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RESEARCH ARTICLE

Molecular diversity of Omani wheat revealed by microsatellites: II. Hexaploid landraces

S. Al Khanjari · K. Hammer · A. Buerkert · M. S. Röder

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Abstract For millennia, wheat (*Triticum* spp.) has been grown in traditional aflaj-irrigation systems of remote mountain oases in Oman. However, little is known about the diversity of the ancient landraces used. Given recent reports about the occurrence of novel germplasm in such material, the objective of this study was to evaluate the genetic diversity of hexaploid wheat (*Triticum aestivum* L.) landraces in relation to their geographic origin using microsatellites. The collection covered most of the cultivation areas in northern Oman where wheat landraces are growing. Total genomic DNA was extracted from six pooled plants representing each accession. A total of 161 wheat accessions were assayed using 35 microsatellite loci in which a total of 305 polymorphic bands were recorded for the 35 microsatellites. The polymorphic information content (PIC) across the 35 microsatellite loci ranged from 0.02 to 0.89 with an average of 0.50. A heterozygosity percentage value of 9.09 was determined and the highest level recorded for accessions from the Batinah district. Rare alleles averaged 1.85 with the highest value being from the Dakhilia district. The results indicated a significant correlation between gene diversity and number of alleles across districts. The correlation coefficient between these two variables over the 35 loci was 0.657, whereby correlation coefficients of 0.718, 0.706, 0.657 and 0.651, respectively, were found for the Batinah, Dhahira, Dakhilia and Sharqia materials. Genetic distances indicated that all landraces were closely related. The cluster analysis discriminated most of the landraces accessions. However, it failed to achieve region-specific groupings of landraces. The present study demonstrated the presence of high diversity in Omani landraces and also indicated the effectiveness of microsatellites to describe it.

Keywords Oasis agriculture · Polymorphic information content · SSR · *Triticum aestivum*

S. Al Khanjari · K. Hammer · A. Buerkert (✉)
Institute of Crop Science, University of Kassel,
D-37213 Witzenhausen, Germany
e-mail: buerkert@uni-kassel.de

S. Al Khanjari
College of Agriculture and Marine Sciences, Sultan Qaboos University, Al Khod, Oman

M. S. Röder
Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstrasse 3,
D-06466 Gatersleben, Germany

Introduction

Only recently Omani wheat landraces, grown in remote mountain oases, have attracted the attention of scientists despite the millenia-old

cultivation history of *Triticum* spp. on the Arabian Peninsula (Schwartz 1939; Guarino 1990; Potts 1993; Zohary and Hopf 1993; Willcox and Tengberg 1995). First morphological studies showed a surprisingly large phenotypic variation and the presence of at least six so far undescribed hexaploid (*T. aestivum* L.) and three tetraploid (*T. durum* Desf., *T. aethiopicum* Jakubc.) botanical wheat varieties (Al-Maskri et al. 2003; Hammer et al. 2004).

The diversity of germplasm has traditionally been described using morphological and agronomical traits (Vavilov 1964; Chapman 1985). However, molecular markers such as microsatellites (SSRs) have been found to be complementary to morphological, pedigree, heterosis and biochemical data (Tolbert et al. 1979; Doebley 1989; Melchinger et al. 1991). Microsatellites have a high potential use for the genetic analysis of self-pollinating crops because of their high degree of polymorphism and they are codominantly inherited (Akkaya et al. 1992; Plaschke et al. 1995; Röder et al. 1995, 2004). Primers flanking the microsatellite locus in the selected DNA sequences even allow to detect multiallelic variation (Johansson et al. 1992; Rongwen et al. 1995). Previously microsatellites have been successfully used in diversity studies of wheat and barley (Koebner et al. 2003; Prasad et al. 2000; Russell et al. 2000; Eujayl et al. 2002; Soleimani et al. 2002; Melchinger et al. 1994). Also, extensive information about their use is available for rice (*Oryza sativa* L.; Ishii and McCouch 2001; Temnykh et al. 2001) and maize (*Zea mays* L.; Mumm and Dudley 1994; Smith et al. 1997; Lu and Bernardo 2001).

Lately, microsatellites have been used to trace the geographic origin of accessions by fingerprinting diverse germplasm from different regions and may thus also help to trace the pre-historic spread of germplasm (Baek et al. 2003; Huang et al. 2002; Li et al. 2002; Röder et al. 2002; Salamini et al. 2002; Zhang et al. 2006).

In view of the above the purpose of this study was to assess the value of molecular markers in unraveling the genetic structure of hexaploid wheat landraces from Oman.

Materials and methods

Plant material

A survey was conducted in the two spring seasons of 2002–2003 across the wheat growing districts of Oman which covered about 80% of the total cultivated area in the country (Fig. 1). At each location, a few randomly chosen farmers were interviewed to identify individuals who still grew landraces of wheat. All of the indicated fields, mostly in remote mountain oases, were visited, whenever physically possible and representative germplasm for each of the 161 hexaploid wheat accessions were collected. Seeds from all accessions were planted in the green house at the Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany (Table 1).

DNA extraction, polymerase chain reaction and amplification

Total genomic DNA was extracted from pooled leaves of six 3-week-old plants grown from representative seeds of any accession. To this end the young seedling leaves of each accession were harvested and frozen in liquid nitrogen. Subsequently, approximately 3–5 g of leaf material were ground into a fine powder and poured into 50 ml propylene tubes.

