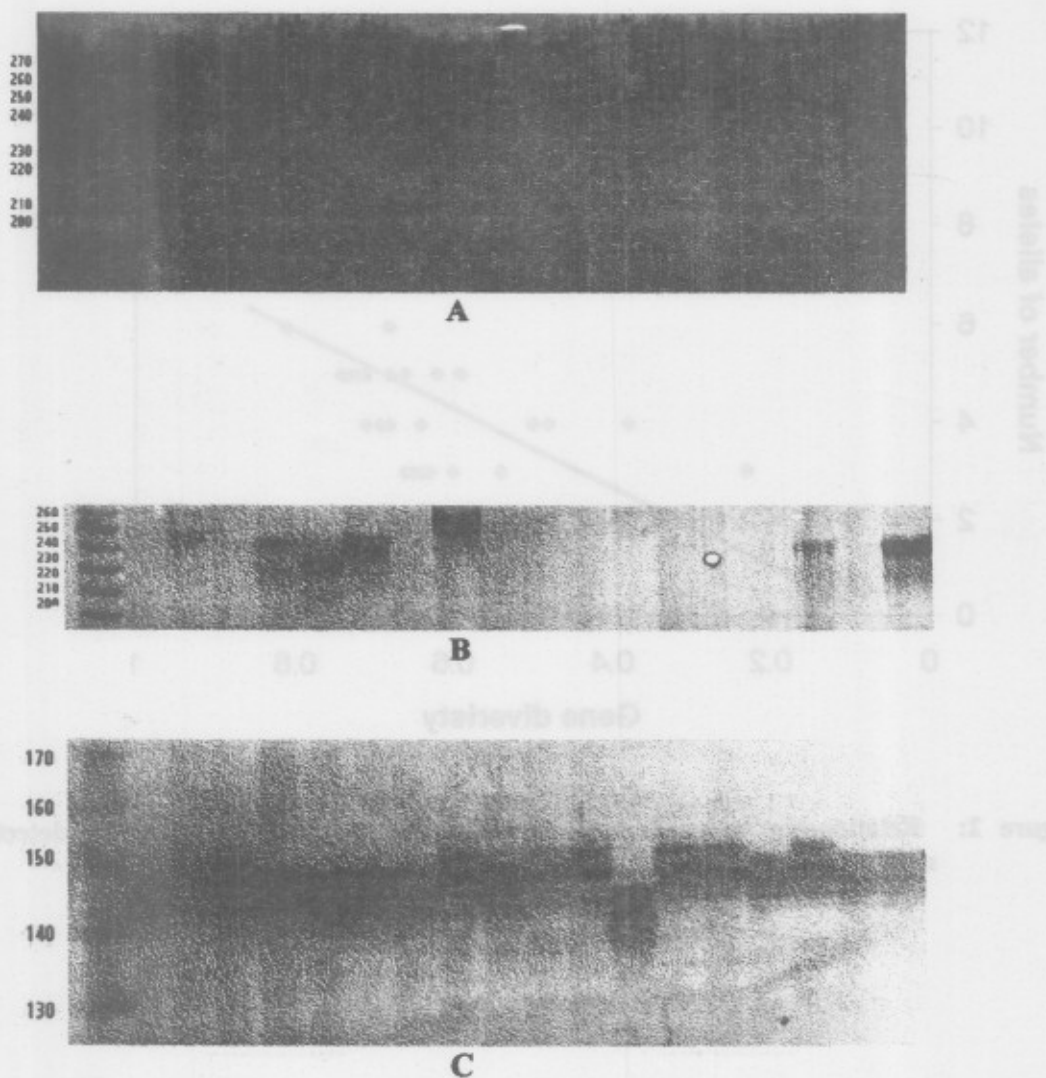


Figure (1): Representative sample of amplification profiles in 19 Egyptian wheat varieties: A) showing one prominent fragment amplified using GWM 368, B) showing two migrating prominent fragments amplified using GWM 140, C) showing two migrating prominent and additional fragment amplified using GWM 155. The molecular weight standard consisted of a 10 bp ladder

