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Breeding for wheat quality to assure food security of a staple crop: the case study of Tajikistan

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Abstract

Background: This study evaluated options and obstacles to strengthening food security through breeding a staple crop in a developing country, using the case of quality of bread wheat in Tajikistan as an example.

Methods: Three wheat varieties and 19 breeding lines were collected from two field trial locations included in the Tajik wheat breeding programme. Grain protein composition as a measure of quality was determined by sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE). Payne scores were calculated in order to predict quality.

Results: There was high variation between and high heterogeneity within several lines and varieties in relation to protein composition. Differences between the same varieties/lines at different locations were also observed. The number of grains analysed from each variety/line allowed prediction of quality, and the majority of materials analysed showed high Payne scores. Based on Payne scores and cluster analyses, a group of varieties/lines with high quality was identified as interesting for further breeding.

Conclusions: This study demonstrated the importance of improving wheat maintenance breeding and early generation seed production and of developing suitable screening methods for quality to secure food supply in developing countries such as Tajikistan.

Keywords: Bread, Food security, Glutenin subunits, Grain protein, Plant breeding, Tajikistan, *Triticum aestivum* L

Background

Food security is one of the main challenges for governments and world leaders and for human populations, not least in developing countries. Food security was defined in 1996 by the World Food Summit as "when all people at all times have access to sufficient, safe, nutritious food to maintain healthy and active life" [1]. For this study, Tajikistan was selected as a case country, due to the fact that more than 70 % of people's income goes to obtaining food and energy and the country's hunger index is considered to indicate a high risk level [2].

Wheat, together with rice and maize, is one of the major staple crops in the world, primarily as a source of protein for human consumption [3, 4]. The highest wheat use and consumption occur in Central and West Asia and North Africa (CWANA region) [5]. Tajikistan has the highest wheat consumption per capita in the world. However, wheat production in Tajikistan, is not high enough to meet the needs of local consumers [6]. Furthermore, most of the wheat consumed is in the form of bread, but the quality of local wheat is often too low for bread production [7]. Improved quality of locally produced grain could have a positive economic impact for farming households in particular.

Since 1991, increasing the amount of locally produced wheat has been a priority for Tajikistan. Therefore, the main strategy of the Tajik wheat breeding programme has been to secure sufficient quantity and quality of wheat for people living in the country [8]. Understanding the pathways to success and major drawbacks in breeding programmes for food security in developing countries would help to improve the efficiency of wheat breeding in such countries. This study focused especially

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on wheat quality for bread production using Tajikistan as a specific case.

The quality of bread wheat is often determined in plant breeding programmes by the composition of the wheat storage proteins, i.e. high-molecular-weight glutenin subunits (HMW-GS) [9]. These proteins are known to be correlated with bread-making quality, and analysis of their compositions is cheap, easy to perform and requires only a limited amount of sample, making them especially valuable as markers in breeding programmes [10]. Gluten strength and elasticity depend to a large extent on the composition of the HMW-GS [11] and on polymerisation of the gluten proteins [12]. Each HMW-GS is encoded by a specific gene, and these genes have been found to be located on group 1 of wheat chromosomes, within loci designated *Glu-A1*, *Glu-B1* and *Glu-D1* [10].

In this study, we investigated the HMW-GS composition of Tajik wheat varieties and breeding lines in order to evaluate options for breeding to improve the bread-making quality of wheat grown in Tajikistan. In addition, the opportunities and difficulties relating to food security improvement using plant breeding in a developing country such as Tajikistan were evaluated and discussed.

Methods

Plant material

Grain samples of 22 bread wheat (*Triticum aestivum* L.) varieties/lines were obtained from the Tajik National Wheat Breeding Programme (Table 1). Three of the varieties were control varieties used in breeding nurseries. One of these, Navruz, was bred by the Tajik Farming Institute and officially released in 1982. This variety is commonly used as a control in official variety testing trials. The second control variety was Alex, also bred by the Tajik Farming Institute, although selected from CIMMYT materials, and officially released in Tajikistan in 2007. The third control variety was Jagger, a widely grown variety in the country from 2000 to 2007, although not officially released. Jagger was bred by Kansas State University and was imported to Tajikistan in the late 1990s. The other 19 breeding lines included in this study were all originally obtained from International Agricultural Research Centres (IARCs). The samples were collected from two different locations where breeding lines were evaluated in 2009: 1) central-west Tajikistan, at the Tajik Farming Institute station in Sharora, Hisor district (38° 29′ N; 68° 38′ E, 739 m asl) and 2) north-east Tajikistan, at the private breeding farm Chilgazi in Isfara district (40° 09′ N; 70° 43′ E, 822 m asl). The breeding lines investigated were all from the Tajik Multilocation Yield Trials nursery, where the last step of selection is carried out and the selected lines are submitted for official variety testing.

