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PROCEEDINGS

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Organization of Wheat Genetic Resources in Collections

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Abstract

Genetic resources have received due attention, with regards to their collection, characterization, maintenance, evaluation and utilization in consequence to grave warnings from the scientific community about genetic erosion of the total germplasm. Consequently, the number of genebanks has grown rapidly since early 1970s when there were fewer than ten, holding perhaps no more than a half million accessions. A total of more than 1300 collections holding approximately 6.1 million accessions are now recorded worldwide (FAO, 1996). Among all agricultural species wheat is the most conserved crop, which is logical since wheat is the most important crop in human being's diet. It is widely accepted that evaluation of genetic resources is an essential preliminary to utilization and further the more information that are available make collection more valuable. Today it is clearly confirmed that core collections are established and organized in order to increase effectiveness of evaluation and utilization of genetic resources.

In this paper we outlined our approach in organizing wheat germplasm, where the breeders evaluate and use the collections. Wheat germplasm was organized in three levels. World collection (whole collection) comprises 2,576 accessions. The collection was preliminarily evaluated for some important characters. The next level is genetic collection (core collection) with 850-900 entries. Genetic collection is grouped in subunits according to the traits considering important for breeding. The evaluation in the genetic collection is highly intensive and it includes more than 50 characters. The third level of wheat genetic resources is Crossing collection. This collection is strictly connected with breeding and comprises (250-300) potential parents intended for crossing.

Keywords: genetic resources, wheat, collection, evaluation

Genebanks and collections as safeguard of PGR

The threat of genetic erosion was first voiced by two scientists, Harlan and Martini in a technical article in the 1930s (FAO, 1996). In the late 1960s the world community began to express serious concern regarding its scale of genetic erosion and to show increasing recognition of the potential value of the genetic resources that were being lost. By the early 1970s this concern was changed to stimulating increased efforts by national, regional and international organizations to conserve genetic resources. In response to the international concern the International Board for Plant Genetic Resources (IBPGR presently IPGRI) genetic resources programs in several International Agriculture Research Centers (IARC) were established.

The number of genebanks in the world and the size of especially *ex situ* collections grew to a great extent during the period from early 1970 to late 1980's in response to increasing awareness of threats to plant genetic diversity. In early 1970's there were fewer than ten genebanks holding around 500,000 accessions. More than 1,300 collections are now recorded in the WIEWS (World Information and Early Warning System) database. According on this database and information provided in Country Reports, approximately 6,1 millions accessions are stored worldwide in *ex situ* germplasm collections including approximately half million accessions stored in field genebanks (FAO, 1996).

Collections vary in crop species covered, extent of the crop genepool covered, type of accession, and origin of material. The most current information from the WIEWS database indicate that 48% of all accessions in genebanks are cereals followed by food legumes with 16%, forages with 10%, vegetable crops with 8%, fruit with 4%, roots and tubers with 4%, fiber crops with 2%, oil crops with 2% and others with 6% (FAO, 1996).

Its has been early emphasized by Frankel (1970) that evaluation is an essential preliminary to utilization and further the more information that is available make the collection more valuable. Three main conceptual categories of *ex situ* collections: base, active and safety duplicate are recognized as serving different purposes (FAO/IPGRI, 1994).

In base collections emphasis is given to conservation and the genebank assumes responsibility for long-term conservation of the germplasm. Accessions in the base collection should therefore be held in optimal conditions for long term storage.

A safety duplicate collection should contain all accessions in the base collection held at distant site or series of sites and preserved for the long-term future.

In active collection emphasis is given to evaluation and utilization in breeding and/or research by genebank experts or by outside users. According to definition of FAO/IPGRI (1994) the additional categories include core and working collection and these related primarily to target evaluation and utilization of selected accessions. Today it is clearly confirmed by majority of Genetic Resources Community that core collection are established and organized in order to increase effectiveness of evaluation and utilization of genetic resources. It is originally described by Frankel (1984) - a core collection is a limited set of accessions of a crop species and its wild relatives which would represent, with a minimum of repetitiveness, the genetic diversity of a crop species and wild relatives. This subset of the whole collection would provide potential users with a large amount of the available genetic variation of the crop genepool in a workable number of accessions. It would therefore be useful to plant breeders seeking new characters which require screening techniques not possible with large collection.

