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Assessment of genetic diversity in Iranian wheat (*Triticum aestivum L.*) cultivars and lines using microsatellite markers

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Abstract

In this study, genetic diversity of 20 wheat genotypes was evaluated using 126 simple sequence repeats (SSR) alleles, covering all three wheat genomes. A total of 1557 allelic variants were detected for 126 SSR loci. The number of alleles per locus ranged from 4 to 19 and the allelic polymorphism information content (PIC) varied from 0.66 (*Xgwm*429) to 0.94 (*Xgwm*212 and *Xgwm*515). The highest polymorphism was observed in *Xgwm212* and *Xgwm515* primers with 19 alleles, while the lowest polymorphism belonged to *Xgwm429* with 4 alleles. The highest number of alleles per locus was detected in the genome A with 594 , compared to 552 and 411 for B and D genomes, respectively. Dendrogram was constructed using Dice similarity coefficient and UPGMA algorithm by NTSYSpc2.0 software and genotypes were grouped in to six clusters. The knowledge about the genetic relationships of genotypes provides useful information to address breeding programs and germplasm resource management. This study also confirms the usefulness of SSR markers to study wheat genetic diversity.

Key words: Genetic diversity, Microsatellite markers, Polymorphism, Wheat (*Triticum aestivum* L.)

Introduction

Wheat (*Triticum aestivum* L.) is the most important and one of the oldest cultivated crops in the world, and understanding its genetics and genome organization using molecular markers is of great value for genetic and plant breeding purposes. Molecular markers are a powerful tool to study the genetic structure of plant populations. In recent years, several molecular assays have been applied to assess genetic diversity among wheat cultivars (Chen *et al.*, 1994). These molecular methods are different in principle, application, type, the amount of detected polymorphism, task and time requirements. Various studies have used SSR markers to investigate genetic diversity in cultivated hexaploid wheat genotypes of *Triticum Aestivum* L. (Senturk Akfirat and Ahu Altinkut Uncuoglu 2013). Microsatellites (Tautz and Renz 1984; Tautz 1989)or simple sequence repeat (SSRs)-based molecular markers are now the marker of choice in most areas of plant genetics. Microsatellites are repeating sequences of 2–6 base pairs of DNA and are among the most stable markers of genetic variation and divergence among wheat genotypes because they are multiallelic, chromosome-specific and evenly distributed along chromosomes (Tautz, 1989). The advantages of SSRs are well documented (Powell *et al*. 1996) and these include: high information content, co-dominant inheritance, reproducibility and locus specificity. The improvement of wheat traits is mainly due to efficient use of wheat germplasm genetic diversity. Determination of genetic diversity is useful for plant breeding and hence production of more efficient plant species under different conditions. Accordingly, 20 of the most common wheat genotypes from different parts of Iran were selected and consequently analyzed for their genetic diversity by microsatellite markers. The aim of this research was to estimate the allelic variation and evaluate the genetic diversity at the expressed sequences among Iranian extremes wheat genotypes and to provide information for wheat breeding and improvement in germplasm management of wheat.

Materials and Methods

Plant Material:

A total of 20 wheat genotypes including salinity tolerant, semi-salinity tolerant and non-tolerant genotypes were used (Table 1) as the source for evaluating genetic diversity and genomics coverage by microsatellite markers. All of them were hexaploid (*Triticum aestivum* L., AABBDD, 2n = 6x = 42), and known as materials of advanced lines and cultivars in Iran.

Table 1. Evaluated wheat genotypes.

1-Roshan	2- Arta	3- Moghan-3	4- S-78-11	5-N-83-3
6-MV-17	7-KRL-4	8- Arg	9-Shotordandan	10-Boolani
11- Shoele	12- Sorghtoghm	13-SNH-9	14- Sistan	15-107-PR-87
16-139-PR-87	17-140-PR-87	18-Kharchia	19- Mahooti	20- Gaspard

DNA Isolation:

