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A DNA fingerprinting-based taxonomic allocation of Kamut wheat

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Abstract

Kamut wheat, said to have been derived from seed found in the Egyptian pyramids, appeared on the market about 25 years ago. We have investigated its taxonomic placement using microsatellite genotyping. In all, 89 accessions of 13 tetraploid wheat species, along with samples of Kamut wheat, were genotyped using two A and B genome wheat microsatellite markers per chromosome, generating 453 alleles (8–33 alleles per locus), and a mean allelic polymorphic information content (PIC) of 0.80. A diversity analysis showed that nine major accession groups could be defined, and these were inconsistent with formal taxonomic classifications of about 10% of the material. Most of these misclassifications are due to either species introgression or seed admixture. Some accessions appear to be duplicates. The Kamut wheats grouped together in a cluster containing three accessions of *Triticum polonicum* and three of *T. durum*, originating from Turkey, Iraq, Iran and Israel. We suggest that Kamut perhaps derived from a natural hybrid between *T. durum* and *T. polonicum*, which occurred in the Fertile Crescent.

Keywords: Kamut wheat; microsatellite markers; tetraploid wheat species; *Triticum* ssp.

Introduction

Kamut wheat has an exciting history (described fully at http://www.kamut.com/english/index.htm). In brief, as reported by Quinn (1999), after the Second World War, a US airman claimed to have taken a handful of grain from a stone box in a tomb near Dashare, Egypt. Thirty-six kernels were given to a friend who sent them to his father, a Montana wheat farmer. According to legend, the grain was dubbed 'King Tut's Wheat'. Soon the novelty wore off and the grain was forgotten. In 1977 a remaining jar of 'King Tut's Wheat' was obtained by the Quinns, another Montana wheat-farming family, who multiplied the seed and introduced the trade name 'Kamut'—an ancient Egyptian word for wheat. In 1990, the US Department of Agriculture recognized the grain as a protected cultivar, which was given the official name 'QK-77'. Kamut is a trademarked wheat that has been widely promoted in Western countries as a unique grain with a unique origin and unusual health and production qualities. No rigorous experimental evidence has been published that addresses or validates these claims. Kamut was described as out-yielding spring wheats when environmental stress occurs during the growing season, but in more ideal growing seasons, its yield is at best equal to that of standard cultivars. Plant height is approximately 130 cm, with good to excellent

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straw strength. Grain protein content is said to be superior to that of common wheat grown under similar environments (Stallknecht *et al.*, 1996).

The taxonomic classification of Kamut is as unclear as its origin. It is thought to have evolved contemporaneously with the free-threshing tetraploid wheats, and is considered to be an ancient relative of modern durum wheats. In the literature it has been variously classified as *Triticum turgidum* ssp. *polonicum*, *T. turgidum* ssp. *turanicum* and *T. turgidum* ssp. *durum* (Stallknecht *et al.*, 1996).

In recent years DNA fingerprinting has become one of the most reliable and powerful tools for genotype identification. Wheat microsatellite markers (Röder *et al.*, 1998), known to be abundant, highly polymorphic, reliable and relatively easy to apply, have been used in numerous studies to generate genotype in large sets of wheat accessions for the estimation of genetic diversity as well as for the investigation of relationships between lines (Plaschke *et al.*, 1995; Donini *et al.*, 1998; Fahima *et al.*, 1998; Ben Amer *et al.*, 2001; Chebotar and Sivolap, 2001; Huang *et al.*, 2002; Röder *et al.*, 2002; Khlestkina *et al.*, 2004a, 2004b). Both Hammer *et al.* (2000) and Alamerew *et al.* (2004) used wheat microsatellites as a taxonomic aid to distinguish diploid from, respectively, tetraploid and hexaploid wheats. The objective of the present study was to use this class of marker to establish the taxomony of Kamut wheat, by comparing its DNA fingerprint with those of other well-characterized tetraploid wheat species.