Table 1 Description of the 22 Tajik wheat varieties/lines included in this study and their origin and source

Sample	Variety/line	Origin	Source/breeder
1	Navruz	TJK	Tajik Farming Institute
2	Alex	TJK/CIMMYT	Tajik Farming Institute
3	Jagger	USA	Kansas State University
4	TNMU/MUNTA	–	–
5	PRINIA/STAR	–	–
6	SHARK/F4105W2.1	–	–
7	VORONA/KAUZ//1D13.1/MLT	–	–
8	TAM200/KAUZ	IWWIP	10 FAWWON
9	1D13.1/MLT//TUI	–	–
10	ARILW PRONGHORN	–	–
11	ESKINA-8	–	–
12	YN/3NPM/VOS83	–	–
13	PASTOR/3/VORONA/CN079	–	–
14	SKAUZ BV 92	CIMMYT	25 ESWYT
15	VORONA SN079	CIMMYT	25 ESWYT
16	SOROCA	CIMMYT	25 ESWYT
17	OTUS TOBA 97	CIMMYT	25 ESWYT
18	KAUZ2/CHEW//BCN/3MILAN	CIMMYT	25 ESWYT
19	CHEN/AEGILOPS SQUAROSA/TAUS/RCN//3/RAV	CIMMYT	25 ESWYT
20	CBRD/KAUZ	CIMMYT	25 ESWYT
21	HUAYUN INIA	CIMMYT	25 ESWYT
22	CMN82A.1294/2*KAUZ//	CIMMYT	12 HRWYT

TJK Tajikistan, *USA* United States of America, *IWWIP* International Winter Wheat Improvement Programme (Turkey), *CIMMYT* International Centre for Maize and Wheat Improvement (Mexico), *FAWWON* Facultative and Winter Wheat Observation Nursery, *ESWYT* Elite Spring Wheat Yield Trial, *HRWYT* High Rainfall Wheat Yield Trial

Samples were obtained from one trial at location 1 and three replicate trials at location 2.

SDS-PAGE

The storage proteins of the grain were fractioned by sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) according to Payne et al. [13], and gels were stained according to Johansson et al. [14]. Samples of single grains of all 22 varieties/lines were run on SDS-PAGE, using 11 different seeds of each variety/line from each of the four locations/replicate field trials, in order to detect variation in the genetic composition of the material ($P > 0.999$) [9]. Thus, a total of 44 grains of each genotype were analysed. The single grains were crushed, and proteins were extracted in the presence of DTT [14]. The gels were stained with Coomassie Brilliant Blue solution [14]. After destaining in distilled water, the gels were scanned with an Epson Perfection V200 Photo Scanner (Epson Co., Japan)

for further reading and evaluation. Identification of band patterns was carried out following the standardised nomenclature proposed by Payne and Lawrence [15] and by comparison with standard and reference samples.

Reference samples used for SDS-PAGE

The Swedish variety Dragon with known HMW-GS (*Glu-A1:*2*, *Glu-B1:*7+9 and *Glu-D1:*2+12) was used as a standard sample on the gels [9]. When difficulties arose with the identification of some specific bands in some sub-samples, the sub-samples were re-run with an additional five reference samples (RS) with corresponding specific bands: RS1: *Glu-A1*:0, *Glu-B1*:17+18, *Glu-D1*:2+12; RS2: 1, 14+15, 2+12; RS3: 21*+21*y, 7+9, 5+10; RS4: 21*+21*y, 14+15, 5+10 and RS5: 21*+21*y, 14+15, 2+12 [16].