The extraction was performed according to Fulton et al. (2000) with an extraction buffer described in Plaschke et al. (1995). Polymerase chain reaction amplifications were performed as described by Röder et al. (1998). All further steps were identical to those mentioned by Al Khanjari et al. (2006).

Microsatellite markers (SSR)

A total of 35 SSR primers were produced from Gatersleben wheat microsatellites (GWM) and one of them from a pseudogliadine gene, Taglgap. The markers were selected based on their uniformity of distribution in the genome level. Approximately three markers for each chromosome of the A, B and D genomes were used in the study. The microsatellite primers used (Table 2) were

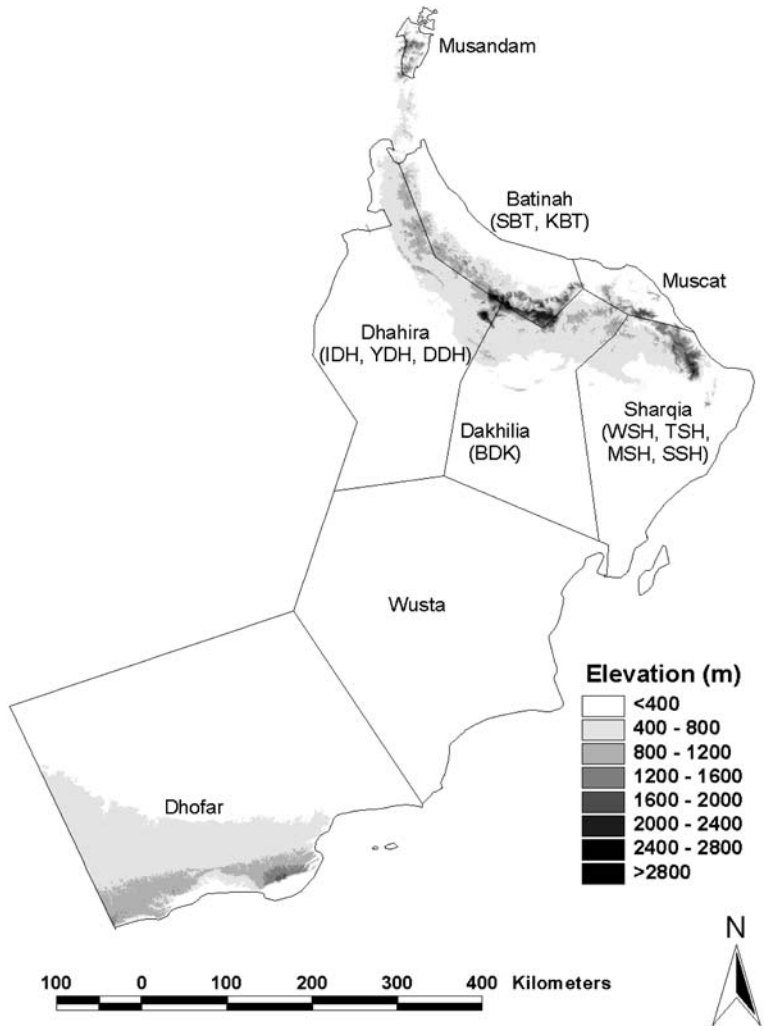

Fig. 1 Map of Oman indicating the four districts Dhahira (*YDH* Yanqul, *DDH* Dank, *IDH* Ibri), Batinah (*SBT* Sohar, *KBT* Khabura), Dakhilia (*BDK* Bahla) and Sharqia (*SSH* Sur, *WSH* Al Raky, *TSH* Taeen, *MSH* Maqta) where the hexaploid wheat landraces were collected

previously described by Röder et al. (1998) and for the primer Taglgap by Devos et al. (1995).

Data analysis

The presence (1) and absence (0) of specific microsatellite alleles was scored in a binary data matrix. 'Chinese Spring' and 'Aztec' were used as controls to standardize different gel runs. The gene diversity also called polymorphic information content (PIC) was computed according to Nei (1973) as:

$$\mathrm{PIC} = 1 - \sum P_{ij}^2$$

where P_{ij} is the allele frequency of the jth allele for the ith marker summed over the number of alleles. Anderson et al. (1993) suggested that gene diversity is the same as the PIC.

Genetic similarity (GS; Dice 1945) was calculated as:

$$\mathrm{GS} = 2N_{ij}/(N_i + N_j)$$

where N_{ij} is the number of fragment common to lines i and j, and $(N_i + N_j)$ is the total number of fragment in both lines.

