Genealogical Analysis in the Czech Spring Wheat Collection and its Use for the Creation of Core Collection

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Abstract: A spring wheat collection of the Czech gene bank included altogether 3270 original accessions in 2005; among them 2123 accessions with pedigree were analyzed using the construction of genetic profiles and subsequent calculation of Renkonen similarity indexes. Genetic diversity was estimated by Shannon diversity index. Subsequently we calculated cluster analysis using coefficients of parentage and in addition, we selected representatives of particular clusters for a core collection. Accessions of the whole analysed set of spring wheat (2123) were progenies of 929 original ancestors and diversity index within the set was $H = 4.17$. In the selected core set we can trace 718 ancestors and the diversity index is $H' = 4.82$. The selected core set is composed of 645 accessions (i.e. 30.4% of the whole set) and it represents 77.3% of genetic diversity in the whole set. The diversity between clusters did not decrease in the core set, which shows the representativeness of selected core accessions. Genealogical analysis provided useful information for the choice of cultivars to a core collection. However, pedigree analysis has to be complemented by other generally applicable approaches such as the use of molecular markers, morphological and agronomical characters. The analysis can also provide valuable information for breeders and researchers.

Keywords: *Triticum aestivum* L.; pedigree analysis; genetic diversity; core collection

The pedigree of a plant genetic resource, if available, can be considered as an important part of data kept in many gene banks. The pedigree is not only one of the identifiers of an accession but also it can provide useful information for breeders, as it confirms breeders' interest in this information. Although pedigree data are available in a part of the collection only, the analysis of pedigree can provide useful information also for collection management and strategy, inclusive of the creation of core collection.

In wheat, researchers apply the pedigree analysis to estimate genetic diversity among cultivars (Sud *et al*. 2005), to evaluate changes in genetic diversity of released cultivars in the course of time (Lang & Bedo 2004) or to classify cultivars for example as for adaptation to stress.

The knowledge of existing genetic diversity in large collections of crop genetic resources is a precondition for their better management and utilization; a core collection can provide an effective tool. The core collection is of limited size

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and its items are chosen to represent the full diversity in the collection. The core collection does not substitute the original one from which it was chosen. However, the existence of the core allows better management of the whole collection and ensures an effective access of users to requested resources. The approach to create a core is often based on analyses of geographical information, characterization and evaluation of data describing morphological and agronomical characters (Polignano *et al.* 1999; Upadhyaya 2003; Upadhyaya *et al.* 2003; Yu Li *et al.* 2004; Dwivedi *et al.* 2005; Reddy *et al.* 2005). An employment of DNA markers can provide reliable results (Varshney *et al.* 2005), particularly by the combination of data from DNA analyses with results of other analysed data and pedigree analyses (Sud *et al.* 2005; van Treuren *et al.* 2006). Opinions differ as for the relative size of the core and whole collection. Most researchers suggest that 10–30% of accessions chosen to the core may represent 70–90% of the genetic diversity of the total collection (van Hintum *et al.* 2000).

An essential precondition is to achieve the objective – expression of genetic diversity of the whole collection in the created core. To reach this aim, accessions can be divided into groups (clusters) in such a way that the variation between groups will increase maximally and the variation within groups will be minimized. Besides other data, we can also include pedigree information in this key step of the creation of core collections. Then, the most typical accessions adequately representing the diversity within a group (cluster) can be chosen for the core collection. The representativeness of such selection and similarity of the genetic diversities in the whole and core collections are to be verified (Rohlf 1998; Martynov *et al.* 2003). Such confirmation may be based on the characteristics used for the creation of core collection or on other parameters.

In this paper, a genealogical approach was used to create a core set of accessions with known pedigree within the whole spring wheat collection in the Czech gene bank and to estimate contributions of particular accessions to genetic diversity in the core set.