Materials and methods

Plant materials

Eighty-nine accessions of 13 tetraploid wheat taxa and 10 independent accessions of Kamut wheat were used in the analysis (Table 1). The 'QK-77' used in the present study was obtained by AGES (Österreichische Agentur für Gesundheit und Ernährungssicherheit, i.e. Austrian Agency for Health and Safety Food) directly from Bob Quinn, the Kamut owner. In addition, five hexaploid wheats, specifically cultivars 'Chinese Spring', 'Aztec', 'Soissons', 'Novosibirskaya 67' and 'Saratovskaya 29', were included as standards. Except for one entry ('01C0200988', originating from Prag-Ruszyne), all materials were re-grown to confirm taxonomic classification by conventional morphology, applying the descriptors of Dorofeev *et al.* (1979).

Microsatellite markers and PCR amplification

Total genomic DNA was extracted from five grains of each accession, as described by Plaschke *et al.* (1995). The 28 selected primer pairs (listed in Table 2) detected a set of microsatellite loci mapping to each arm of the 14 A and B genome chromosomes present in tetraploid wheat (Plaschke *et al.*, 1995; Röder *et al.*, 1995, 1998), and all amplification reactions were performed as described previously (Plaschke *et al.*, 1995; Röder *et al.*, 1998). Fragment separation was effected using an automated laser fluorescence sequencer (ALF Express, Amersham-Biosciences), and fragment size was calculated via Fragment Analyser version 1.02 software (Amersham-Biosciences) by comparison with internal size standards. The bread wheat cultivars were included as template controls, as the fragment sizes at all the loci amplified from their DNAs are well characterized.

Statistical analysis

The presence/absence of each fragment was encoded as a 1/0 score, generating a binary data matrix. These binary data allowed for the computation of a pair-wise similarity matrix (Dice, 1945), which was subjected to cluster analysis using the unweighted pair-group method of arithmetical means (UPGMA) algorithm in NTSYS-pc, version 2.0 (Rohlf, 1998). Gene diversity was calculated as $1 - \Sigma P_{ij}^2$ (Nei, 1973), where P_{ij} is the frequency of the jth allele at the ith locus, summed across all alleles of the locus. This coefficient is identical to the allelic polymorphic information content (PIC), as defined by Anderson *et al.* (1993).

Results

Microsatellite marker analysis and gene diversity

All of the microsatellite primer pairs generated polymorphic fragments in the test material, but some primer pairs amplified poorly or not at all from the template of certain accessions. In these cases, null alleles were assigned where amplification failed in repeated experiments. Allele sizes, the number of alleles per locus and the gene diversity coefficients are presented in Table 2. In total, 453 alleles were detected, ranging from eight (*Xgwm415*, chromosome 5AS) to 33 (*Xgwm459*, chromosome 6AS) alleles per locus. The mean number of alleles per locus was higher in the B genome (17.1 alleles per locus) than in the A genome (15.2 alleles per locus). Gene diversity varied from 0.36 (*Xgwm415*, chromosome 5AS) to 0.95 (*Xgwm540*, chromosome 5BS), with a mean of 0.80. The mean gene diversities for the A and B genome loci were, respectively, 0.77 and 0.83.

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Table 1. Tetraploid and hexaploid wheat accessions used in the present study (taxonomic classification follows Dorofeev *et al.*, 1979)