Genetic distance (GD) among group pairs was calculated following (Nei and Li 1979).

$$(\mathrm{GD}_{xy}) = 1 - (2N_{xy}/N_x + N_y)$$

To calculate allele frequency (A_{xy}) from one group of variation to another in each locus the formula of Khlestkina et al. (2004) was used:

Table 1 OMTRI (Oman *Triticum*) accession numbers of hexaploid wheat landraces from Oman used for molecular genetic analysis in this diversity study

District	Region	OMTRI	Total
Batinah			
	Sohar (SBT)	125, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179	22
	Khabura (KBT)	180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191	12
Dhahira			
	Ibri (IDH)	51, 54, 55, 56, 57, 58, 59, 60, 61, 62, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117	31
	Dank (DDH)	50, 63, 64, 65, 66	5
	Yanqul (YDH)	52, 53, 67, 68, 69, 70, 71, 72, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 118, 119, 120, 121, 122	37
Dakhilia			
	Bahla (BDK)	30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45,46, 47, 48, 49	20
Sharqia			
	Sur (SSH)	123, 124, 157, 158	4
	Taeen (TSH)	139, 140, 141, 142, 143, 144, 156	7
	Al Raky (WSH)	126, 127, 128, 129, 130, 131, 132, 134, 135, 136, 137, 138, 155	13
	Maqta (TMSH)	145, 146, 147, 148, 149, 150, 151, 152, 153, 154	10
Total			161

$$\text{Allele frequency variation} = \sum |P_{xi} - P_{yi}|/N_{xy} \times 100\%$$

where P_{xi} and P_{yi} are the frequencies of the ith allele in regions X and Y, respectively, and N_{xy} is the total number of alleles for the two groups X and Y.

The allelic frequency variation (A_{xy}) was calculated separately for each of the 35 loci and then for all of them as an average.

All fragments were used to generate a GS matrix with the software NTSYS (Numerical Taxonomy and Multivariate Analysis System, vers. 2.1) for PC (Rohlf 2002). The relationships among accessions were analysed using the un-weighted pair-group methods (UPGMA) and principal component analysis (PCA; Sneath and Sokal 1973).

Results

Microsatellites

The 35 wheat microsatellite markers used revealed a total of 305 alleles. Their fragment size ranged from 77 bp in *GWM3* located on chromosome 3DS to 265 bp in *Taglgap* on chromosome 1BS. The average number of alleles/locus was 8.70 and the largest number of alleles (28 alleles) was detected at locus *GWM459*. The lowest number of alleles (2 alleles) was at *GWM261* (Table 2).

District-wise analysis of diversity parameters was based on different numbers of accessions. Averages of allele numbers were different for each district. With 245 the allele number was highest in the Dhahira district followed by Batinah (198), Sharqia (161) and Dakhilia (126). The average allele numbers per district were strongly correlated to the number of investigated accessions ($r = 0.93$).

The number of rare alleles (frequency < 0.02) significantly varied between markers ranging from 0 for *GWM357*, *GWM155*, *GWM655, GWM192A* and *GWM192D* to 5 on *GWM540* with total alleles averaging 1.76 (Table 2). The highest number of rare alleles was observed for Batinah (67) followed by Dhahira (57), Dakhilia (38) and Sharqia (36) (Table 3). The eight unique alleles were found at *GWM752, GWM18, GWM3, GWM192B, GWM898, GWM408, GWM44* and*GWM333*.

Heterozygosity was observed for all microsatellite loci but the heterozygosity level varied

Table 2 List of the 35 microsatellite loci of chromosome locations used to evaluate allele variation, rage of fragment size, genetic diversity, polymorphism information content (PIC), allele number, rare alleles, heterozygosity (H) and allele variation (AV) of 161 hexaploid wheat landraces from Oman

SSR and chromosomal location	Fragment size range	PIC	Allele no.	Rare alleles	H (%)	AV (%)
XGWM357-1AL	120–126	0.49	4	0	2	1.31
XGWM752-1AS	Null, 120–154	0.71	6	1	8	1.97
XGWM18-1BS	177–193	0.47	8	1	16	2.62
Taglgap-1BS	Null, 212–265	0.49	9	2	6	2.95
XGWM458-1DL	Null, 108–170	0.32	8	2	7	2.62
XGWM337-1DS	110–168	0.41	11	2	15	3.61
XGWM95-2AS	Null, 129–124	0.17	8	3	5	2.62
XGWM619-2BL	143–179	0.54	9	3	32	2.95
XGWM157-2DL	Null, 98–112	0.2	8	2	6	2.62
XGWM261-2DS	Null, 163–175	0.29	4	2	3	1.31
XGWM155-3AL	Null, 129–149	0.53	7	0	27	2.30
XGWM720-3AS	130–182	0.73	15	3	36	4.92
XGWM655-3BL	Null, 158–172	0.65	8	0	12	2.62
XGWM389-3BS	Null, 102–160	0.67	14	3	23	4.59
XGWM3-3DS	Null, 77–85	0.41	6	1	4	1.97
XGWM160-4AL	176–198	0.52	7	2	7	2.30
XGWM192-4AS	128–134	0.02	2	0	1	0.66
XGWM192-4BL	Null, 191–225	0.71	11	1	13	3.61
XGWM513-4BL	143–151	0.39	6	2	16	1.97
XGWM898-4BS	103–115	0.23	4	1	10	1.31
XGWM192-4DL	Null, 134–140	0.27	4	0	1	1.31
XGWM186-5AL	Null, 126–152	0.54	13	3	34	4.26
XGWM415-5AS	120–134	0.91	11	2	10	3.61
XGWM408-5BL	Null, 175–183	0.34	6	1	10	1.97
XGWM540-5BS	114–138	0.65	10	5	34	3.28
XGWM190-5DS	200–214	0.55	7	2	12	2.30
XGWM459-6AS	Null, 162–190	0.89	28	2	26	9.18
XGWM680-6BS	123–147	0.38	6	1	7	1.97
XGWM325-6DS	Null, 122–142	0.74	7	1	24	2.30
XGWM631-7AS	Null, 190–204	0.39	6	2	20	1.97
XGWM297-7B(C)	Null, 150–178	0.71	10	2	15	3.28
XGWM333-7BL	148–166	0.16	6	1	4	1.97
XGWM577-7BL	Null, 126–224	0.72	13	2	10	4.26
XGWM437-7DL	Null, 98–118	0.55	11	3	28	3.61
XGWM 44-7DS	Null, 152–186	0.78	12	1	28	3.93