MATERIALS AND METHODS

A spring wheat (*Triticum aestivum* L.) collection of the Czech gene bank includes 3598 accessions, out of which 328 are probably duplicates, and in 1147 accessions pedigrees are absent or for some reasons they could not be used for the analysis. Therefore, we could include 2123 accessions in the set we considered as a whole collection. The pedigree analysis, inclusive of the construction of genetic profiles (the spectrum of original ancestors included in the full extended pedigree of the cultivar, Martynov *et al.* 2003) and calculation of the matrix of similarity indexes were carried out by means of Information and Analytical System of Genetic Resources GRIS3.5 (Martynov & Dobrotvorskaya 2000). The Renkonen similarity index was calculated according to the formula:

$$p_{ij} = \Sigma\min \{x_{ki}, x_{kj}\}$$

where:

x_{ki}, x_{kj} – contributions of the k^{th} ancestor in the i^{th} and j^{th} accession, respectively

Σmin – mean summarized minimal contributions of the k^{th} ancestor in two compared accessions (Rohlf 1998)

Further we used modified Shannon diversity index (Martynov *et al.* 2003) to characterize genetic diversity within a set of accessions of known pedigree:

$$H = -\sum_{i=1}^{A} \bar{R}_i \ln \bar{R}_i$$

where:

$\bar{R}_i = \Sigma R_{ij}/N$ – average coefficient of parentage of the i^{th} ancestor

R_{ij} – coefficient of parentage between the i^{th} ancestor and j^{th} cultivar

N – number of accessions in a set

A – number of landraces

ln – symbol of the natural logarithm

This index estimates genetic diversity based on a set of landraces providing genetic profiles. Further we calculated the cluster analysis based on the matrix of coefficients of parentage, using an unweighted pair-group method (algorithm UPGMA) and software package NTSYS 2.02c (Rohlf 1998). Coefficient of parentage (R_{ij} in the formula) is an indirect measure of genetic diversity among genotypes based on the probability that alleles at a certain locus are identical by descent (Dreisigacker *et al.* 2004); coefficients of parentage for all possible pairs of cotton cultivars were calculated by Bowman *et al.* (1997)

RESULTS AND DISCUSSION

In 2005 the spring bread wheat (*T. aestivum* L.) collection in the Czech gene bank included 3270 original accessions, among them 65.7% were bred cultivars, 28.6% breeders' lines and genetic stock and only 5.9% and 1.4% were represented by landraces and wild relatives, respectively. Applicable pedigree data were available for 2123 accessions, i.e. for 65% of the total number of original accessions or 75.5% of the part of the collection with pedigree data (bred cultivars, breeders' lines, genetic stock). Because the pedigree analysis can refer only to bred materials as mentioned above, about 75% of all these materials were analysed.

Contributions of original ancestors to genetic diversity within the gene pool of the Czech spring wheat collection

We were able to trace pedigrees of analysed accessions up to the original ancestors and then calculate the coefficients of parentage between each cultivar and its original ancestor; these coefficients correspond to the relative genetic contribution of an original ancestor to the pedigree of a cultivar.

For the whole set with known pedigree (2123 accessions), 929 original ancestors were identified, among them 530 landraces, 90 old varieties and 273 lines with unknown pedigree. The geographical origin of landraces and local old varieties covers 61 countries of five continents: Europe – 332, Asia – 154, America – 79, Africa – 43, Australia – 12 landraces. Original ancestors from Russia (54 landraces), Portugal (48 landraces), former Czechoslovakia (39 landraces) and Germany (34 landraces) were most frequently found in the analysed set. The following incidence of landraces and local old varieties in pedigrees of accessions was recorded:

Less than 1%	466
1–5%	72
6–20%	39
More than 20%	43

The majority of the landraces (466 or 75.8%) are present in pedigrees of a very small number of accessions, among them 319 (51.9%) enter only into the pedigree of a single accession.

Among original ancestors, lines of unknown pedigree (273 or 29.4%) account for a significant portion; it is the result of incomplete information on pedigree. The major part of such lines was found in the pedigree of a very small number of accessions, and therefore these lines usually have low incidence (less than 1%).

Pedigree analysis and identification of original ancestors for the creation of soybean core collection were applied by Gai and Zhao (2001). They analyzed the pedigree of 651 cultivars and selected core accessions among 384 identified ancestors.

Cluster analyses

We were able to identify and characterize 210 clusters which showed diversity within the cluster on the level corresponding to Renkonen similarity index $p_{ij} \geq 0.5$; among them we found 11 large clusters (20–437 cultivars in a cluster), 72 average (5–19 cultivars) and 127 small (2 to 4 cultivars) ones (Table 1).