Payne quality score

The Payne quality score system [17] was applied to evaluate the quality of the Tajik wheat varieties and breeding lines. This scoring system was developed in order to facilitate quality determination of wheat based directly on its HMW-GS composition (Table 5). In the system, the protein subunit bands (designated according to Payne and Lawrence [15]) obtained on the electrophoretic gels are allocated a specific value (from 1 to 4) based on their contribution to bread-making quality evaluated in a number of studies [17]. Thus, a variety or breeding line can obtain a Payne quality score ranging from 3 to 12. Each genotype has three sets of genes on three different chromosomes with alleles encoding HMW-GS.

Statistical analyses

Basic statistical calculations of means and frequencies were carried out using Microsoft Excel. The statistical package Minitab v. 16 [18] was used for the clustering analyses applying Manhattan Distance to compare similarity of the varieties/lines based on HMW-GS composition. Analysis of molecular variance (AMOVA) was applied using the Arlequin software [19] in order to calculate the extent of variation within and between the varieties/lines analysed as regards composition of HMW-GS.

Results

HMW-GS composition

Most of the varieties/lines analysed showed either HMW-GS 1 or 2* encoded by *Glu-A1*, and several of the varieties/lines also showed presence of both these subunits. Only one line, SKAUZ BV 92, was found to have the null allele, as well as both the 1 and 2* alleles (Table 2). On comparing the frequencies of various alleles in the entire material, HMW-GS 2* was found to be the most frequent and was present in 65.4 % of the grains analysed, while HMW-GS 1 was found in 34.5 % of the grains analysed (Table 3). Among the HMW-GS encoded by *Glu-B1*, HMW-GS 7+9 was found in all except one of the varieties/lines analysed, while HMW-GS 7+8 was found in 12 of the varieties/lines analysed (Table 2), and these two alleles were present in 62.6 and 22.5 %, respectively, of the seeds analysed (Table 3). Some varieties/lines with HMW-GS 13+16 and 17+18 encoded by *Glu-B1* were also found in the Tajik wheat material (Table 2), although at lower frequencies (Table 3). HMW-GS 5+10 was the most commonly found subunit (17 varieties/lines; Table 2) encoded by *Glu-D1* and HMW-GS 2+12 (15 varieties/lines) was the next most common. These alleles were present in 74.3 and 16.6 %, respectively, of the seeds analysed (Table 3).

Variation in protein composition between and within varieties and lines

In total, 12 different HMW-GS combinations were identified in the Tajik wheat materials: three in *Glu-A1*, five in *Glu-B1* and four in *Glu-D1* (Table 3). In general, a high degree of heterogeneity was observed within the varieties/lines investigated. Only one breeding line (ESKINA-8) was found to be totally homogeneous for HMW-GS encoded on all three loci of the three different chromosomes (Table 2). In total, seven varieties/lines were found to be homogeneous at *Glu-A1*, two varieties/lines were homogeneous at *Glu-B1* and six varieties/lines were homogeneous at *Glu-D1* (Table 4). The majority of the 22 varieties/lines showed two alleles from each of the loci, i.e. 63.6, 59.2 and 50.0 % of the varieties/lines showed two alleles encoded on *Glu-A1, Glu-B1* and *Glu-D1*, respectively. Despite this large variation in HMW-GS composition within the varieties/lines, AMOVA analyses showed higher between (61.71–77.60 %) than within (21.10–27.58 %) variety/line variation in protein composition for all three loci when the variation in HMW-GS composition was compared locus by locus (Table 5). However, when the genetic variation at all three loci was compared simultaneously, higher within (87.34 %) than between (13.32 %) variety/line variation was observed (Table 5).

Variation in protein composition between locations/replicate field trials

In general, most of the cultivars/lines showed variations in protein composition between the different locations/replicate field trials. Only seven of the 22 varieties/lines were homogeneous for protein composition encoded by *Glu-A1*, and these lines all contained 2* (results not shown). Two of the 22 lines were homogeneous, showing 7+9 over the four replicate trials, for protein subunits encoded by *Glu-B1*, and five lines (one with 2+12, one with 4+12 and three with 5+10) were homogeneous for subunits encoded by *Glu-D1* (results not shown).