Table 3 Comparison of gene diversity (polymorphism information content, PIC values) of cultivated bread wheat landraces among the different districts of Oman

	Dhahira	Batinah	Sharqia	Dakhilia	Total
No. of accession	74	34	33	20	161
Allele numbers	245	198	161	126	305
Average no. of alleles per marker	7.00	5.67	5.00	5.57	8.70
No. of rare alleles	57	67	36	38	61
No. of unique alleles	5	1	1	0	8
Heterozygosity %	9.00	10.57	12.57	14.38	9.09
Average PIC value	0.45	0.48	0.42	0.33	0.5

among microsatellite markers. It was highest at locus *GWM186* of chromosome 5A and lowest at *GWM192* of chromosome 4D. The highest percentage of heterozygosity was in Dakhilia district (14.4%) and the lowest in Sharqia (12.6%, Table 3)

The allelic frequency variation within loci indicated the highest variation for *GWM459* and

the lowest for *GWM192A* with 9.2 and 0.7%, respectively (Table 2).

Analysis of gene diversity

The PIC-value reflecting the gene diversity of the 35 microsatellite loci ranged from 0.02 at locus *GWM 192A* to 0.89 at locus *GWM459* with an average of 0.50 (Table 2). The gene diversity differed between districts (Table 3). The correlation coefficient between gene diversity and numbers of alleles over the 35 microsatellites loci was 0.66 with district-specific differences (Fig. 2).

Genetic distance

Genetic distance values indicated that some of the landraces were closely related. Averages of GD over regions ranged from 0.88 between Sharqia and most of the other regions to 0.19 between Bahla and Dhank (Table 4). The assessment of genetic similarities coefficients on the regional level yielded approximately 12,880 pairs. The 161 Omani hexaploid wheat landraces ranged from 0.06 to 0.89 with a mean of 0.46. The low GS coefficient values indicate the presence of high gene diversity in Omani hexaploid wheat landrace accessions.

Cluster analysis

The GS values between accessions used to produce a dendrogramme ranged from 0.19 between Sohar and Yanqul to 0.81 between Bahla and Dhank. The accessions clustered in two groups: one group consisted of the material from Sharqia, Batinah and Dhahira comprising accessions 159SBT, 161SBT, 50DDH of the botanical variety *T. aestivum* var. *maqtaense* A. Filat. et K. Hammer, 53YDH, 90YDH, 126YDH and 158SSH (most accessions were from farmers' seed stocks). The second group was larger and divided into two subgroups of which one comprised Sharqia Sur (123SSH, 124SSH, 155WSH, 157SSH *T. aestivum* var. *pseudohostianum* (Flaksb.) Mansf.). However, the analysis could not group the accessions according to districts. This was particularly true for accessions from Dakhilia which were scattered and mixed with accessions from other districts (Fig. 3).

Principal component analysis

The analysis for the ten collection regions separated the accessions into two clearly separated groups with Sur and Yanqul in the first quadrant and the other regions in the third quadrant (Fig. 4). The first three principal components had Eigenvalues of 47.7, 5.1 and 3.3%. The

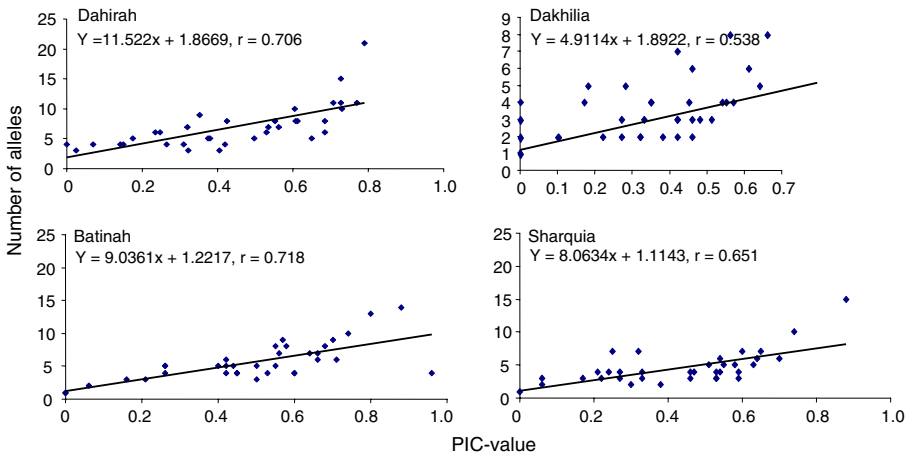

Fig. 2 Correlation between gene diversity and the number of alleles over 35 microsatellite loci in hexaploid wheat landraces. The accessions were analyzed separately for their collection districts in Oman (Dhahira, Batinah, Sharqia and Dakhilia)

Table 4 Nei's gene distances between the different collection regions of hexaploid wheat landraces from Oman