The detected clusters explain 83.5% of genetic diversity in the part of the spring wheat collection (2123 accessions) with known pedigree. Out of 210 clusters, which include totally 1773 accessions, 295 accessions were chosen for the core set, i.e.16.6%. These accessions and other 350 accessions with known pedigree that did not fall into any cluster increased the size of the core set up to 645 (i.e.30.4% of the whole set with known pedigree).

In Table 2, there are characteristics of 11 large clusters and dominant original ancestors. Such ancestors are referred to as dominant in which the highest mean coefficients of parentage (*COP*) between ancestor and derived cultivars were found and which were present in pedigrees of all cultivars within the cluster. These ancestors determine the structure of clusters within the whole set to a significant extent. Nevertheless, as reported by van Treuren *et al.* (2006), the contribution of the parent to the offspring can be skewed, possibly due to disproportionate selection or involvement of backcrossing during the breeding process. Also the results obtained by Sud *et al.* (2005) call for a caution in the interpretation of pedigree analyses. They document a low correlation of *COP* values based on pedigree analysis and genetic similarity values based on microsatellite markers (r = 0.285). With respect to these limitations of pedigree analyses, more cluster representatives included in the core collection can increase the reliability of this approach. Therefore, we used the ratio 1:10 when selecting cluster representatives for the core set.

Table 1. The results of cluster analysis based on Renkonen similarity indexes and done in the set of spring wheat accessions with known pedigree of the Czech gene bank collection

Cluster parameters	Whole set	Core set
Number of accessions	2123	645
Number of clusters	210	–
Number of accessions in all clusters	1773	295
Number of accessions outside clusters	350	350
Number of original ancestors	929	718
Average weighted number of ancestors per cluster	25	18
Average weighted Shannon diversity index in a cluster	2.25	2.15
Shannon diversity index	4.17	4.82
Average weighted correlation coefficient between ancestor contributions in whole set and core set	0.98	

Cluster 15, the largest one, contains short-straw cultivars carrying genes reducing stem height, *Rht1* and *Rht2*. The donor of rust resistance Kenya C-9906 (Kenya 324) occurs in the pedigree of cultivars belonging to this cluster. This line got into the pedigrees via Sonora 64 cultivar and its progeny and via Kentana 48 cultivar. All cultivars in this cluster were bred using CIMMYT breeding material. In this cluster the cultivars from Mexico (63%), countries of South America (13%) and Australia (7%) are prevailing. The other cultivars of cluster 15 have been developed in North America, countries of Asia, Africa and South Europe.

All cultivars of the second largest cluster, cluster 62 (82 accessions), were the offspring of the Canadian cultivar Marquis. In the pedigree of cultivars in this cluster, the input of Marquis's parents (landraces Hard Red Calcutta and Ostka Galycijska) was maximal. Hard Red Calcutta and Ostka Galycijska dominate in cluster 17 but their input into this cluster was only of a half size. The highest number of cultivars in this cluster comes from North America (Canada and USA).

In cluster 27, the fourth largest with 57 accessions, there are mainly cultivars from North and South Americas while the Japanese landrace Akakomugi (donor of *Rht8* gene) has a high average input via the Italian cultivar Mentana and its progeny.

Cluster 13 (52 accessions) is characterised by a high input of the landrace Crimean; it includes the progeny of crosses of II-8156 from CIMMYT. In this cluster cultivars from Mexico (52%), Australia (17%), Asia and Africa (25%) prevail that carry the reduced stem height genes *Rht1* and *Rht2*.

Cultivars from Italy prevail (67%) in cluster 90 jointly with cultivars from other countries which were bred on the basis of Italian cultivars Ardito, Balilla, Damiano, Mentana, Villa Glori – the offspring of Japanese landrace Akakomugi. The cultivars of this cluster are very closely related to Akakomugi landrace.

All other clusters are smaller than 40 accessions. Cluster 4 contains Russian cultivars bred on the basis of cultivars from Saratov Breeding Station (now South-East Agricultural Research Institute). For this group of cultivars, a high input of Poltavka (landrace from the Saratov region) is characteristic. The cultivars with high drought tolerance and good rheological and bread making quality prevail in cluster 4.

Two thirds of accessions in cluster 45 originate from Australia and the rest of the cultivars has been bred from Australian material.

Brazilian cultivars dominate in cluster 59. The pedigree of these cultivars contains Brazilian landraces Polyssu and Turco – Colonias, Fronteira, Trintecinco and others.