Table 2 HMW-GS composition from the three encoding loci and Payne scores and clustering for the 22 Tajik wheat varieties/lines analysed

Sample	Variety/line	*Glu-A1*	*Glu-B1*	*Glu-D1*	Payne score			Cluster
					Lowest	Highest	Average	
1	Navruz	2*	7+9/20	2+12/5+10	6	9	8.86	II
2	Alex	1/2*	7+9/17+18	2+12/5+10	7	10	9.59	III
3	Jagger	1/2*	7+9/13+16	2+12/5+10	7	10	8.98	I
4	TNMU/MUNTA	1/2*	7+8/7+9/17+18	2+12/4+12/5+10	6	10	9.50	III
5	PRINIA/STAR	1/2*	7+8/7+9	2+12/5+10	7	10	8.93	II
6	SHARK/F4105W2.1	2*	7+8/7+9	2+12/5+10	7	10	9.77	III
7	VORONA/KAUZ//1D13.1/MLT	1/2*	7+8/7+9	2+12/4+12/5+10	6	10	9.59	III
8	TAM200/KAUZ	2*	7+8/7+9/17+18	2+12	7	8	7.98	IV
9	1D13.1/MLT//TUI	1/2*	7+8/7+9	2+12/5+10	7	10	8.91	I
10	ARILW PRONGHORN	1/2*	7+9	5+10	9	9	9.00	I
11	ESKINA-8	2*	7+9	4+12	6	6	6.00	IV
12	YN/3NPM/VOS83	2*	7+8/7+9	5+10	9	10	9.95	III
13	PASTOR/3/VORONA/CN079	1/2*	7+9/7+8	2+12/4+12/5+10	6	10	8.86	I
14	SKAUZ BV 92	0/1/2*	7+9/13+16	2+12/5+10	5	10	8.93	II
15	VORONA SN079	1/2*	7+8/7+9/13+16/17+18	2+12/2+10/5+10	8	10	9.39	III
16	SOROCA	2*	7+8/13+16	2+12/5+10	8	10	8.18	IV
17	OTUS TOBA 97	1/2*	7+8/7+9	2+12/5+10	7	10	7.11	IV
18	KAUZ2/CHEW//BCN/3MILAN	1/2*	7+8/7+9/13+16	2+12/5+10	7	10	8.86	I
19	CHEN/AEGILOPS SQUAROSA/TAUS/RCN//3/RAV	1/2*	7+9/13+16	2+10/2 +12/5+10	7	10	8.07	IV
20	CBRD/KAUZ	1/2*	7+8/7+9/17+18	5+10	9	10	9.23	II
21	HUAVUN INIA	2*	7+8/7+9/13+16/17+18	2+12/5+10	7	10	9.02	II
22	CMN82A.1294/2*KAUZ//	1/2*	7+8/7+9/17+18	5+10	9	10	9.86	III

Table 3 Frequency of different HMW-GS in the Tajik wheat varieties/lines analysed

Locus	Allele	HMW-GS	Frequency (%)
Glu-A1	a	1	34.5
	b	2*	65.4
	c	0	0.1
Glu-B1	b	7+8	22.5
	c	7+9	62.6
	f	13+16	5.6
	i	17+18	9.1
	e	20	0.2
Glu-D1	a	2+12	16.6
	c	4+12	5.0
	d	5+10	74.3
	e	2+10	4.1

HMW-GS high-molecular-weight glutenin subunits

Thus, these resulted in only one line, Eskina-8, being homogeneous for all protein subunits evaluated over all four replicate trials at the two locations (Table 2). However, AMOVA analyses showed that protein composition was more stable over locations/replicate trials than between and within varieties/lines (Table 5). The frequencies of protein subunits between the different locations/replicate trials were in general found to vary, although the relative variation was higher for rare alleles than for common alleles (Table 6). However, the variation in protein composition between the different locations/replicate trials did not result in large variations in Payne score for the wheat materials in the different replicate trials (Table 6).