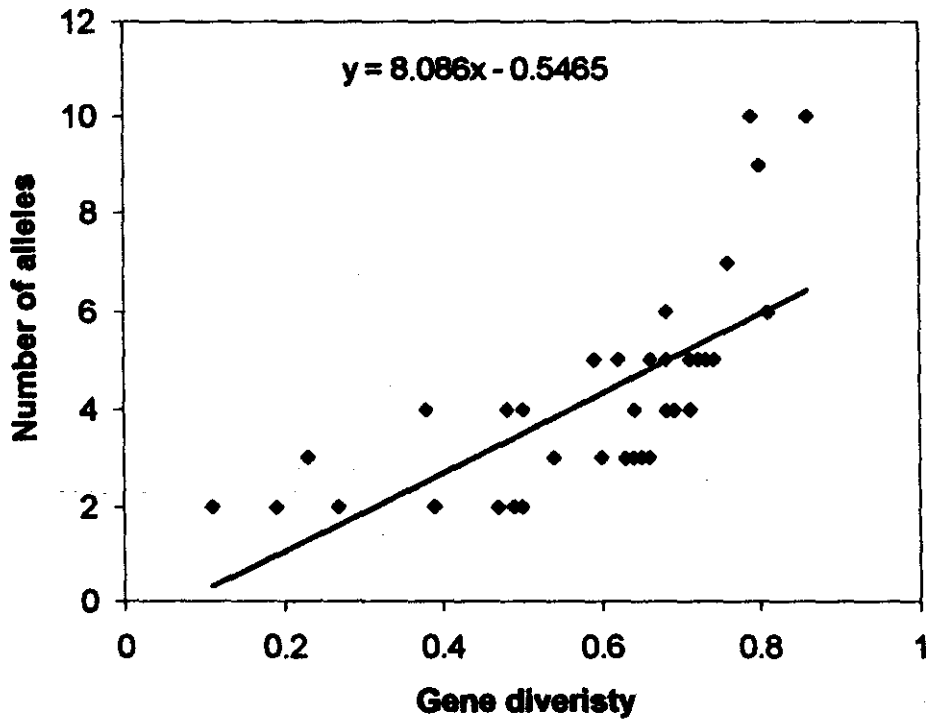


Figure 2: Relationship between gene diversity and the number of alleles detected by 42 microsatellite loci in 19 Egyptian wheat varieties.

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REFERENCES

Ahmad, M. (2002) Assessment of genomic diversity among wheat genotypes as determined by simple sequence repeats. *Genome* 45: 646-651.

Anderson, J. A.; J. A. Churchill; J. E. Autrique; S. D. Tanksley and M. E. Sorrells (1993). Optimizing parental selection for genetic linkage maps. *Genome* 36: 181-186.

Barlow, K. K. and C. J. Driscoll (1981) Linkage studies involving two chromosomal male-sterility mutants in hexaploid wheat. *Genetics* 98: 791-799.

Bassam B. J., G. Caetano-Anolles and P. M. Gresshoff (1991) Fast and sensitive silver staining of DNA in polyacrylamide gels. *Anal. Biochem.* 196: 80-83.

Brian G. J., A. J. Collins, P. Stephenson, A. Orry, J. B. Smith and M. D. Gale (1997) Isolation and characterization of microsatellites from hexaploid bread wheat. *Theor Appl Genet* 94:557-563.

Byoko, E. V., K. S. Gill, L. Mickelson-Young, S. Nasuda, W. J. Raupp, J. N. Zeigel, S. Singh, D. S. Hassawi, A. K. Fritz, D. Namuth, N. L. V. Lapitan and B. S. Gill (1999) A high density genetic linkage map of Theor Appl Genet, the D genome progenitor of bread wheat. *Theor Appl Genet* 99: 16-26.