	Accession number/cultivar name	Species	Genome designation	Source of seeds	Provenance	Cluster determined in Fig. 1
01	'Kamut Boku'	? ['Kamut']	[AABB]	BOKU, Vienna, Austria (via USA)	Unknown	IX
02	'Grano Kamut'	? ['Kamut']	[AABB]	Health food shop, Venice, Italy	Unknown	IX
03	'Kamut Neuform'	? ['Kamut']	[AABB]	Shop, Vienna, Austria	Unknown	IX
04	'Kamut Ernte'	? ['Kamut']	[AABB]	Market, Tulln, Austria	Unknown	IX
05	'QK-77'	? ['Kamut']	[AABB]	AGES Vienna, Austria	Unknown	IX
06	'Kamut Bioleben'	? ['Kamut']	[AABB]	Supermarket, Vienna, Austria	Unknown	IX
07	'KAMUT'	? ['Kamut']	[AABB]	AGES Vienna, Austria (from Bob Quinn)	Unknown	IX
08	TRI 16 772	? ['Kamut']	[AABB]	IPK Gatersleben, Germany (via Italy)	Unknown	IX
09	TRI 18 957	? ['Kamut']	[AABB]	IPK Gatersleben, Germany (via France)	Unknown	IX
10	WA 7382 'Kamut'	? ['Kamut']	[AABB]	IPK Gatersleben, Germany (via Canada)	Unknown	IX
11	PI 251925	*T. turanicum* Jakubz.	AABB	NSGC Aberdeen, UK	Unknown	VIII
12[a]	01C0200988	*T. turanicum* Jakubz.	AABB	Prag-Ruszyne, Czech Republic	Unknown	V
13	TRI 10 343	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Uzbekistan	VIII
14	TRI 11 532	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iraq	VIII
15	TRI 11 533	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iraq	VIII
16	TRI 17 462	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Uzbekistan	VIII
17	TRI 3287	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Europe	VIII
18	TRI 4326	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iran	VIII
19	TRI 5254	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Europe	VIII
20	TRI 6243	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iran	VIII
21	TRI 680	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Europe	VIII
22	TRI 909	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Europe	VIII
23	TRI 11 949	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Unknown	VIII
24	TRI 18 614	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Turkmenistan	VIII
25	TRI 18 625	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iran	VIII
26	TRI 18 865	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Russia	VIII
27	TRI 18 866	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Uzbekistan	VIII
28	TRI 18 868	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Kazakhstan	VIII
29	TRI 18 869	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Tajikistan	VIII
30	TRI 18 870	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Tajikistan	VIII
31	TRI 18 871	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Tajikistan	VIII
32	TRI 8872	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Tajikistan	VIII
33	TRI 9485	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Greece	VIII
34[a]	TRI 9517	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Azerbaijan	VII
35	TRI 9925	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Europe	VIII
36	TRI 17 461	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Pakistan	VIII
37[a]	TRI 6070	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iran	III
38[a]	TRI 6075	*T. turanicum* Jakubz.	AABB	IPK Gatersleben, Germany	Iran	III
39	1510	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	VIII
40	42 101	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	VIII
41[a]	42 102	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	IV
42[a]	40 103	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	IV

Table 1. *Continued*

	Accession number/cultivar name	Species	Genome designation	Source of seeds	Provenance	Cluster determined in Fig. 1
43[a]	42 104	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	IV
44[a]	42 105	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	IX
45[a]	43 542	*T. turanicum* Jakubz.	AABB	BAZ Braunschweig, Germany	Unknown	III
46	'Ambrodur'	*T. durum* Desf.	AABB	Saatzucht Dr. Franck, Germany	Germany	VII
47	'Extradur'	*T. durum* Desf.	AABB	Probstdorfer Saatzucht, Austria	Austria	VII
48	'Helidur'	*T. durum* Desf.	AABB	Probstdorfer Saatzucht, Austria	Austria	VII
49	'Heradur'	*T. durum* Desf.	AABB	Probstdorfer Saatzucht, Austria	Austria	VII
50	'Prowidur'	*T. durum* Desf.	AABB	Probstdorfer Saatzucht, Austria	Austria	VII
51	'Superdur'	*T. durum* Desf.	AABB	Probstdorfer Saatzucht, Austria	Austria	VII
52	'Topdur'	*T. durum* Desf.	AABB	Probstdorfer Saatzucht, Austria	Austria	VII
53	TRI 9515	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Azerbaijan	IX
54	TRI 5992	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Iran	VII
55	TRI 6183	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Iran	VII
56	TRI 8154	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Iraq	IX
57	TRI 8155	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Iraq	IX
58	TRI 9514	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Azerbaijan	VII
59	TRI 18 260	*T. durum* Desf.	AABB	IPK Gatersleben, Germany	Italy	VII
60	TRI 18 482	*T. dicoccoides* (Koern. ex Aschers. Et Graebn.) Schweinf.	AABB	IPK Gatersleben, Germany	Turkey	II
61	TRI 18 535	*T. dicoccoides* (Koern. ex Aschers. Et Graebn.) Schweinf.	AABB	IPK Gatersleben, Germany	Turkey	II
62[a]	'BVAL_212017'	*T. dicoccon* Schrank	AABB	Genebank Linz, Austria	Unknown	IX
63	TRI 5860	*T. dicoccon* Schrank	AABB	IPK Gatersleben, Germany	Iran	II
64	TRI 18 207	*T. dicoccon* Schrank	AABB	IPK Gatersleben, Germany	Georgia	II
65	TRI 18 210	*T. dicoccon* Schrank	AABB	IPK Gatersleben, Germany	Azerbaijan	II
66	TRI 18 519	*T. dicoccon* Schrank	AABB	IPK Gatersleben, Germany	Turkey	II
67	TRI 18 520	*T. dicoccon* Schrank	AABB	IPK Gatersleben, Germany	Turkey	II
68	TRI 12 911	*T. jakubzineri* Udacz. et Schachm.	AABB	IPK Gatersleben, Germany	Uzbekistan	V
69	TRI 17 540	*T. jakubzineri* Udacz. et Schachm.	AABB	IPK Gatersleben, Germany	Uzbekistan	V
70	TRI 11 946	*T. karamyschevii* Nevski	AABB	IPK Gatersleben, Germany	Georgia	III
71	TRI 12 750	*T. karamyschevii* Nevski	AABB	IPK Gatersleben, Germany	Georgia	III
72	TRI 17 437	*T. karamyschevii* Nevski	AABB	IPK Gatersleben, Germany	Georgia	III
73[a]	TRI 18 539	*T. araraticum* Jakubz.	AAGG	IPK Gatersleben, Germany	Turkey	II
74	TRI 18 472	*T. araraticum* Jakubz.	AAGG	IPK Gatersleben, Germany	Iraq	I
75	TRI 18 512	*T. araraticum* Jakubz.	AAGG	IPK Gatersleben, Germany	Iran	I
76	TRI 2376	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Europe	VI
77	TRI 3428	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Turkey	IX
78	TRI 5915	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Iran	IX
79	TRI 17 452	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Kazakhstan	VI
80	TRI 17 454	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Georgia	VI
81	TRI 17 457	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Israel	IX
82	TRI 18 270	*T. polonicum* L.	AABB	IPK Gatersleben, Germany	Turkey	VI
83	TRI 3433	*T. timopheevii* (Zhuk.) Zhuk.	AAGG	IPK Gatersleben, Germany	Turkey	I