Germplasm and evaluation

Few categorizations of germplasm resources have been suggested. Frankel (1977) emphasized that crop genetic resources can be grouped into four categories:

1. High yielding, varieties in current use and obsolete cultivars
2. Primitive varieties or landraces of traditional pre-scientific agriculture

3. Wild and weedy relatives

4. Specialized genetic and cytogenetic stock including induced mutations.

Plant genetic resource as given by the International Undertaking on Plant Genetic Resources in 1989, is the reproductive or vegetable propagating material of following categories of plants:

1. Wild and weedy species, near relatives of cultivated varieties

2. Primitive cultivars (landraces)

3. Obsolete cultivars

4. Cultivated varieties (cultivars) in current use

5. Special genetic stocks.

Wilkes (1993) has recently defined another classification of germplasms. According to the classification germplasms resources can be organized into six categories:

1. Cultivars in current use

2. Obsolete cultivars - often the elite cultivars of 20-or 50 years ago that can be found in the parentage of current cultivars

3. Primitive cultivars or landraces

4. Wild and weedy relatives of crop plants

5. Special genetic stock including induced mutations

6. Co-adapted genetic stocks in which two forms are existing:

a) two distinct crops

b) crop and symbiotic (such as crop and its unrelated weed or crop and nodule forming bacteria).

The **types of data** that have traditionally been recorded to evaluate, select and use PGR are:

- disease and pest resistance

- adaptation and abiotic stress reaction

- productivity and quality performances.

The groups of data mentioned above are traditionally used for describing PGR. These data basically name each accession, describe its history related to place of development or collection and describe its morphological and agronomic characteristics.

Descriptors play the key role in characterization and evaluation of PGR. A descriptor is generally defined as an identifiable and measurable trait of a plant accession. It includes a descriptor name, descriptor definition and possible list of descriptor states and codes. The selection of descriptors made during the establishment of databases would determine not only the size of the database but also usefulness of the database to the users. The use of descriptor lists that have been developed by an international group of crop-specific experts will assist in compatibility of data during exchange. IPGRI has been responsible for publishing over 60 crop-specific descriptors each of which follows a standard format for descriptor categories (Perry and Ayad 1995). Concerning these descriptors, their respective lists have to be unrestricted in the future. Descriptor lists published by IPGRI use the following definition for GR data management. (Le Blanc and Faberova, 1996).

Characterization descriptors: enable an easy and fast discrimination between phenotypes. Characterization information generally concerns strongly heritable characters, which are independent of the environment. In addition they may include a limited number of additional traits thought desirable by consensus of users of particular crop.

Evaluation descriptors: in contrast to previous one, descriptors in this category are related mainly to traits, which are susceptible to environment differences, but they are generally useful in crop improvement. They include yield, agronomic performance, stress susceptibility and biochemical and cytological traits; biochemical and / or molecular characterization also may be involved in these descriptors.

In case of wheat, for the EWDB (European Wheat Data Base) it was decided to use a joint category for characterization and evaluation. The minimal list of descriptors was established according to their low level of interaction with the environment or the importance of information for users;

The minimal list of description include evaluation of following traits:

- Growth habit (growth class in the country of collection)
- Principal attribute (the most useful traits of accession)
- Principal utilization (way of main utilization)
- Morphological descriptors (awnedness, pericarp colour, spike density)
- Cytological characteristics and identified genes (1B/1R translocation, Rht genes)
- Gel electrophoresis patterns (glutenins subunits, gliadines)
- Plant height
- Protein content
- 1000-kernel weight
- Yield level
- Lodging
- Cold susceptibility
- Biotic stress susceptibility (susceptibility to main disease in Europe)

Evaluating of wheat genetic resources in wheat collection in Novi Sad

The wheat collection of the Institute of Field and Vegetable Crops in Novi Sad (Yugoslavia) was established in 1939. Initially it consisted of 200-300 genotypes of domestic variety, landraces (populations) and several foreign varieties. The main purpose of the collection was to study the entries for major traits and to use them in breeding programs.

Starting from 1965, the collection was organized in three levels: World collection, Genetic collection and Crossing block (Denčić and Borojević 1991). These collections have remained until today.

World collection includes: current cultivars, obsolete cultivars, advanced lines and landraces. The collection is comprise of 1,838 genotypes from 43 countries of origin (Table.1) and they are grown annually.