Cluster 104 covers cultivars from Germany (63%) and cultivars from other European countries that were derived from the old German cultivar Heines Kolben and its progeny. Heines Kolben was selected in the 19th century from the French landrace Saumur de Mars (Breustedts Teutonen, Heines Koga I, Koga II, Peko and others).

Table 2. Characteristics* of large clusters set up within the part of spring wheat collection with known pedigree (2123 accessions) of the Czech gene bank

Cluster					Selected core set			
No.	Dominant ancestors**	*n*	*na*	*H*	*n'*	*na'*	*H'*	*r*
4	Poltavka (0.532)	33	58	1.38	3	41	1.58	0.99
13	Crimean (0.149), Goldendrop (0.069), Ostka Galicyjska (0.086)	52	81	2.74	5	48	2.56	0.98
15	Crimean (0.104), Kenya C-9906 (0.107)	437	231	3.02	44	128	2.97	1.00
17	Crimean (0.109), Hard Red Calcutta (0.145), Ostka Galicyjska (0.117)	63	100	2.80	6	64	2.60	0.99
27	Akakomugi (0.133), Polyssu (0.075), Rieti (0.066)	57	80	2.88	5	55	2.72	0.99
45	Crimean (0.102), Gaza (0.151), Goldendrop (0.097), Ostka Galicyjska (0.131)	22	65	2.41	2	40	2.16	0.92
59	Polyssu (0.279), Turco (0195)	22	66	2.05	2	43	1.93	0.97
62	Hard Red Calcutta (0.302), Ostka Galicyjska (0.232)	82	73	1.82	8	54	1.93	0.99
90	Akakomugi (0.283), Rieti (0.158), Mediterranean (0.081)	49	68	2.20	5	35	2.13	0.97
104	Saumur de Mars (0.221)	27	58	2.21	3	23	2.02	0.97
133	LV-Halland via Halland (0.109), Hard Red Calcutta (0.073), Mediterranean (0.100), Saumur de Mars (0.077)	23	46	1.92	3	28	1.73	0.96

*n – number of accessions, na – number of original ancestors in a cluster, H – Shannon diversity index, n'– number of selected accessions, na' and H' – number of original ancestors and Shannon diversity index in a selected group, respectively, r – correlation coefficient between mean ancestor contributions in cluster and selected group

**in brackets there are mean coefficients of parentage (*COP*) between ancestor and derived cultivars

Swedish cultivars dominate in cluster 133 (87%). All cultivars in this cluster have been bred with participation of the progeny of Swedish landrace Halland (Karn I, Karn II, Sveno) and old German cultivar Heines Kolben.

The genetic basis of most cultivars was formed by the following original ancestors: Ostka Galicyjska (POL), Mediterranean (Europe), Hard Red Calcutta, Etawah, Indian G, Pusa 107 (IND), Crimean (UKR), Zeeuwse (NLD), Rieti, Iumillo (*T. durum*), Carosella, Sicilian Squarehead (ITA), Akakomugi, Daruma (JPN), Red Straw, Goldendrop (GBR), Ladoga, Yaroslav Emmer (RUS), Polyssu, Turco (BRA), Redchaff (USA), Marroqui (MAR), Gaza, Red Egyptian (EGY), Kenya C-9906 (KEN). The clusters included in Table 2 differ from each other in the ratio of contributions of these ancestors and presence of other dominant ancestors. For example, in cluster 62 two original ancestors – Hard Red Calcutta (*COP* = 0.302) and Ostka Galicyjska (*COP* = 0.232) dominate. In cluster 17, Crimean (*COP* = 0.109) dominates jointly with these two ancestors with the contributions 0.145 and 0.117, respectively. In some clusters, only one original ancestor with the high average contribution is dominant. For example, in cluster 4 Poltavka (*COP* = 0.532) dominates and in cluster 104 Saumur de Mars (*COP* = 0.221) is dominant.

Diversity parameters of clusters

As mentioned above, when selecting representatives from large clusters we followed the principle of proportionality (1:10); small clusters (15 accessions or less) are represented only by one accession. A degree of representativeness of the selected core set towards the cluster was estimated by Shannon diversity index and coefficient of correlation between the mean contributions of original ancestors into the cluster and into the selected accession. In addition, the total numbers of ancestors in a cluster and in the selected core were considered (Martynov *et al.* 2003). The representativeness of selected core accession and its relation to the whole cluster was verified; the applied procedure is explained on the example

of cluster 35 containing 14 cultivars, all from the Czech Republic (Table 3).