Table 1. *Continued*

	Accession number/cultivar name	Species	Genome designation	Source of seeds	Provenance	Cluster determined in Fig. 1
84	TRI 5351	*T. timopheevii* (Zhuk.) Zhuk.	AAGG	IPK Gatersleben, Germany	Georgia	I
85	TRI 13 604	*T. timopheevii* (Zhuk.) Zhuk.	AAGG	IPK Gatersleben, Germany	Georgia	I
86	TRI 17 542	*T. timopheevii* (Zhuk.) Zhuk.	AAGG	IPK Gatersleben, Germany	Russia	I
87	TRI 16 601	*T. militinae* Zhuk. et Migusch.	AAGG	IPK Gatersleben, Germany	Bulgaria	I
88	TRI 17 488	*T. militinae* Zhuk. et Migusch.	AAGG	IPK Gatersleben, Germany	Georgia	I
89	TRI 758	*T. turgidum* L.	AABB	IPK Gatersleben, Germany	Turkey	VI
90	TRI 5888	*T. turgidum* L.	AABB	IPK Gatersleben, Germany	Iran	VI
91	TRI 9547	*T. turgidum* L.	AABB	IPK Gatersleben, Germany	Armenia	IX
92[a]	TRI 17 236	*T. turgidum* L.	AABB	IPK Gatersleben, Germany	Turkey	IV
93	TRI 3422	*T. carthlicum*	AABB	IPK Gatersleben, Germany	Caucasus	IV
94	TRI 9535	*T. carthlicum* Nevski	AABB	IPK Gatersleben, Germany	Armenia	IV
95	TRI 15 127	*T. carthlicum* Nevski	AABB	IPK Gatersleben, Germany	Georgia	IV
96	TRI 17 185	*T. carthlicum* Nevski	AABB	IPK Gatersleben, Germany	Turkey	IV
97	TRI 6177	*T. ispahanicum* Heslot	AABB	IPK Gatersleben, Germany	Iran	II
98	TRI 7260	*T. ispahanicum* Heslot	AABB	IPK Gatersleben, Germany	Iran	II
99	TRI 17 436	*T. ispahanicum* Heslot	AABB	IPK Gatersleben, Germany	Iran	II
100	'Aztec'	*T. aestivum* L.	ABBDD	IPK Gatersleben, Germany	France	II
101	'Chinese Spring'	*T. aestivum* L.	ABBDD	IPK Gatersleben, Germany	China	III
102	'Soissons'	*T. aestivum* L.	ABBDD	IPK Gatersleben, Germany	France	III
103	'Novosibirskaya 67'	*T. aestivum* L.	ABBDD	ICG Novosibirsk, Russia	Russia	III
104	'Saratovskaya 29'	*T. aestivum* L.	ABBDD	ICG Novosibirsk, Russia	Russia	III

[a] Taxonomic re-classification necessary.