Christiansen, M. J., S. B. Anderson and R. Ortiz (2002). Diversity changes in an intensively bred wheat germplasm during the 20th century. *Mol. Breed.* 9: 1-11.

Devos, K.M. and M.D. Gale. (1992). The use of random amplified polymorphic DNA markers in wheat. *Theor. Appl. Genet.* 84:567-572.

Devos, K. M., T. Millan and M. D. Gale (1993) Comparative RFLP maps of the homoeologous group-2 chromosomes of wheat, rye and barley. *Theor. Appl. Genet* 85: 784-792.

Dreisigacker, S., P. Zhang, M. L. Warburton, M. Van Ginkel, D. Hoisington, M. Bohn and A. E. Melchinger (2004). SSR and pedigree analyses of genetic diversity among CIMMYT wheat lines targeted to different mega-environments. *Crop Sci.* 44: 381-388.

Fahima, T., M. S. Roder, K. Wendhake, V. M. Kirzhner and E. Nevo (2002). Microsatellite polymorphism in natural populations of wild emmer wheat, *Triticum dicoccoides* in Israel. *Theor. Appl. Genet.* 104: 17-29.

Fahmi, A.I., H. H. Nagaty, R. A. Eissa, M. I. Sherif and M. I. Abd El-Hameed (2004). Comparison of genetic relationships based on morphological, RAPD and microsatellite markers in hexaploid wheat. *Alex. J. Agric. Res.* 49: 45-60.

Hayden, M. J. and P. J. Sharp (2001)a Targeted development of informative microsatellites (SSR) markers. *Nucl Acids Res* 29:e44.

Hayden, M. J. and P. J. Sharp (2001)b Sequence tagged microsatellite profiling (STMP): a rapid technique for developing SSR markers. *Nucl Acids Res* 29:e43.

Huang, X. Q., A. Borner, M. S. Roder and M. W. Ganal (2002) Assessing genetic diversity of wheat (*Triticum aestivum* L.) germplasm using microsatellite markers. *Theor Appl. Genet* 105: 699-707.

Kobiljiski, B., S. Quarrie, S. Dencic, J. Kirby and M. Ivesges (2002). Genetic diversity of the Novi Sad wheat core collection revealed by microsatellites. *Cell. Mol. Biol. Lett.* 7: 685-694.

Li, Y-C., A. B. Korol, T. Fahima, A. Beiles and E. Nevo (2002). Microsatellites: genomic distribution, putative functions and mutational mechanisms: a review. *Molecular Ecology* 11: 2453-2465.

Li, Y-C, T. Fahima, M. S. Roder, V. M. Kirzhner, A. Beiles, A. B. Korol and E. Nevo (2003) Genetic effects on microsatellite diversity in wild emmer wheat (*Triticum dicoccoides*) at the Yehudiyya microsite, Israel. *Heredity* 90: 150-156.

Litt, M., X. Hauge and V. Sharma (1993) Shadow bands seen when typing polymorphism dinucleotide repeats: some causes and cures. *Biotechniques* 15: 280-283.

Liu, B. H. and J. Y. Deng (1986) A dominant gene for male sterility in wheat. *Plant Breed* 97: 204-209.

Ma, X. F., M. K. Wanous, K. Houchins, M. A. Rodriguez Milla, P. G. Goicoechea, Z. Wang, M. Xei and J. P. Gustafson (2001) Molecular linkage mapping in rye (*Secale cereale* L.). *Theor Appl Genet* 102: 517-523.

Prasad, M., R. K. Varshney, J. K. Roy, H. Balyan, and P. K. Gupta (2000). The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat. *Theor. Appl. Genet.* 100: 584-592.

Reide, C. R. and J. A. Anderson (1996) Linkage of RFLP markers to an aluminum tolerance gene in wheat. *Crop Sci.* 36: 905-909.