The complete genetic profile of all 14 cultivars in cluster 35 includes 55 original ancestors. Shannon diversity index of this cluster (H = 2.56) corresponds to the accepted ratio of representatives (1:10), therefore cluster 35 can be represented by one accession. The cultivar Leguan was selected as such a representative because its genetic profile includes 44 coincident original ancestors of the whole cluster and Shannon diversity index (H' = 2.50) is close to that of the whole cluster. The

Table 3. The original ancestors of 14 cultivars of cluster 35 and one selected representative of the cluster – cultivar Leguan

Name of original ancestor	Contribution		Name of original ancestor	Contribution	
	cluster*	Leguan		cluster*	Leguan
Kenya C-9906	0.14900	0.14062	Gaza	0.00474	0.00391
Saumur de Mars	0.09443	0.07251	Polyssu	0.00429	0.00391
Crimean	0.06601	0.06231	Marchfelder	0.00363	0.01172
LV-Kremenchug via Artemovka	0.05022	0.07031	Mouton a Epi Rouge	0.00349	–
Ostka Galicyjska	0.04722	0.05163	Turco	0.00322	0.00293
Hard Red Calcutta	0.02932	0.03735	Yaroslav Emmer	0.00300	0.00274
Goldendrop	0.02916	0.02651	Red Straw	0.00276	0.00235
Marroqui	0.02877	0.02637	Krajova Postoloprty	0.00272	0.00879
Ladoga	0.02699	0.02832	Rieti	0.00263	0.00342
LV-Seignora via Blaue Dame	0.01774	0.02124	LV-UKR via Lutescens 17	0.00251	0.01172
LV-Seignora via Grune Dame	0.01774	0.02124	Kolben	0.00223	–
Mediterranean	0.01565	0.01263	Carosella	0.00193	0.00165
TR.TI	0.01447	0.01328	Banatka (UKR)	0.00188	0.00879
Kenya BF-4-3-B-10-V-1	0.01332	0.01172	Etawah	0.00184	0.00157
Red Egyptian	0.01332	0.01172	Egyptian Na 101	0.00112	–
LV-Odessa via Noe	0.01288	0.00366	Indian G	0.00110	0.00092
Iumillo	0.01049	0.00959	Pusa 107	0.00067	0.00055
Gehun	0.00989	0.00806	Zeeuwse	0.00066	0.00085
Onega	0.00989	0.00806	Barleta	0.00047	0.00220
Daruma	0.00914	0.00781	LV-URY via Klein Universal Ii	0.00047	0.00220
Klastersko Hradistska Jarka	0.00893	–	Sicilian Squarehead	0.00044	0.00037
Loosdorfer	0.00893	–	Mouton	0.00042	–
Weihenstephaner GKI-1716	0.00725	0.02344	Introduction From GBR	0.00040	–
DHE-516	0.00656	0.00195	Ble Seigle	0.00028	–
Akakomugi	0.00527	0.00684	LV-ENG via Prince Albert	0.00014	–
Redchaff	0.00514	0.00439	LV-Sahara via El Krelof	0.00013	–
Chinese 165	0.00492	0.00146	Squarehead Type from Norfolg	0.00006	–
LV-Skania via Kotte	0.00492	0.00146			

*Cluster 35 includes Czech cultivars Leguan, Linda, Rena, Sandra, Saxana, and breeders lines HE-331, ST-174, ST-44-74, ST-57, ST-58, ST-70, ST-777, UH-209, UH-23

coefficient of correlation between the inputs of original ancestors within the whole cluster and the cultivar Leguan is high (r = 0.97). Thus, the cultivar Leguan adequately represents cluster 35.

The number of original ancestors in all clusters of the collection (accessions with known pedigree) varied from 1 to 231, i.e. on average na = 25, and Shannon diversity index from 0 to 3.22 with average weighted value H = 2.25. The number of ancestors selected from clusters for the core set was a bit lower and ranged from 1 up to 128 with average na' = 18, and Shannon diversity index from 0 to 3.06 with average weighted value H' = 2.15; it corresponds to 95.4% of diversity in clusters. Despite of the decreased number of ancestors and diversity index in the selected core set, the average weighted coefficient of correlation between the ancestor contributions (computed by the use of Z-transformation) showed a high value (r = 0.98). Obviously the lost original ancestors had low incidence in pedigrees, and therefore the contributions of such ancestors were low or close to zero.