Payne quality score

Payne score was calculated for each of the 22 varieties/breeding lines based on their relative frequencies of protein subunits, and these calculations resulted in relatively high Payne scores for most of the materials analysed. A total of 10 varieties/lines had a Payne score of 9 or above and nine varieties/lines had a Payne score of 8 or above. The lowest Payne score was obtained for the homogeneous line

Table 4 Frequency of varieties/lines containing different numbers of alleles, presented for each locus encoded on different chromosomes

Amount of alleles found	*Glu-A1*		*Glu-B1*		*Glu-D1*	
	Number of varieties/lines	Frequency (%)	Number of varieties/lines	Frequency (%)	Number of varieties/lines	Frequency (%)
1	7	31.9	2	9.1	6	27.3
2	14	63.6	13	59.1	11	50.0
3	1	4.5	5	22.7	5	22.7
4			2	9.1		
Sum	22	100	22	100	22	100

Eskina-8 (Table 2). Based on the distribution of HMW-GS, the similarity between the varieties/lines was calculated. Clustering applying the Manhattan Distance test resulted in the material being separated into four groups (Fig. 1). These groups were clearly correlated to Payne score values, with varieties/line with the highest scores clustering into group III and varieties/lines with the lowest scores clustering into group IV (Table 2).

Discussion

The results obtained in this study clearly revealed both opportunities and difficulties for plant breeding in a developing country such as Tajikistan if it is to secure food of sufficient quantity and quality for its population. Furthermore, the study confirmed that the fast, simple and reliable SDS-PAGE method used for determination of protein composition can be valuable in developing plant breeding for food security in Tajikistan. Wheat bread is the main staple food and contributes a significant amount of daily calorie intake for the Tajik population [5]. Thus, both yield and the bread-making quality of wheat are important for the food security of the Tajik people. The objective of plant breeding programmes in Tajikistan is to develop high-yielding bread wheat varieties with good bread-making quality in order to assure food security for the country [8]. In the present study, we used Tajikistan as a case of a developing country and we used the bread-making quality of bread wheat, determined and selected for in many breeding programmes as protein composition as a measure of a breeding character to secure food.

Table 5 Analysis of molecular variance (AMOVA) as percentage of variation between and within the Tajik wheat varieties and lines analysed and between replicates for the different loci encoding HMW-GS

Source of variation	*df*	Percentage of variation			
		Glu-A1	*Glu-B1*	*Glu-D1*	Total[a]
Between varieties/lines	21	66.54	66.71	77.6	13.32
Between replicates	66	10.86	10.71	1.30	0.65
Within varieties/lines	880	22.60	27.58	21.10	87.34

[a]*df* for total is 21, 66 and 2816, respectively

The results revealed quite a large variation in protein composition in the wheat varieties/lines evaluated. The presence of genetic variation between cultivars and lines is always viewed as positive in a plant breeding perspective, since variation is a necessity for improvement. Furthermore, desirable subunits correlated with good quality and high gluten strength, such as 2* in *Glu-A1*, 7+8 in *Glu-B1* and 5+10 in *Glu-D1*, were abundant in the Tajik materials. The high Payne quality scores that were generally obtained for the Tajik wheat material were related to the presence of these HMW-GS. In all, 17 varieties/lines from among a total of 22 evaluated contained HMW-GS 5+10 or mixtures of 5+10 and 2+12. The HMW-GS 5+10 is known to be the main contributor of gluten strength and good bread-making quality. The high content of 5+10 in the Tajik wheat might be the result of breeding work in the former USSR based on the variety Bezostaya 1, which contains HMW-GS 2*, 7+9 and 5+10, as this variety was probably also used in breeding of some of the current Tajik varieties/lines [20]. According to Yesimbekova and Bulatova [21], 90 % of Central Asian winter wheat varieties have 7+8 and 7+9 in their relevant loci in *Glu-B1*. Similarly, in this study, we found that these alleles were prevalent and overall comprised 85 % of alleles in *Glu-B1*.