Roder, M. S., V. Korzum, K. Wendehake, J. Plaschke, M. H. Tixier, P. Leroy and M. W. Ganal (1998) A microsatellite map of wheat genetics 149: 2007-2023.

- Rodriguez, S. and C. Zapata (2002) Typing dinucleotide repeats under non-denaturing conditions with single-base resolution and high sizing precision. *Mol Biotechnol* 21:117-122.
- Snedecor, G. W. and W. G. Cochran (1976) *Statistical methods* 5th ed., Iowa State University, Ames, Iowa, USA.
- Sourdille, P., Singh-S, Cadalen-T, Brown-Guedira-G-L, Gay-G, Qi-L, Gill-B-S, Dufour-P, Murigneux-A, Bernard-M (2004) Microsatellite-based deletion bin system for the establishment of genetic-physical map relationships in wheat (*Triticum aestivum* L.). *Funct Integr Genomics* 4: 12-25
- Varshney, R.K., R. Sigmund, A. Börner, V. Korzun, N. Stein, M. E. Sorrells, P. Langridge and A. Graner (2005) Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. *Plant Science* 168: 195-202.
- Xie, D. X., K. M. Devos, G. Moore and M. D. Gale (1993) RFLP-based genetic maps of the homoeologous group 5 chromosomes of bread wheat (*Triticum aestivum* L.). *Theor Appl Genet* 87: 70-74.

الملخص العربي

مرقات التتابع الدقيقة (الميكروساتيليتات) كمرقات للطرز الجينية في القمح المصري

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قسم الوراثة - كلية الزراعة - جامعة المنيا - شبين الكوم.

أظهرت الدراسات السابقة أن مرقات التتابع الدقيقة (الميكروساتيليتات) تغطي تغيرات كبيرة و أنها سهلة الاستخدام في القمح المدلسي و لذلك فإن هذه الدراسة أجريت لتحقيق الأهداف التالية: (١) تقدير مستوى التنوعات بين ١٩ صنف قمح مصري و (٢) دراسة مدى قدرة مرقات التتابع الدقيقة (الميكروساتيليتات) بصورة عامة و تخصيص بعضها في تعريف الطرز الجينية للقمح المصري. اشتملت الدراسة على ٤٢ مرقة من مرقات التتابع الدقيقة (الميكروساتيليتات) ذات مواقع محددة على الولد و عشرون زوج من الكروموسومات و موزعة بحيث يتواجد مرقة واحد من مرقات التتابع الدقيقة (الميكروساتيليتات) لكل ذراع كروموسومي لكل من جينومات A و B و D.

و قد أوضحت النتائج أن العدد الكلي للأليلات التي تم تحديدها كان ١٧٢ و تراوح عدد الأليلات للموقع الولد بين ٢ و ١٠ و كان متوسط عدد الأليلات للموقع الولد ٤,١ و تراوحت قيم محتوى الاختلافات المصوبة بين 0.11 و 0.86 و أظهر ٢٠ موقع من ٤٢ تحت الدراسة (٧١,٤٢%) قيم محتوى اختلافات 0.5 أو أعلى و كان متوسط قيم محتوى الاختلافات هو 0.57 و أوضحت هذه الدراسة أن 7 مرقات فقط من ٤٢ تحت الدراسة لها القدرة على التفريق بين التسعة عشر تركيب وراثي من الأماح المصرية و على ذلك فإن المجموعة المستخدمة من ٤٢ من مرقات التتابع الدقيقة (الميكروساتيليتات) ذات فائدة عالية في تقدير الاختلافات و تحديد بصمة الـ DNA للطرز الجينية للأماح المصرية و أخيراً فإن هذه المجموعة من مرقات التتابع الدقيقة (الميكروساتيليتات) يمكن أن تستخدم كمجموعة مرجعية من المرقات على مدى واسع من التطبيقات البحثية في القمح المصري