High correlations between Shannon diversity indexes for clusters and selected cluster representatives can be used as criteria for successful choice to the core set. In our study, the coefficient of correlation calculated for 210 clusters and principal cluster representatives equalled $r_{(H, H')}$ = 0.91. Such a close correlation proves indirectly a high similarity of genetic diversity in the whole set and selected core set.

The value of Shannon diversity index depends mainly on the number of original ancestors. This is confirmed by the high correlation (r = 0.70) between the number of original ancestors and Shannon diversity index in 210 clusters of the whole set. The coefficient of determination (d = r^2 = 0.49) shows that we could explain only about a half of variation in diversity index through variability in the number of ancestors. The remaining variation is caused by other factors, in particular by the mean incidence of original ancestors in pedigrees. Typically, if the number of ancestors decreases, diversity index either decreases or in some cases remains unchanged or even slightly increases (see Table 2). For example, a decrease in the number of ancestors from 58 to 41 in selected ancestors of cluster 4 increased the index of diversity from H = 1.38 in the cluster to H' = 1.58 in the selected part. In cluster 62, a decreased number of ancestors from 73 to 54 resulted in a slight increase (from H = 1.82 to H' = 1.93) of diversity index. This can be explained by the increased mean incidence of original ancestors in the pedigrees of selected cultivars.

Creation of core set

When selecting accessions for the core set, we have two categories: representatives of clusters and separate accessions that do not belong to any cluster. Therefore, total numbers of original ancestors, weighted mean values of Shannon diversity indexes in the original set and selected core set and number of accessions outside clusters are essential indicators for effective choice to the core set. Of course, pedigree analysis cannot refer to bred materials of unknown pedigree, landraces and wild relatives, respectively. However, these materials, especially landraces and wild relatives, are usually an essential source of genetic diversity in the collection and they cannot be omitted during the creation of the core collection. In general, pedigree analysis can be considered as one of the possible tools for the core development, when combined with other methods, preferably with DNA markers and/or morphological characters; at the same time, molecular markers can help to verify the pedigree (Varshney *et al*. 2005). We should also have in mind possible limits of pedigree analyses due to incorrect data, disproportionate selection or involvement of backcrossing during the breeding process. However, these limitations do not cast doubt on the applicability of pedigree analysis, especially in large collections with a high proportion of accessions with known pedigree.

The cluster analysis was aimed to maximize the between-cluster variation and to minimize the within-cluster one. The comparison of Shannon indexes calculated for the whole and core collections (H = 4.17 and H' = 4.82, respectively) shows that between-cluster diversity did not decrease in the core set. A slight increase in the value of Shannon index, as well as an increase in other diversity parameters, can be assigned to the smaller size of the core set (van Hintum *et al*. 2000).

In our study we found that the accessions of the whole analysed set of spring wheat (2123 accessions) were progenies of 929 original ancestors and diversity index within the set was H = 4.17. In the selected core set, 718 ancestors were traced and the diversity index equalled H' = 4.82. The selected core set consists of 645 accessions

(i.e. 0.4% of the whole set) and accounts for 77.3% of genetic diversity in the whole set. Results of our earlier study on pedigree analyses in winter wheat (Martynov *et al*. 2003) were similar. The studied core set of winter wheat comprised 25.5% of the whole collection and harboured 76% of its genetic diversity.

Genealogical analysis carried out in the Czech spring wheat collection proved to be one of the useful tools for the choice of cultivars into a core collection. This analysis can effectively complement other generally applicable approaches such as the use of isozymes (Balfourier *et al*. 1998), molecular markers (Roussel *et al*. 2004), morphological and agronomical characters and special software like MSTRAT, enabling to do a sampling procedure for different sets of traits (Gouesnard *et al*. 2001). The pedigree analysis can also provide valuable information for breeders and researchers, for example as concerns original ancestors, genetic differences between cultivars and pedigree structure (the pedigree of wheat cultivars is available on line http//genbank.vurv.cz/wheat/pedigree/).

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