Region	Sur	Yanqul	Dhank	Bahla	Ibri	Sohar	Khabura	Maqta	Al Raky	Taeen
Sur										
Yanqul	0.88									
Dhank	0.86	0.79								
Bahla	0.88	0.76	0.19							
Ibri	0.88	0.76	0.41	0.35						
Sohar	0.86	0.81	0.49	0.49	0.46					
Khabura	0.88	0.73	0.22	0.21	0.36	0.50				
Maqta	0.85	0.85	0.46	0.41	0.54	0.61	0.42			
Al Raky	0.80	0.78	0.31	0.28	0.33	0.49	0.31	0.47		
Taeen	0.88	0.70	0.43	0.42	0.54	0.60	0.43	0.55	0.45	

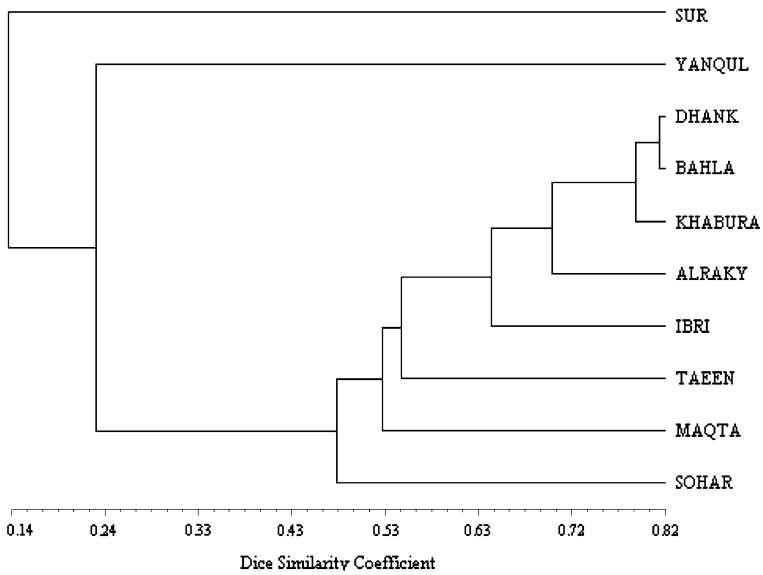

Fig. 3 Dendrogram of Omani landraces accessions grouped for ten regions of Oman according to UPGMA using Dice's similarity coefficients

results of PCA of the individual accessions showed the distribution of the landrace accessions spreading in three quadrants only. Some of Sharqia's accessions were relatively grouped and distanced from the others. Accessions from Batinah, Sharqia and Dhahira clustered together in two quadrant boxes (Fig. 5).

Discussion

In this study 35 microsatellites revealing 305 alleles from the 161 hexaploid wheat landraces were enough to discriminate all accessions. These results are in contrast with the minimum number of alleles reported by Zhang et al. (2002) who suggested a minimum of 350–400 alleles were needed to detect genetic relationships among common wheat varieties (Zhang et al. 2002). They examined 43 Chinese wheat varieties with 90 polymorphic SSR to determine the minimum number of alleles required to detect genetic relationships in their accessions. In a study of the French bread wheat, however, a set of 41 wheat microsatellite markers (WMS) was enough to detect 609 alleles from 559 landraces and registered varieties (Roussel et al. 2004).

The average allele number obtained in the present investigation of Omani hexaploid wheats was 8.70. This compares well with previous results on genetic diversity of wheat using microsatellite analysis. Khlestkina et al. (2004) detected average allele numbers of 6.6 in 54 common spring wheat varieties and Prasad et al. (2000) found

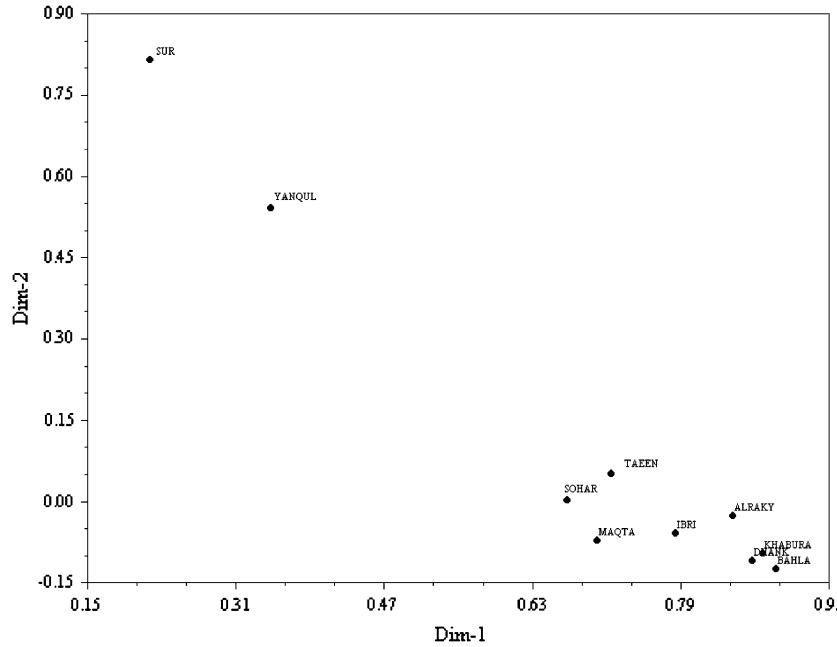

Fig. 4 Results of a principal component analysis (PCA) of 161 hexaploid wheat accessions from Oman. The grouping for the ten collection regions is based on Dice's similarity coefficients