Total genomic DNA was extracted from leaf tissue for each line and cultivar. Young leaves from four-week old plants were cut as tissue samples for DNA extraction. Genomic DNA was extracted by mini prep_ isolation method (Dellaporta 1983) with minor modifications. 0.2g of young leaves were frozen in liquid N_2, mixed with 400 l of extraction buffer (50 mM Trisbase pH 8, 300 mM NaCl, 25 mM EDTA pH 8 and 1% SDS) and incubated at 65℃ for 30 min. 200 l sodium acetate 5 mM was added to each tube and placed about 10 min on ice. 500 l chloroform/ isoamyl alcohol (24: 1) was added and mixed well. The mix was centrifuged at 12000 g for 15 min. The supernatant was precipitated with an equal volume of ice-cold isopropanol and centrifuged at 5000 g for 15 min. In this stage DNA was recovered by centrifuging. The pellet was hooked out by sterile pipettes, washed in 70% ethanol and air dried and suspended in 300 l of 1x TBE buffer. Both DNA quantity and quality were estimated using UV spectrophotometer (Carry 50) by measuring absorbencies at A260 and A280 nm and 1% agarose gel electrophoresis and comparing band intensity with DNA ladder of known concentrations. DNA samples were diluted to 50ng/ l for SSR reactions. (Dellaporta *et al.*, 1983).

Microsatellite Markers Analysis:

To test the genetic diversity of wheat genotypes, 126 SSR markers dispersed throughout the genome were used in this study. Genomic SSR primer information was obtained from two sources. The first primer set was obtained from Röder *et al*.,(1998) from a conventional genomic library and designated as *GWM*, and the second one was obtained from Grain genes database (http:// graingenes.org). Microsatellite amplifications were carried out as reported by Röder *et al*. (Röder *et al*.,1998). Polymerase chain reaction (PCR) and fragment analysis were performed according to (Devos *et al*., 1995) and (Röder *et al*., 1998). PCR reactions were performed in a volume of 25 µL in Perkin-Elmer (Norwalk, CT) thermo cyclers. The reaction mixture contained 3 µL of each primer, 1.5 µL of each deoxy nucleotide, 1.5 µL $MgCl_2$, 1 unit Taq polymerase, and 50–100 ng of template DNA. After 3 min at 94˚C, 45 cycles were performed with 1 min at 94˚C,. 1 min at either 50, 55, or 60˚C (depending on the individual microsatellite), 2 min at 72˚C, and a final extension step of 10 min at 72˚C. Amplification products were separated on denaturing 8% polyacrylamide gel electrophoresis. Gel running times were adapted to fragment size, i.e. extended running times were used for the separation of larger fragments. The amplified fragments were detected using the silver staining methods and 100 bp size marker as described by (Bassam *et al*., 1993). The base material for the present study consisted of 126 microsatellite for all genomes.

Data analysis

The amplified bands were scored manually as 0 (absent) or 1 (present). Matrix similarity of genotypes was calculated using NTSYSpc.2.1 (Rohlf Fj .,1998)) with Sanh-clustering using the UPGMA (Unweighted Paired Group Method Using Arithmetic Averages) method. We used the Dice genetic similarity coefficient (Dice Lr., 1945; Nei M, Li Wh ., 1979). The results are presented graphically in dendrogram. The term polymorphism information content (PIC) was originally introduced into human genetics by Botstein *et al* (1980). It refers to the value of a marker for detecting polymorphism within a population, depending on the number of detectable and the distribution of their frequency. The polymorphic information content (PIC) was employed for each locus to assess the informative of each marker. The PIC for each marker was calculated according to formula of Nei (1973):

$$H_e = 1 - \sum_{i=1}^{n} P_i^2$$

where n is the total number of alleles detected for a locus of a marker and P_{ij} the frequency of the j th allele in the set of 20 investigated genotypes. The following parameters were estimated: the percentage of polymorphic loci and gene diversity, and other calculations were performed using the AlphaEaseFC4.0 software.

Results and Discussion

Microsatellite Polymorphism:

Twenty wheat cultivars of diverse origins were evaluated using 126 microsatellite markers. These microsatellites were selected on the basis of their known genetic locations to give a uniform coverage for all three wheat genomes (A, B and D) and a total of 1557 polymorphic alleles were detected at 126 loci (Table 2). A wide range of allelic variants was observed for each locus (Table 2). The number of alleles per locus ranged from 4 to 19, with the average number of 12.35 alleles per locus (Table 2). The largest number of alleles per locus occurred in the A genome which is accounted to be 594, compared to 552 for genome B and 411 for genome D (table 3). Microsatellite PIC values ranged from 0.66 to 0.94 (Table 2). Approximately 88.8% of microsatellite markers that used all chromosomes had a PIC value greater than 0.70, which indicates a high level of polymorphism for the majority of markers. The highest polymorphism was observed in *Xgwm212* and *Xgwm515* primers with 19 alleles at chromosome location 5D and 2A, respectively. The high percentage of polymorphism detected by microsatellites markers has been reported in Portuguese bread wheat cultivars (98.5%) (Carvalho *et al*., 2010), in Chinese barley accessions (98.13%) (Hou *et al*., 2005), and in Mediterranean faba bean cultivars (98.9%) (Terzopoulos and Bebeli, 2008).

Table 2: Wheat microsatellite marker name, chromosomal location, no. of alleles, and gene diversity for the microsatellite markers used in this study.

	Primer	**Ch.**	**Allele No**	**Major Allele. Frquency**	**PIC**	**Gene Diversity**
1	*Xgwm135*	1A	9	0.25	0.8272	0.845
2	*Xgwm357*	1A	11	0.15	0.8798	0.89
3	*Xgwm550*	1B	13	0.3	0.8551	0.865
4	*Xgwm11*	1B	12	0.2	0.8745	0.885
5	*Xgwm18*	1B	13	0.15	0.903	0.91
6	*Xgwm498*	1B	10	0.55	0.6609	0.675
7	*Xgwm140*	1B	10	0.55	0.6609	0.675
8	*Xgwm153*	1B	12	0.2	0.8804	0.89
9	*Xgwm642*	1D	13	0.25	0.876	0.885
10	*Xgwm232*	1D	13	0.2	0.8806	0.89
11	*Xgwm636*	2A	13	0.2	0.8921	0.9
12	*Xgwm47.1*	2A	8	0.5	0.6661	0.695
13	*Xgwm339*	2A	15	0.2	0.8982	0.905
14	*Xgwm312*	2A	17	0.1	0.9312	0.935
15	*Xcfa2043a*	2A	10	0.55	0.6609	0.675
16	*Xbarc353.2*	2A	11	0.2	0.8685	0.88
17	*Xwmc261*	2A	18	0.1	0.9367	0.94
18	*Xcfa2058*	2A	12	0.2	0.8691	0.88
19	*Xgpw2206*	2A	11	0.25	0.8579	0.87
20	*Xwmc109d*	2A	16	0.15	0.9202	0.925
21	*Xgwm47.2*	2A	13	0.2	0.8921	0.9
22	*Xgwm294b*	2A	10	0.25	0.8456	0.86
23	*Xgwm515*	2A	19	0.1	0.9422	0.945
24	*Xwmc296*	2A	14	0.3	0.8614	0.87
25	*Xgwm95*	2A	14	0.2	0.8979	0.905
26	*Xgwm328*	2A	15	0.2	0.9038	0.91

Table 2: continued

	Primer	Ch.	Allele No	Major Allele. Frquency	PIC	Gene Diversity
27	*Xwmc170*	2A	16	0.1	0.9256	0.93
28	*Xgwm10*	2A	18	0.1	0.9367	0.94
29	*Xgwm512*	2A	7	0.45	0.7069	0.735
30	*Xgwm372*	2A	14	0.3	0.8614	0.87
31	*Xcfa2121b*	2A	14	0.2	0.8923	0.9
32	*Xgwm249*	2A	8	0.6	0.5965	0.615
33	*Xgwm257*	2B	12	0.15	0.8857	0.895
34	*Xgwm410.2*	2B	15	0.2	0.9038	0.91
35	*Xgwm429*	2B	4	0.4	0.6654	0.715
36	*Xgwm539*	2D	13	0.15	0.8917	0.9
37	*Xgwm261*	2D	11	0.3	0.8364	0.85
38	*Xgwm102*	2D	14	0.15	0.9032	0.91
39	*Xwmc11*	3A	13	0.25	0.8702	0.88
40	*Xgwm369*	3A	14	0.15	0.9087	0.915
41	*Xgwm674*	3A	13	0.15	0.903	0.91
42	*Xgwm494*	3A	1	1	0	0
43	*Xgwm162*	3A	11	0.35	0.7974	0.815
44	*Xgwm391*	3A	8	0.55	0.6445	0.665
45	*Xwmc291*	3B	14	0.15	0.9087	0.915
46	*Xwmc326*	3B	12	0.2	0.8804	0.89
47	*Xcfa2170*	3B	1	1	0	0
48	*Xbarc84*	3B	13	0.25	0.876	0.885
49	*Xbarc206*	3B	15	0.15	0.909	0.915
50	*Xwmc687*	3B	11	0.35	0.8165	0.83
51	*Xgwm108*	3B	13	0.3	0.8551	0.865
52	*Xgwm340*	3B	14	0.15	0.9032	0.91
53	*Xgwm285*	3B	12	0.2	0.8745	0.885