Table 2. Designation, chromosomal location (Röder *et al.*, 1998; and unpublished data), size range, number of alleles and gene diversity values across 28 A and B genome microsatellite loci

Designation	Chromosome arm location	Range of allele size (bp)	Number of alleles	Gene diversity
Xgwm357	1A (cent)	103–145	11	0.78
Xgwm1097	1AS	null, 103–177	13	0.71
Xgwm95	2AS	null, 104–130	11	0.72
Xgwm312	2AL	181–253	23	0.9
Xgwm720	3AS	null, 126–174	20	0.91
Xgwm155	3AL	null, 125–165	15	0.88
Xgwm601	4AS	null, 149–173	14	0.86
Xgwm1081	4AL	131–167	9	0.69
Xgwm415	5AS	101–133	8	0.36
Xgwm126	5AL	null, 185–199	9	0.78
Xgwm459	6AS	null, 105–195	33	0.94
Xgwm1089	6AL	110–170	18	0.82
Xgwm631	7AS	162–214	11	0.6
Xgwm698	7AL	null, 153–213	18	0.79
Xgwm18	1BS	null, 146–212	20	0.85
Xgwm268	1BL	null, 183–259	31	0.94
Xgwm148	2BS	null, 136–198	18	0.85
Xgwm619	2BL	null, 135–179	15	0.69
Xgwm389	3BS	null, 116–152	15	0.83
Xgwm655	3BL	null, 121–203	15	0.79
Xgwm898	4BS	null, 100–120	11	0.78
Xgwm513	4BL	null, 137–155	10	0.79
Xgwm540	5BS	105–135	15	0.95
Xgwm408	5BL	null, 147–195	15	0.77
Xgwm680	6BS	103–157	12	0.71
Xgwm219	6BL	103–235	21	0.88
Xgwm46	7B (cent)	null, 145–195	20	0.91
Xgwm577	7BL	null, 128–218	22	0.88
Total			453	
Mean			16.2	0.80

Cluster analysis

A dendrogram, derived from the UPGMA cluster analysis (Fig. 1), defines nine major groups (see also Table 1). Group I, with genetic similarity coefficients (GS) ranging from 0.26 to 0.92, was the most distantly separated and included accessions of *T. araraticum*, *T. timopheevii* and *T. militinae*. Group II (GS 0.15–0.73) included several species, and could be divided into three subgroups: (1) *T. dicoccum* and *T. isphahanicum*; (2) *T. dicoccoides*; and (3) a single accession of *T. araraticum* and one control *T. aestivum* cultivar. A morphological re-classification suggested that the *T. araraticum* line may have experienced introgression from *T. dicoccoides*. Group III (GS 0.18–1.00) contained the remaining four bread wheat controls, three accessions of *T. turanicum* (re-classified as containing genetic material from *T. aestivum*) and a small subgroup of *T. karamyschevii*. Group IV (GS 0.28–0.57) was largely composed of the *T. carthlicum* accessions, although it also included one *T. turgidum*, re-classified as *T. carthlicum*, and three *T. turanicum* accessions, which were mixtures either between *T. aestivum* and *T. carthlicum* or between *T. turgidum*, *T. durum* and *T. carthlicum*. Group V consisted of two closely related (GS 0.98) *T. jakubzineri* accessions and a much more distantly related (GS 0.24) accession of *T. turanicum*, which was the one entry not re-classified. Group VI (GS 0.29–0.56) was made up of *T. polonicum* and *T. turgidum* accessions. Group VII (GS 0.26–0.88) was the *T. durum* group, but also included one *T. turanicum* accession showing evidence of *T. durum* introgression. Group VIII contained only *T. turanicum* accessions. The final group (group IX) consisted of five small subgroups: (1) one *T. turgidum* accession (the most distal from the other subgroups); (2) one *T. turanicum* accession similar to Kamut; (3) a subgroup of *T. durum*; (4) a subgroup of *T. polonicum* including one *T. durum* accession; and (5) all 10 Kamut wheats, six of which (including 'QK-77')