The two types of characters are evaluated in the collection:

a) Quantitative characters whose expressions are dependent upon both genotype and environment such as

- Winterhardiness
- Earliness
- Intensity of lodging
- Disease resistance
- Insect resistance
- Plant height
- Drought tolerance

Table 1. Countries of origin of the wheat germplasm held in the world collection

Continent	Country and no. of accessions
Europe	Yugoslavia (684), Croatia (69), Bosnia and Herzegovina (287), Macedonia (5), Austria (53), Belgium (7), Bulgaria (90), Czech Republic (97), Finland (2), France (17), United Kingdom (37), Germany (17), Hungary (86), Israel (11) Italy (73), Kyrgyzstan (1), Moldavia (17), The Netherlands (8), Poland (6), Romania (17), Slovakia (21), Spain (4), Sweden (5), Switzerland (5), Turkey (12), Ukraine (67), Russia (177)
North America	USA (114), Canada (8), Mexico (22)
South America	Argentina (31), Brazil (6), Chile (4), Colombia (3)
Asia	Afghanistan (3), South Korea (1), India (2), Israel (3), Japan (17), China (70), Pakistan (1)
Africa	Algeria (14), Angola (8), Egypt (7), South African Republic (3), Kenya (2), Lesotho (6), Nigeria (1), Tunisia (2)
Australia	Australia (34), New Zealand (33)

For each character every year we measure the mean, standard deviation (σ), coefficient of variation (CV) and especially record genotypes with high and low value of analyzed traits.

b) The characters, which are under lesser pressure of the environment, such as:

- Growth habit
- Type of tillering
- Colour of leaves
- Position of leaves
- Spike form
- Colour of anthers
- Spike glaucosity
- Colour of spike
- Presence of awns or scurs

These characters are screened periodically.

The World Collection is the "first look" at the germplasm collection for researches to identify quickly the desired trait as well as to estimate the general variability of mentioned characters.

The next level in organizing the wheat collection is so-called **Genetic collection**. The objectives of the genetic collection are to increase the efficiency of germplasm

evaluation and utilization, and to provide manageable and representative set of wheat accessions for use in scientific research and breeding (what is in our case most important).

We use the term genetic collection instead of core collection because when the collection was established the term core collection was still unknown and second reason is that in constituting genetic collection the main principles of core collection which refer to "minimum repetitiveness" and "maximum genetic diversity" are not to strict respect. Nevertheless we can consider genetic collection as a kind of modified core collection such as Brown (1995) pointed out in part when he discuss about modification of core concept.

Table 2. The accessions grouped in sub-units of the genetic collection

Sub-unit	Example genotypes	Total no.
Winter hardiness	Mironovska.808, Bankut 1205, Centurk, Partizanka, MV-19...	20
Plant height	Norin 10, Aobakomughi, S. Cerros, Tom Thumb, Ai-bian...	120
Earliness	Norin 61, Tanori, Peking 11, Rusalka, Nizija	36
Resistance to leaf rust	Lee, Thatcher, Marquis, Bezostaja 1, Purdue 5392	47
Resistance to powdery mildew	Adder, Benni, Dina, Caldwell, NS 5-92...	22
Bread-making quality	Jubilejnaja 50, Bezostaja 1, Centurk, Elkon, Atlas 66...	38
Leaf architecture	Sremica, Mexico 120, Resistante, Semilia Eligulata, Sadovo S..	45
High tillering capacity	Tanori 71, Magnif 41, NE 11, NS 46/98...	5
Low tillering capacity	ZG 238/82, L 154, Osprey (Tin), Bodalin (Tin)..	12
Spike architecture	Bolonjska, ZG-195, Mexico 3, Pema, Intro 604..	107
Long leaf area duration	Red Coat, Partizanka, Purdue 5392, Szegedi 60, Buck Cin, Pobeda, Hersonska 90, ...	40
Glume size	NS 50-14, Mironovska 10, Raduša, S. Cerros ...	6
Resistance to insects	Vel, Bean, Harf, Ruler, Downy, Kharkof ...	35
Resistance to lodging	Novos. 100, Kratka, Ana, Fundulea 490, Recital, WLRGP-91-26	22
Leaf chlorose	Lira, Florida, Don.polupat. Caldwell, Centurk	23
Solidness of upper internode	GSN 17, UC 66206, W 53/86, Rogosija s.k.Z.P, Sun 25....	7
Genetic and cytogenetic stock	Mutations, Wheat-rye translocation, isogenic lines, etc.	103