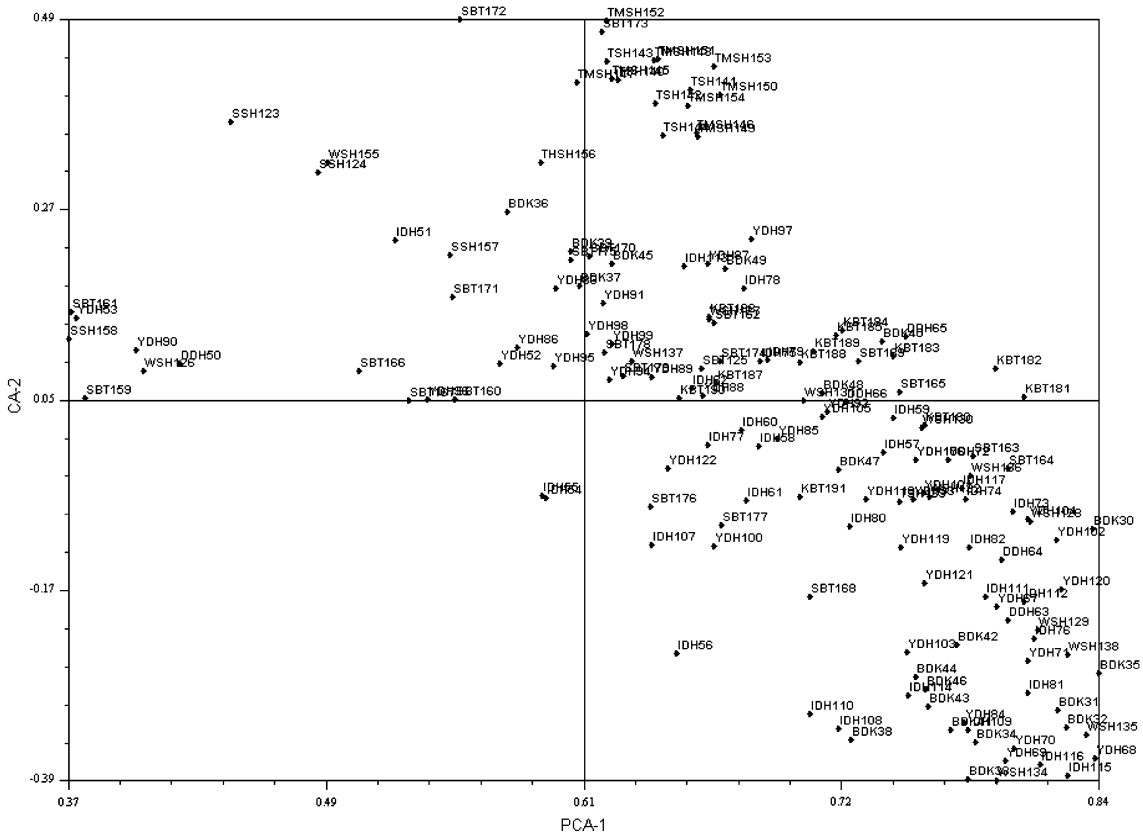

Fig. 5 Results of a principal component analysis (PCA) of 161 hexaploid wheat accessions from ten regions of Oman. The grouping is based on Dice's similarity coefficients

averages allele numbers of 7.4 in 55 varieties. Manifesto et al. (2001) reported an average allele number of 10.5 from 500 European wheat varieties, whereas Huang et al. (2002) investigated with microstallites nearly 1,000 accessions of hexaploid wheat originating from all over the world and thereby recorded an average allele number of 18.1.

The average gene diversity (PIC) obtained in the present investigation was comparable with previous results on genetic diversity of wheat using microsatellite analysis. Khlestkina et al. (2004) found a PIC-value of 0.70 in 54 common spring wheat varieties, while Prasad et al. (2000) reported a PIC-value of 0.71 in their 55 elite wheat genotypes. Analysing 105 Argentinean wheat varieties, Manifesto et al. (2001) reported an average gene diversity (PIC) of 0.72. For 500 European and world-wide collected wheats Röder et al. (2002) and Huang et al. (2002) found respective PIC values of 0.67 and 0.77. The highly significant ($P < 0.001$) correlation coefficient of 0.635 between gene diversity and number of alleles per locus for the 161 cultivated landraces (Fig. 2) confirms previous findings by Huang et al. (2002) and Roussel et al. (2004). However, it contradicts results of Prasad et al. (2000) who reported that the PIC value was uncorrelated with the number of alleles in their material.

The relatively large number of rare alleles in Batinah and Sharqia may be due to the sample size or modern commercial activities. High frequencies of rare alleles have also been reported in *Triticum urartu* Thum. ex Gandil. (Moghaddam et al. 2000), in *Aegilops tauschii* Coss. (Dudnikov 1998), in European wheat varieties (Röder et al. 2002) and for the Gatersleben wheat collection (Huang et al. 2002). Similarly, Roussel et al. (2004) reported that on average about 72% of the total number of alleles had a frequency lower than 5% and were therefore considered as rare.