Table 2: continued

	Primer	Ch.	Allele No	Major Allele. Frquency	PIC	Gene Diversity
54	*Xgwm547*	3B	15	0.2	0.9038	0.91
55	*Xgwm341*	3D	17	0.15	0.9258	0.93
56	*Xgwm664*	3D	11	0.25	0.8518	0.865
57	*Xgwm114*	3D	13	0.35	0.8296	0.84
58	*Xgwm3*	3D	15	0.15	0.9145	0.92
59	*Xgwm314*	3D	17	0.1	0.9312	0.935
60	*Xgwm161*	3D	14	0.15	0.9087	0.915
61	*Xgwm165*	4A	14	0.15	0.9032	0.91
62	*Xgwm601*	4A	13	0.2	0.8863	0.895
63	*Xgwm610*	4A	13	0.2	0.8863	0.895
64	*Xgwm637*	4A	10	0.55	0.6609	0.675
65	*Xgwm350*	4A	15	0.15	0.909	0.915
66	*Xgwm160*	4A	8	0.6	0.5965	0.615
67	*Xgwm66*	4B	14	0.2	0.8923	0.9
68	*Xgwm251*	4B	7	0.6	0.5877	0.61
69	*Xgwm368*	4B	11	0.4	0.7859	0.8
70	*Xgwm495*	4B	15	0.15	0.9145	0.92
71	*Xgwm113*	4B	9	0.3	0.8234	0.84
72	*Xgwm107*	4B	18	0.1	0.9367	0.94
73	*Xgwm165*	4D	15	0.3	0.8676	0.875
74	*Xgwm194*	4D	17	0.15	0.9258	0.93
75	*Xgwm609*	4D	13	0.2	0.8863	0.895
76	*Xgwm6*	4D	14	0.25	0.8821	0.89
77	*Xbarc48.4*	4D	13	0.15	0.8973	0.905
78	*Xgpw345*	4D	10	0.25	0.8456	0.86
79	*Xgwm624*	4D	10	0.2	0.8507	0.865
80	*Xgwm186*	5A	12	0.2	0.8691	0.88

Table 2: continued

	Primer	Ch.	Allele No	Major Allele. Frquency	PIC	Gene Diversity
81	*Xgwm639*	5A	18	0.1	0.9367	0.94
82	*Xgwm595*	5A	11	0.5	0.7119	0.725
83	*Xgwm410.2*	5A	15	0.15	0.9145	0.92
84	*Xgwm443*	5A	16	0.2	0.9096	0.915
85	*Xgwm415*	5A	4	0.45	0.6398	0.69
86	*Xgwm205*	5A	8	0.35	0.7898	0.81
87	*Xgwm335*	5B	11	0.3	0.8364	0.85
88	*Xgwm554*	5B	15	0.1	0.9199	0.925
89	*Xgwm271*	5B	13	0.2	0.8751	0.885
90	*Xgwm604*	5B	18	0.1	0.9367	0.94
91	*Xgwm190*	5D	10	0.25	0.8398	0.855
92	*Xgwm174*	5D	11	0.35	0.8165	0.83
93	*Xgwm212*	5D	19	0.1	0.9422	0.945
94	*Xgwm654*	5D	11	0.25	0.8289	0.845
95	*Xgwm121*	5D	5	0.35	0.7352	0.77
96	*Xgwm565*	5D	14	0.3	0.8614	0.87
97	*Xgwm169*	6A	16	0.1	0.9256	0.93
98	*Xgwm427*	6A	13	0.35	0.8296	0.84
99	*Xgwm613*	6B	15	0.3	0.8676	0.875
100	*Xgwm644*	6B	15	0.2	0.9038	0.91
101	*Xgwm70*	6B	13	0.15	0.903	0.91
102	*Xgwm219*	6B	11	0.35	0.8165	0.83
103	*Xgwm518*	6B	10	0.4	0.7722	0.79
104	*Xbarc196*	6D	9	0.25	0.8334	0.85
105	*Xwmc416*	6D	7	0.5	0.6732	0.7
106	*Xgwm469*	6D	16	0.15	0.9202	0.925
107	*Xgwm325*	6D	13	0.25	0.876	0.885