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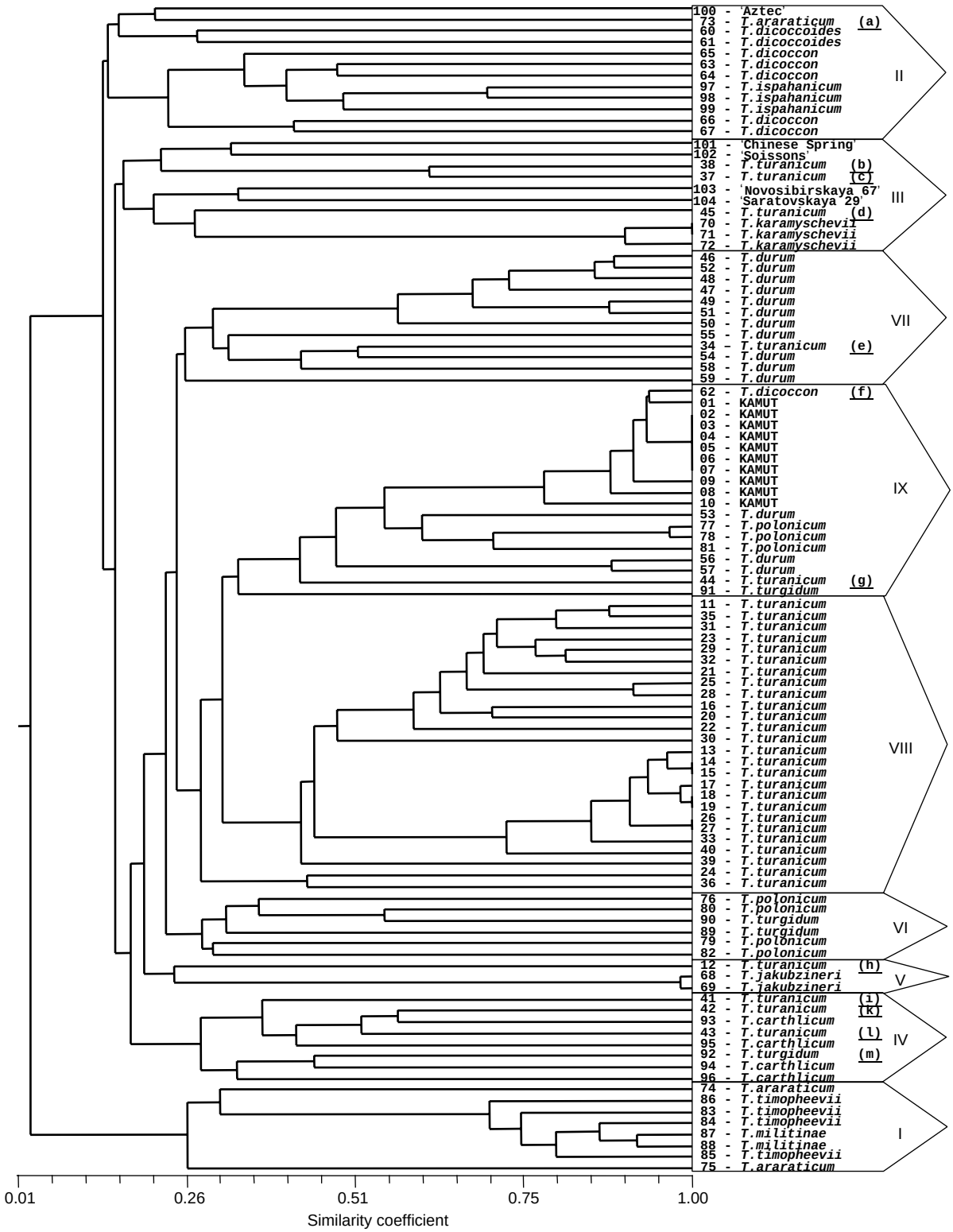