Wheat growing and breeding were a low priority in Tajikistan and the other Central Asian countries during the Soviet era due to the profitability of growing cotton in this region. The need for better and more modern food crop varieties arose after the 1990s, when the countries achieved independence [22]. Therefore, national wheat breeding programmes were developed, international collaborations were established and in the late 1990s, the diversity of wheat varieties was enriched by exchange of breeding and genetic materials. This definitely brought not only many new opportunities but also constraints to breeders and growers [22]. Wheat grain currently produced in Tajikistan is considered as being of lower quality, and some farmers prefer to use "improver" flour imported from Kazakhstan or Russia [23]. However, not all farmers can afford buying this flour. Early selections in breeding of high-quality candidate varieties/lines can have a significant impact in improving

Table 6 Frequency of different alleles encoded on three loci on different chromosomes in Tajik wheat material obtained from two locations (L) and three replicate (rep) field trials at one of these locations, and Payne scores of the wheat material from each location

Location/rep	*Glu-A1*			*Glu-B1*					*Glu-D1*				Payne score
	0	1	2*	7+8	7+9	13+16	17+18	20	2+12	4+12	5+10	2+10	
L1rep1	0	34.3	65.7	23.3	63.2	7.4	6.2	0	17.8	4.6	74.8	2.9	8.85
L2rep1	0	30.6	69.4	24.8	58.7	6.2	10.3	0	16.9	5.0	79.0	4.1	8.88
L2rep2	0.4	39.3	60.3	23.1	64.0	3.7	8.3	0.9	14.9	5.8	74.8	4.6	8.85
L2rep3	0	33.9	66.1	19.0	64.5	5.0	11.6	0	16.9	4.5	73.6	5.0	8.84

locally produced grain and thereby contribute to improving food security. According to results from the present study, screening of lines as related to HMW-GS composition will definitely help in improving selection of quality lines and in the long-term perspective of food security for the Tajik people.

The large variation in protein composition observed in the present study can also be seen as problematic and a drawback for the breeding programme in Tajikistan, since a large part of the variation is within, and not between, the varieties/lines. Furthermore, heterogeneity was also found for some of the same varieties/lines grown at different locations. Despite the fact that the seeds planted were collected from breeding plots, the breeding materials showed high heterogeneity with a mixture of variants. This can be explained by poor maintenance of breeding plots, which is a common practical problem in developing countries. The original samples were most likely obtained pure from IARCs, and most of them might have been analysed for protein composition, as commonly carried out at CGIAR centres. However, during the selection years, the levelling of off-types increased, probably due to mistakes during the selection process, resulting in genetic differentiation of the breeding lines at different locations. However, one part of the explanation of the heterogeneity might also be that pure HMW-GS compositions were not evaluated and bred for in the breeding programmes to obtain new lines/varieties. Previous studies have identified several "biotypes" being present especially of various gliadin alleles in pure varieties from, e.g. Australia and elsewhere [24].

Jagger is an American variety bred at Kansas State University, and the basic seed material of Jagger was brought to Tajikistan, during the late 1990s in the form of humanitarian aid. Due to its early ripening and high yield capacity, this variety was widely distributed throughout the country shortly after its introduction [25]. It was also the leading variety in wheat cropping areas of Kansas State for several years [26]. According to Pike and MacRitchie [27], who conducted tests on the protein composition of some wheat varieties in the USA, Jagger contains subunit 1 in *Glu-A1*, 17+18 in *Glu-B1* and 5+10 in *Glu-D1*. However, the seed samples of Jagger analysed in the present study showed 1/2*, 7+9/13+16 and

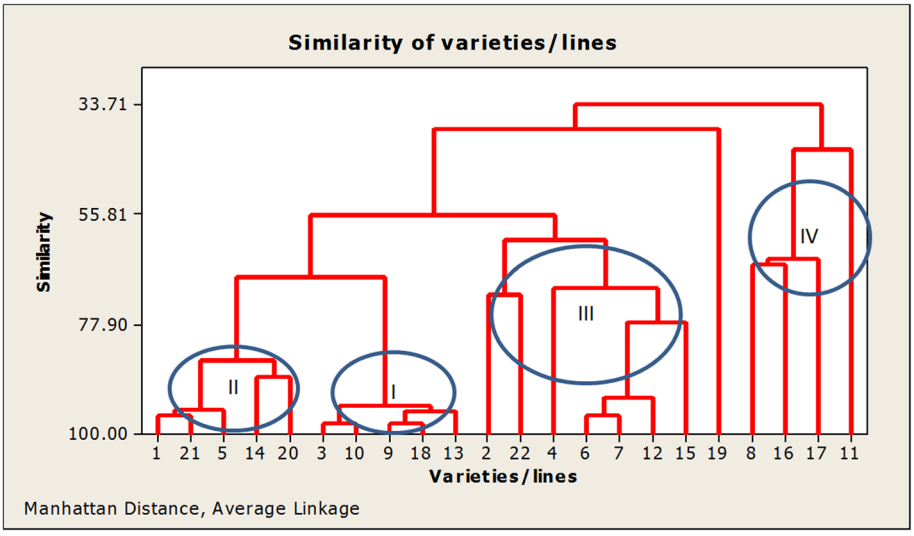

Fig. 1 Similarity of varieties/lines estimated with cluster analysis based on the Manhattan Distance test. Numbers and names of the varieties/lines are presented in Table 1