Table 2: continued

	Primer	Ch.	Allele No	Major Allele. Frquency	PIC	Gene Diversity
108	*Xgwm635*	7A	10	0.3	0.8299	0.845
109	*Xgwm332*	7A	8	0.35	0.7898	0.81
110	*Xgwm282*	7A	11	0.4	0.7859	0.8
111	*Xgwm260*	7A	6	0.35	0.7626	0.79
112	*Xgwm569*	7B	12	0.25	0.87	0.88
113	*Xgwm400*	7B	11	0.4	0.7859	0.8
114	*Xgwm297*	7B	15	0.1	0.9199	0.925
115	*Xgwm333*	7B	11	0.2	0.8743	0.885
116	*Xgwm43*	7B	15	0.15	0.909	0.915
117	*Xgwm274*	7B	15	0.25	0.8881	0.895
118	*Xgwm611*	7B	13	0.25	0.8702	0.88
119	*Xgwm146*	7B	15	0.25	0.8881	0.895
120	*Xgwm577*	7B	12	0.4	0.7927	0.805
121	*Xgwm46*	7B	17	0.1	0.9312	0.935
122	*Xgwm295*	7D	13	0.25	0.8702	0.88
123	*Xgwm44*	7D	12	0.35	0.823	0.835
124	*Xgwm437*	7D	16	0.25	0.894	0.9
125	*Xgwm37*	7D	8	0.3	0.798	0.82
126	*Xgwm121*	7D	4	0.35	0.6804	0.73
	Average		12.35	0.2666	106.57	105.15
	Total		1557	33.75	0.8466	0.8354

Mohammadi *et al*. (2009) reported the high values of SSR-based gene diversity and polymorphic information content (PIC) of 0.7 and 0.66 for 27 Iranian local commercials and adapted wheat cultivars. The monomorphism SSR markers Xgwm494 and Xcfa2170 were at chromosome location 3A and 3B respectivelty. The highest number of microsatellite loci in the existing microsatellite coverage of wheat is on the A genome and the lowest is on the D genome (Table 3).

Table 3. Means of polymorphic information contents (PIC) for SSR markers located on each chromosome.

Chromosome	No of markers on each chromosome	No of polymorphic alleles	PIC
1A	2	20	0.8534
2A	22	293	0.8528
3A	5	60	0.8247
4A	6	73	0.8070
5A	7	84	0.8244
6A	2	29	0.8775
7A	4	35	0.7920
Average A Genomes	48	594	0.8361
1B	6	70	0.8058
2B	3	31	0.8183
3B	9	120	0.8807
4B	6	74	0.8234
5B	4	57	0.8920
6B	5	64	0.8525
7B	10	136	0.8729
Average B Genomes	43	552	0.8538
1D	2	26	0.8783
2D	3	38	0.8770
3D	6	87	0.8935
4D	7	92	08793
5D	6	70	0.8373
6D	4	45	0.8257
7D	5	53	0.8131
Average D Genomes	33	411	0.8574

In order to distinguish the best clustering and similarity coefficient calculation methods, the cophenetic correlation, a measure of the correlation between the similarity represented on the dendrograms and the actual degree of similarity, was calculated for each method combination. Among different methods, the highest value (r=0.70) was observed for UPGMA clustering method based on Dice (Nie & Li) similarity coefficient (Table 4). Therefore, the dendrogram constructed based on this method was used for depicting genetic diversity of genotypes (Fig. 1). Cluster analysis (Fig. 1) divided the 20 genotypes into Six groups.

Table 4. Comparison of different methods for constructing dendrogram.