The cluster analysis discriminated most of the hexaploid landraces accessions in our study. However, it did not group the landraces according to their geographic location. Similar results were obtained by Khlestkina (2004) for old and modern Siberian spring wheat varieties. Also Huang (2002) reported that not all accessions originating from the same region clustered in the same group, indicating that the genetic diversity of *T. aestivum* is not completely related to geographic distribution. In contrast, Alamerew et al. (2004) reported that all of his accessions could be separated, clustering in two large groups.

The results of our study might also show the effects of seed exchange between farmers within or even between districts. The Sharqia data indicated a high genetic diversity within a district which may reflect the effects of cultural isolation and distinct agricultural practices. On the other hand there is the observation that farmers will give different names to wheat landraces based on their agronomic performance or minor phenotypic differences regardless of the outcome of morphological or molecular genetic studies.

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References

Alamerew S, Chebotar S, Huang XQ, Röder MS, Börner A (2004) Genetic diversity in Ethiopian hexaploid and tetraploid wheat germplasm assessed by microsatellite markers. Genet Resour Crop Evol 51:559–567

Al-Maskri A, Nagieb M, Hammer K, Filatenko AA, Khan I, Buerkert A (2003) A note about *Triticum* in Oman. Genet Resour Crop Evol 50:83–87

Anderson JA, Churchill GA, Autrique JE, Sorrells ME, Tanksley SD (1993) Optimizing parental selection for genetic linkage maps. Genome 36:181–186

Akkaya SM, Bhagwat AA, Cregan PB (1992) Length polymorphism of simple-sequence repeat DNA in soybean. Genetics 132:1131–1139

Baek HJ, Beharav A, Nevo E (2003) Ecological-genomic diversity of microsatellites in wild barley, *Hordeum spontaneum*, populations in Jordan. Theor Appl Gen 106:397–410

Chapman C (1985) Genetic resources of wheat. A survey and strategy for collection. IBPGR, Rome

Devos KM, Bryan GJ, Collins AJ, Gale MD (1995) Application of two microsatellite sequences in wheat

storage proteins as molecular markers. Theor Appl Gen 90:247–252
Dice LR (1945) Measures of the amount of ecologic association between species. Ecology 26:297–302
Doebley J (1989) Isozyme evidence and the evolution of crop plants. In: Soltis DE, Soltis PS (eds) Isozymes in plant biology. Chapman and Hall, London, pp 165–191
Dudnikov AJU (1998) Allozyme variation in Transcaucasian populations of *Aegilops squarrosa*. Heredity 80:248–258
Eujayl ME, Sorrells M, Baum P, Wolters W, Powell W (2002) Isolation of EST-derived microsatellite markers for genotyping the A and B genomes of wheat. Theor Appl Gen 10:399–407
Fulton TM, Grandillo S, Beck-Bunn T, Fridman E, Frampton A, Petiard V, Uhlig J, Zamir D, Tanksley D (2000) Advanced backcross QTL analysis of a *Lycopersicon esculentum* × *Lycopersicon parviflorum* cross. Theor Appl Gen 100:1025–1042
Guarino L (1990) Crop collecting in the Sultanate of Oman in the context of the Arabian Peninsula. FAO/IPGRI PGR Newsl 77:27–33
Hammer K, Filatenko AA, Alkhanjari S, Al-Maskri A, Buerkert A (2004) Emmer (*Triticum dicoccon* Schrank) in Oman. Genet Resour Crop Evol 51:111–113
Huang Q, Börner A, Röder S, Ganal W (2002) Assessing genetic diversity of wheat (*Triticum aestivum* L.) germplasm using microsatellite markers. Theor Appl Gen 105:699–707
Ishii T, Xu Y, McCouch SR (2001) Nuclear- and chloroplast-microsatellite variation in A-genome species of rice. Genome 44(4):658–666
Johansson M, Ellegren H, Andersson L (1992) Cloning and characterization of highly polymorphic porcine microsatellites. J Hered 83:196–198
Koebner R, Donini P, Reeves J, Cooke R, Law J (2003) Temporal flux in the morphological and molecular diversity of UK barley. Theor Appl Gen 106:550–558
Khlestkina EK, Röder MS, Efremova TT, Börner A, Shumny VK (2004) The genetic diversity of old and modern Siberian varieties of common spring wheat as determined by microsatellite markers. Plant Breed 123:122–127
Li YC, Korol AB, Fahima T, Beiles A, Nevo E (2002) Microsatellites: genomic distribution, putative functions and mutational mechanisms: a review. Mol Ecol 11:2453–2465
Lu H, Bernardo R (2001) Molecular marker diversity among current and historical maize inbreds. Theor Appl Gen 103:613–617
Manifesto MM, Schlatter AR, Hop HE, Suarez EY, Dubcovsky J (2001) Quantitative evaluation of genetic diversity in wheat germplasm using molecular markers. Crop Sci 41:682–690
Melchinger AE, Messmer MM, Lee M, Woodman WL, Lamkey KR (1991) Diversity and relationships among U.S. maize inbreds revealed by restriction fragment length polymorphisms. Crop Sci 31:669–678
Melchinger AE, Graner A, Singh M, Messmer M (1994) Relationships among European barley germplasm. I. Genetic diversity among winter and spring cultivars revealed by RFLPs. Crop Sci 34:1191–1199
Moghaddam M, Ehdaie K, Waines JG (2000) Genetic diversity in populations of wild diploid wheat *Triticum urartu* Thum. ex Gandil. revealed by isozyme markers. Genet Resour Crop Evol 47:323–334
Mumm RH, Dudley JW (1994) A classification of 148 U.S. maize inbreds. I. Cluster analysis based on RFLPs. Crop Sci 34:842–851
Nei M (1973) Analysis of gene diversity in subdivided populations. Proc Natl Acad Sci USA 70:3321–3323
Nei M, Li WH (1979) Mathematical model for studying genetic variation in terms of endonucleases. Proc Natl Acad Sci USA 76:5269–5273
Prasad M, Varshney RK, Roy JK, Balayan HS, Gupta PK (2000) The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat. Theor Appl Gen 100:584–592
Plaschke J, Ganal MW, Röder MS (1995) Detection of genetic diversity in closely related bread wheat using microsatellite markers. Theor Appl Gen 91:1001–1007
Potts D (1993) Rethinking some aspects of trade in the Arabian Gulf. World Archae 24:423–439
Röder MS, Huang XQ, Ganal MW (2004) Wheat microsatellites in plant breeding-potential and implications. In: Loerz H, Wenzel G (eds), Molecular markers in plant breeding. Springer, Berlin Heidelberg New York, pp 255–266
Röder MS, Plaschke J, Koenig SU, Börner A, Sorrels ME, Tanksley SD, Ganal MW (1995) Abundance, variability and chromosomal location of microsatellites in wheat. Mol Gen Genet 246:327–333
Röder MS, Korzun V, Wendehake K, Plaschke J, Tixier MH, Leroy P, Ganal MW (1998) A microsatellite map of wheat. Genetics 149:2007–2023
Röder MS, Wendehake K, Korzun V, Bredemeijer G, Laborie D, Bertrand L, Isaac P, Rendell S, Jackson J, Cooke RJ, Vosman B, Ganal MW (2002) Construction and analysis of a microsatellite-based database of European wheat varieties. Theor Appl Gen 106:67–73
Rohlf FJ (2002) Numerical taxonomy and multivariate analysis system. NTSYS version 2.11a. Applied Biostatistics Inc., New York
Rongwen J, Akkaya MS, Bhagwat AA, Lavi U, Gregan PB (1995) The use of microsatellite DNA markers for soybean genotype identification. Theor Appl Gen 90:43–48
Roussel V, Koenig J, Beckert M, Balfourier F (2004) Molecular diversity in French bread wheat accessions related to temporal trends and breeding programmes. Theor Appl Gen 108:920–930
Russell JR, Ellis RP, Thomas WTB, Waugh R, Provan J, Booth A, Fuller J, Lawrence P, Young G, Powell W (2000) A retrospective analysis of spring barley germplasm development from 'foundation genotypes' to currently successful cultivars. Mol Breed 6:553–568
Salamini F, Ozkan H, Brandolini A, Schafer-Pregl R, Martin W (2002) Genetics and geography of wild cereal domestication in the near east. Nat Rev Gen 3:429–441