Fig. 1. UPGMA-based dendrogram based on genetic similarity between Kamut wheat and 13 tetraploid wheat species. After taxonomic re-classification, the following changes were considered necessary: (a) *Triticum araraticum* with *T. dicoccoides* introgression; (b) *T. turanicum* with *T. aestivum* introgression; (c) *T. turanicum* with *T. aestivum* introgression; (d) *T. aestivum*; (e) *T. turanicum* with *T. durum* introgression; (f) Kamut; (g) Kamut-like *T. turanicum*; (h) no re-classification performed; (i) mixture between *T. carthlicum* and *T. aestivum*; (k) mixture between *T. carthlicum* and *T. aestivum*; (l) mixture between *T. carthlicum, T. durum* and *T. turanicum*; (m) *T. carthlicum*.

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clustered with a GS of 1.00. The Kamut subgroup also included an emmer accession (*T. dicoccum*), re-classified as Kamut.

Discussion

The cluster analysis showed that many species map across more than a single group, and in the subsequent morphology-based re-classification, it was apparent that the original species designation in several cases was faulty. This demonstrates that DNA fingerprinting can be powerful as a means of detecting errors in morphological taxonomic classification, as it can highlight problems caused both by seed admixture and cross-species introgression. About 10% of the accessions used in the present study proved to have been incorrectly assigned. In addition, the genotyping exercise has identified a number of duplicate accessions. Thus in addition to the homogeneous Kamut wheats, there were no genotypic differences between either the pair of *T. karamyschevii* accessions (group III), or the three pairs of *T. turanicum* accessions (group VIII). The *T. karamyschevii* accessions came independently to the Gatersleben collection, one from the Institute of Botany, Tblisi, Georgia, and the other from the VIR, St Petersburg, Russia, and thus could well be identical to one another.

As predicted on the basis of genome content (Dorofeev *et al.*, 1979), the AAGG tetraploids *T. timopheevii*, *T. militinae* and *T. araraticum* clustered together into a single group (I), which was separated from the AABB and AABBDD wheats. Dorofeev *et al.* (1979) classified *T. dicoccoides*, *T. dicoccum*, *T. ispahanicum* and *T. karamyshevii* into a discrete group among the AABB tetraploids, and this grouping was confirmed by the DNA fingerprinting analysis, since these four species fell into two clusters (groups II and III) separated from the other tetraploid species. Interestingly, all five hexaploid wheats were allocated to these same two clusters.

Within the Kamut cluster (group IX), the six identical accessions all originated from Austria, including 'QK-77'. The other four samples were distinguishable from one another. In this same cluster were one accession of *T. turgidum*, three of *T. polonicum*, three of *T. durum* and, although more distantly related, one of *T. turanicum* with a Kamut-like ear morphology. The *T. polonicum* and *T. durum* accessions in this cluster originated from regions around the Fertile Crescent (Turkey, Iraq, Iran, Israel and Azerbaijan). The remaining *T. polonicum* accessions formed a separate group (group VI) together with those of *T. turgidum*. A separate cluster (group VII) contained all the other *T. durum* accessions, including modern Austrian and German cultivars. Based on these findings, we suggest that Kamut could well be the outcome of a natural hybridization event between *T. durum* and *T. polonicum*, which took place in the Near East. This suggestion is supported by the spike morphology comparisons (Fig. 2).

Fig. 2. Typical spikes of (from left to right) *Triticum durum* (TRI 9515), Kamut ('QK-77') and *T. polonicum* (TRI 17 457).

Kamut has been frequently recommended as a wheat substitute in diets of patients allergic to bread wheat (Stallknecht *et al.*, 1996). However, recent studies have established that there is no allergenic difference between bread wheat and Kamut, and indeed Kasarda (2001) has shown that since Kamut grain contains glutens, coeliac patients should avoid them as much as bread and durum wheats. Similarly, Simonato *et al.* (2002) have strongly recommended that all individuals suffering a serious allergy to wheat should avoid consuming Kamut. These conclusions are hardly surprising considering the close taxonomic relationship between Kamut and standard pasta wheats, as revealed in this study by the application of molecular markers.