Analysis Method	Cophenetic coefficient (r)		
	Simple Matching	Jaccard	Dice (Nie & Li)
UPGMA	0.58	0.68	0.70*
Complete Linkage	0.51	0.66	0.59

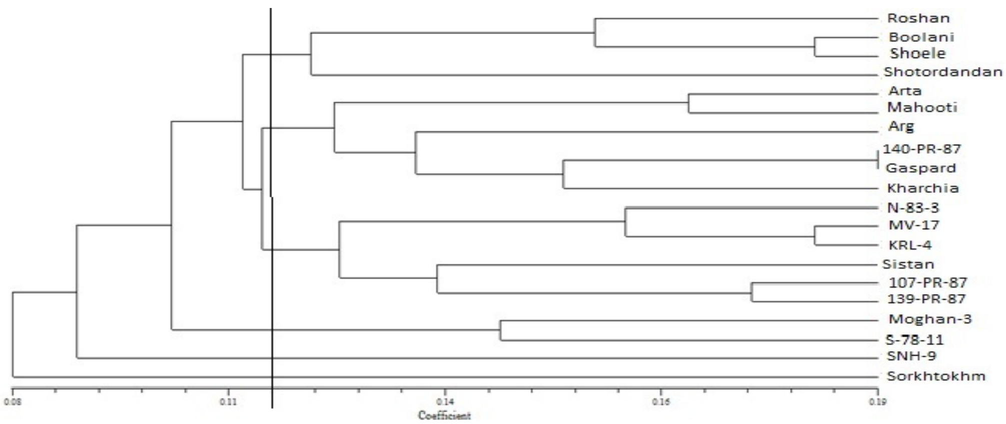

Fig. 1. A dendrogram based on genetic similarities discriminated all the wheat genotyping used in this study.

The first included the wheat genotyping Roshan, Boolani, Shoele and Shotordandan. The second cluster was divided into two sub accessions. Group 2 contains wheat genotyping Arta, Mahooti, Arg, 140-PR-87, Gaspard, Kharchia. In group 2 the highest similarity value was observed between 140-PR-87 and Gaspard genotypes. Most of wheat genotypes were placed in group 3 and 4. Group 3 contains 6 genotypes as N-83-3, MV-17, KRL-4, Sistan, 107-PR-87, 139-PR-87. Group 4 contains 2 Genotypes as Moghan-3 and S-78-11. In groups 5 and 6 were only two genotypes SNH-9 and Sorkhtokhm, respectively. The genetic distances between studied genotypes were represented in Table 6. The highest genetic distance was recorded between Sorkhtokhm and Mahooti with the highest similarity index (0.960). On the other hand, the two most distantly related cultivars were Gaspard and 140-PR-87 with low similarity index (0.811) (Table 5). Since only a wide genetic base gives the opportunity to select genotypes with a trait of interest, it is essential to understand the extent and distribution of genetic variation. This type of information is particularly important for wheat as an important crop grown in the world and especially in Iran and as a result of a wide range of genetic diversity observed among all genotypes. The results have shown that it is possible both to classify the genetic diversity of elite genotypes and select genotypes or cultivars for the highest genetic diversity using SSRs, as indicated by cluster analysis. Several authors reported a narrow genetic diversity in wheat when assessed with RAPD and DNA amplification fingerprinting (DAF) (Abdollahi Mandoulakani *et al*., 2010), AFLPs (Khalighi *et al*., 2008; Shoaib and Arabi, 2006). The knowledge about the genetic relationships of genotypes also provides useful information to address breeding programs and germplasm resource management. This type of investigation on genetic diversity is helpful for developing appropriate science based strategies for wheat breeding (Landjeva *et al*.,2006) and it can be a good tool of selecting genotypes in breeding programs. In conclusion, this study confirms the usefulness of SSR markers to study wheat genetic diversity. Only 36% of all primer pairs flanking wheat.

Table 5: Similarity matrix for the 20 wheat genotypes based on their microsatellite markers.

G:Genotypes , 1.Roshan,2.Arta,3.Moghan-3, 4.S-78-11, 5.N-83-3,6.MV-17, 7.KRL-4, 8.Arg, 9.Shotordandan, 10.Boolani, 11.Shoele, 12.Sorkhtokhm, 13.SNH-9, 14.Sistan, 15.107-PR-87, 16.139-PR-87, 17.140-PR-87, 18.Kharchia, 19.Mahooti, 20.Gaspard.