5+10/2+12, respectively. Maintaining genetic purity in the early generation of plant breeding is extremely important for bringing the right planting materials to growers. Thus, the urgent need for improvements in early generation of seed production, as well as in maintenance breeding of new and best varieties, are important issues to consider. The findings of the present study showed that purity and maintenance of protein composition in the wheat material evaluated are more or less absent. There is also a high risk of the lines containing mixtures of other characters than those relating to bread-making quality. On the other hand, for some other characters, e.g. resistance to diseases and pests, variety mixtures have been shown to be more beneficial than pure varieties [28]. Variety mixtures containing different genes for resistance to diseases and pests might be of particular importance in developing countries, e.g. Tajikistan, where pesticides are used to only a limited extent by small-scale, poor farmers. The main problem within a breeding programme in a developing country such as Tajikistan, is thus perhaps not the existence of mixtures but the fact that pure lines were expected and did not exist.

Studies examining protein composition in wheat in other former Soviet Union States have reported high purity [29]. If heterogeneous wheat materials such as those analysed in the present study are to be used in breeding programmes in developing countries or elsewhere, it is highly important to choose an evaluation method for quality of the material to capture the variation. Thus, a certain number of grains need to be evaluated, as was done in the present study. With the method applied, including separate analyses of 11 seeds of each variety/line, nearly all variation was captured ($P > 0.999$). The method also allowed selection of most interesting grains through the analyses of half of the grain, making it possible to plant the other half of the grain with the intact embryo. Another method to screen suitable varieties/lines for use in breeding or selection for variety testing is to apply size exclusion high-performance liquid chromatography (SE-HPLC) to evaluate the amount and size distribution of polymeric proteins [30, 31]. The SE-HPLC method has also been found to be fast and reliable in a number of studies, capturing both genetic and environmental variation in protein composition [32]. However, SE-HPLC analyses demand more advanced equipment and skills than SDS-PAGE, which may limit their common application in Tajik wheat breeding programmes. International collaboration in this regard may be an option.

As related to food security, this study clearly shows an option for the Tajik wheat breeding programme to reach the objective to improve the quality of locally cultivated wheat for bread production. However, to reach the goal, active efforts are important in determining most suitable protein composition for the Tajik wheat and to screen and select suitable lines/varieties based on protein composition.

Conclusions

The present study highlighted both opportunities and difficulties in wheat breeding for food security in a developing country such as Tajikistan. Large genetic variation was found in the HMW-GS composition, which determines bread-making quality in wheat, a factor of the utmost importance for achieving food security in Tajikistan. Large variation among breeding materials is a prerequisite to perform breeding. However, larger genetic variation was found within the breeding lines/varieties than between them. This high within-variety/line variation needs to be taken into consideration in future breeding work. Moreover, methods to evaluate quality need to be carefully chosen, and consequently, lines with high purity have to be developed.

Abbreviations

AMOVA: Analyses of molecular variance; CGIAR: Consultative Group on International Agricultural Research; CIMMYT: International Maize and Wheat Improvement Centre; HMW-GS: High-molecular-weight glutenin subunits; IARCs: International Agricultural Research Centres; SDS-PAGE: Sodium dodecyl sulphate polyacrylamide gel electrophoresis.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

All authors planned jointly the study, the hypothesis and the objectives. BH and MM collected the plant materials and performed the laboratory analyses. HM was responsible for the Tajik part of the experiments and managed the field experiments in Tajikistan. EJ provided overall coordination for the project and obtained reference samples from Italy. BH, EJ and LG evaluated the results. BH drafted the manuscript. All authors contributed to manuscript improvement and read and approved the final manuscript.

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