Schwartz O (1939) Flora des tropischen Arabien. Mitteilungen aus dem Institut für Allgemeine Botanik in Hamburg 10, pp 339

Smith JSC, Chin ECL, Shu H, Smith OS, Wall SJ, Senior ML, Mitchell SE, Kresovich S, Ziegle J (1997) An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L.). Theor Appl Gen 95:163–173

Sneath PHA, Sokal RR (1973) Numerical Taxonomy. Freeman. San Francisco, p 573

Soleimani VD, Soleimani BR, Baum DA, Johnson AD (2002) AFLP and pedigree-based genetic diversity estimates in modern cultivars of durum wheat [*Triticum turgidum* L. subsp. *durum* (Desf.) Husn.]. Theor Appl Gen 104:350–357

Temnykh S, DeClerck G, Lukashova A, Lipovich L, Cartinhour S, McCouch S (2001) Computational and experimental analysis of microsatellites in rice (*Oryza sativa* L.): frequency, length variation, and genetic marker potential. Genome Res 11:1441–1452

Tolbert DM, Qualset CO, Jain SK, Craddock JC (1979) A diversity analysis of a world collection of barely. Crop Sci 19:789–794

Vavilov NI (1964) World resources of cereals, legumes, flax cultivars and their utilization in breeding. Wheat. Nauka, Moskow and Leningrad

Willcox G, Tengberg M (1995) Preliminary report on the archaeobotanical investigations at Tell Abraq with special attention to the chaff impressions in mud brick. Arabian Archae Epig 6:129–138

Zhang P, Dreisigacker S, Buerkert A, Alkhanjari S, Melchinger AE, Warburton ML (2006) Genetic diversity and relationships of wheat landraces from Oman investigated with SSR markers. Genet Resour Crop Evol (in press)

Zhang XY, Li CW, Wang LF, Wang HM, You GX, Dong YS (2002) An estimation of the minimum number of SSR alleles needed to reveal genetic relationships in 19 wheat varieties. Information from large-scale planted varieties and cornerstone breeding parents in Chinese wheat improvement and production. Theor Appl Gen 106:112–117

Zohary D, Hopf M (1993) Domestication of plants in the Old World – The origin and spread of cultivated plants in West Asia, Europe, and the Nile Valley. Clarendon Press, Oxford