G	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	…..																			
2	0.889	…..																		
3	0.937	0.897	…..																	
4	0.897	0.874	0.858	…..																
5	0.889	0.874	0.921	0.874	…...															
6	0.929	0.889	0.905	0.921	0.834	…..														
7	0.889	0.921	0.9291	0.858	0.850	0.818	……													
8	0.897	0.889	0.913	0.881	0.881	0.874	0.866	…..												
9	0.937	0.881	0.921	0.921	0.889	0.897	0.881	0.897	……											
10	0.866	0.881	0.874	0.905	0.874	0.897	0.881	0.905	0.874	…..										
11	0.826	0.913	0.905	0.913	0.913	0.913	0.889	0.881	0.834	0.818	…..									
12	0.897	0.937	0.937	0.905	0.929	0.929	0.929	0.913	0.944	0.897	0.913	…..								
13	0.944	0.897	0.921	0.921	0.905	0.921	0.905	0.897	0.905	0.905	0.929	0.921	…..							
14	0.897	0.889	0.897	0.881	0.889	0.850	0.889	0.889	0.889	0.881	0.842	0.913	0.905	….						
15	0.866	0.897	0.897	0.929	0.881	0.897	0.881	0.897	0.905	0.897	0.889	0.913	0.921	0.842	…..					
16	0.889	0.897	0.905	0.921	0.881	0.881	0.850	0.897	0.905	0.905	0.897	0.905	0.921	0.889	0.826	…..				
17	0.850	0.866	0.881	0.889	0.889	0.897	0.889	0.874	0.889	0.866	0.897	0.897	0.905	0.866	0.874	0.818	…..			
18	0.897	0.897	0.905	0.897	0.905	0.874	0.889	0.905	0.881	0.905	0.897	0.905	0.913	0.905	0.897	0.897	0.834	…..		
19	0.881	0.834	0.858	0.905	0.897	0.874	0.929	0.921	0.913	0.881	0.913	0.960	0.889	0.889	0.921	0.937	0.874	0.881	…..	
20	0.889	0.858	0.866	0.889	0.889	0.88	0.850	0.826	0.874	0.866	0.866	0.913	0.889	0.874	0.874	0.866	0.811	0.866	0.842	…

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ارزیابی تنوع ژنتیکی کولتیوارها و لاین‌های ایرانی گندم نان با استفاده از نشانگرهای ریزماهواره

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چکیده

در این مطالعه، تنوع ژنتیکی ۲۰ ژنوتیپ گندم با استفاده از ۱۲۶ نشانگر ریزماهواره که هر ۳ ژنوم گندم را تحت پوشش قرار می‌داد مورد ارزیابی قرارگرفت. در مجموع ۱۵۵۷ باند توسط ۱۲۶ نشانگر مربوطه تشخیص داده شد. تعداد باندهای مربوط به هر نشانگر بین ۴ تا ۱۹عدد بوده و مقدار اطلاعات چند شکلی بین ۰/۶۶ تا ۰/۹۴ متغیر بود. بیش‌ترین میزان تنوع مربوط به نشانگرهای *Xgwm212* و *Xgwm515* با ۱۹ باند بود. در حالی‌که کم‌ترین تنوع متعلق به نشانگر *Xgwm429* با تعداد ۴ باند بود. بیش‌ترین تعداد باندها مربوط به یک مکان ژنی در ژنوم A با ۵۹۴ باند و مکان‌های دیگر با ۵۵۲ و ۴۱۱ باند به ترتیب مربوط به ژنوم‌های B و D بودند. دندروگرام مربوطه با استفاده از ضریب تشابه دایس و روش UPGMA و با نرم‌افزار NTSYSpc2.0 رسم شد و ژنوتیپ‌های مورد بررسی در شش کلاستر گروه‌بندی شدند. دانش حاصل درباره‌ی ارتباطات ژنتیکی ژنوتیپ‌ها اطلاعات مفیدی را برای انجام پروژه‌های اصلاحی و مدیریت منابع ژنتیکی در اختیار قرار می‌دهد. همچنین این مطالعه نشان می‌دهد نشانگرهای ریزماهواره برای مطالعه‌ی تنوع ژنتیکی گندم مفید می‌باشد.

کلمات کلیدی: تنوع ژنتیکی، نشانگرهای ریزماهواره، چندشکلی، گندم نان.