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References

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

Anderson JA, Churchill GA, Antrique JE, Tanksley SD and Sorrels ME (1993) Optimising parental selection for genetic linkage maps. *Genome* 36: 181–188.

Ben Amer IM, Börner A and Röder MS (2001) Detection of genetic diversity in Libyan wheat genotypes using wheat microsatellite markers. *Genetic Resources and Crop Evolution* 48: 579–585.

Chebotar SV and Sivolap YM (2001) Differentiation, identification and characterization of *Triticum aestivum* L. varieties from Ukrainian breeding programs by using STMS analysis. *Cytology and Genetics* 35: 18–27 (in Russian).

Dice LR (1945) Measures of the amount of ecologic association between species. *Ecology* 26: 297–302.

Donini P, Stephenson P, Bryan GJ and Koebner RMD (1998) The potential of microsatellites for high throughput genetic diversity assessment in wheat and barley. *Genetic Resources and Crop Evolution* 45: 415–421.

Dorofeev VF, Filatenko AA, Migushova EF, Udachin RA and Jakubziner MM (1979) *Flora of Cultivated Plants*. Leningrad: Kolos, Leningrad Branch (in Russian).

Fahima T, Röder MS, Grama A and Nevo E (1998) Microsatellite DNA polymorphism divergence in *Triticum dicoccoides* accessions highly resistant to yellow rust. *Theoretical and Applied Genetics* 96: 187–195.

Hammer K, Filatenko AA and Korzun V (2000) Microsatellite markers—a new tool for distinguishing diploid wheat. *Genetic Resources and Crop Evolution* 47: 497–505.

Huang XQ, Börner A, Röder MS and Ganal MW (2002) Assessing genetic diversity of wheat (*Triticum aestivum* L.) germplasm using microsatellite markers. *Theoretical and Applied Genetics* 105: 699–707.

Kasarda DD (2001) Grains in relation to celiac disease. *Cereal Foods World* 46: 209–210.

Khlestkina EK, Huang XQ, Quenum FJB, Chebotar S, Röder MS and Börner A (2004a) Genetic diversity in cultivated plants—loss or stability? *Theoretical and Applied Genetics* 108: 1466–1472.

Khlestkina EK, Röder MS, Efremova TT, Börner A and Shumny VK (2004b) The genetic diversity of old and modern Siberian varieties of common spring wheat determined by microsatellite markers. *Plant Breeding* 123: 122–127.

Nei M (1973) Analysis of gene diversity in subdivided populations. *Proceedings of the National Academy of Sciences of the USA* 70: 3321–3323.

Plaschke J, Ganal MW and Röder MS (1995) Detection of genetic diversity in closely related bread wheat using microsatellite markers. *Theoretical and Applied Genetics* 91: 1001–1007.

Quinn RM (1999) Kamut®: ancient grain, new cereal. In: Janick J (ed.) *Perspectives on New Crops and New Uses*. Alexandria, VA: ASHS Press, pp. 182–183.

Röder MS, Plaschke J, König SU, Börner A, Sorrells ME, Tanksley SD and Ganal MW (1995) Abundance, variability and chromosomal location of microsatellites in wheat. *Molecular and General Genetics* 246: 327–333.

Röder MS, Korzun V, Wendehake K, Plaschke J, Tixier M-H, Leroy P and Ganal MW (1998) A microsatellite map of wheat. *Genetics* 149: 2007–2023.

Röder MS, Wendehake K, Korzun V, Bredemeijer G, Laborie D, Bertrand L, Isaak P, Rendell S, Jackson J, Cooke RJ, Vosman B and Ganal MW (2002) Construction and analysis of a microsatellite-based database of European wheat varieties. *Theoretical and Applied Genetics* 106: 67–73.

Rohlf FJ (1998) *NTSYS-pc: Numerical Taxonomy and Multivariate Analysis System*, version 2.0. New York: Applied Biostatistics.

Simonato B, Pasini G, Giannattasio M and Curioni A (2002) Allergenic potential of Kamut wheat. *Allergy* 57: 653–654.

Stallknecht GF, Gilbertson KM and Ranney JE (1996) Alternative wheat cereals as food grains: Einkorn, Emmer, Spelt, Kamut, and Triticale. In: Janick J (ed.) *Progress in New Crops*. Alexandria, VA: ASHS Press, pp. 156–170.