Based on evaluating data from World collection, data gotten from the owners of germplasm, data from previous scientific researches and data published in literature about accessions, the genetic collection is grouped in subunits according to the traits considered important for breeding or scientific purpose (Table 2). For example - in subunit "winterhardiness", all genotypes which posses high level of resistance to low temperatures are included. By doing that we always try to include genotypes from different place of origin and as much as possible different in expression of other traits such as plant height, tillering capacity, leaf architecture, leaf size, etc. so in each subunits of genetic collection include accessions with

highest value of certain character with maximum variability for other traits. In last few years attempts have been made whenever possible to establish subunits according to genes which have been identified to control certain traits such as *Rht* genes for stem height (Table.3), *Lr* genes for resistance to leaf rust, *Sr* genes for resistance to stem rust, *Ppd* genes for photoperiodic reaction, *Vrn* genes for vernalization etc. In 15 subunits of genetic collection 600-700 genotypes are grown annually.

Table 3. The wheat genetic collection sub-unit "Plant height" arranged according to *Rht* Genes

No.	Genotype	Gene(s)	Count. of orig.	Growth habit*
19	Maris Hunts.	<i>Rht 0</i>	UK	W
25	Bank. 1205	<i>Rht 0</i>	Hungary	W
26	Siete Cerros	<i>Rht B1b (4A)</i>	Mexico	S
38	Banks	<i>Rht B1b</i>	Austria	S
39	Aobakomug.	<i>Rht D1d (4D)</i>	Japan	W
61	Durin	<i>Rht D1d</i>	UK	W
62	Norin 10	<i>Rht B1b+Rht D1d</i>	Japan	W
71	Cajeme 71	<i>Rht B1b+Rht D1d</i>	Japan	I
72	Tom Thumb	<i>Rht B1c (4A)</i>	Tibet	W
77	Min. Dwarf	<i>Rht 3</i>	Belgium	S
78	Akakomughi	<i>Rht 8 (2D)</i>	Japan	S
84	Sava	<i>Rht 8</i>	Yugoslavia	W
85	Ai-bian	<i>Rht D1c (4D)</i>	Japan	I
119	Burt M 860	<i>Rht 20</i>	USA	W

* W – winter, S – spring, I – facultative (winter/spring)

The evaluation in the collection is very intensive and it includes:

- The data for the purpose of EWDB management so-called **joint category for characterization and evaluation**
- The data which is requested by UPOV (most of them are independent of environment and serve mostly for identification and protection)
- The other data which are important for breeding.

There are 55 characters evaluating in genetic collection. If available, the international scale of scoring is used but if it is not, we used our own scale and/or descriptions. Out of 55 characters 28 are periodically evaluated (during 3-4 succession years) because of their low susceptibility to environment and other 27 characteristics are evaluated every season (Tab.4). Besides the mentioned evaluation, certain number of accessions are evaluated for special purpose such as: drought resistance under artificial conditions (mobile roofs and greenhouse); biochemical markers such as: glutenin and gliadin subunits (determined by Glu alleles); root characteristics in seedling stage; presence of wheat/rya translocation (1B/1R); rate of photosynthesis etc.

All accessions in genetic collection are grown in 7 replications. The first replication is used only for presentation (students, foreign and domestic scientists etc.) Another three replications are used for evaluating. The rest are used for

measuring the effect of diazotrophs microorganisms, which are inoculated on the seed before sowing. The evaluation of the last three replications is not complete and it includes only the important breeding traits such as: yield, quality, plant height etc.

The third level of wheat collection is crossing block. Just as its name says crossing block is strictly connected with breeding and comprises potential parents intended for crossing. In principle, crossing block includes cultivars and advanced lines from genetic collection whose genetic base is known to certain degree. The basic criterion genotypes must fulfill to be included in the crossing block is to possess desirable genes / traits intended to be recombined in new varieties. Crossing block usually consists of 300-350 genotypes.

Table 4. Traits evaluated in the wheat genetic collection in Novi Sad

Traits evaluated periodically (3-4 years)	Traits evaluated each year
1. Coleoptile coloration	1. Winter hardiness in the field
2. Coleoptile length	2. Number of leaves
3. Growth habit	3. Time of ear emergence
4. Tiller coloration	4. Vegetative period of flowering
5. Winter hardiness in cold chambers	5. Plant height
6. Coloration of auricles	6. Ear length
7. Coloration of leaves	7. Ear density
8. Leaves position in flowering	8. No. ears/m ²
9. Frequency of plants with recurved flag leaves	9. Lodging resistance
10. Flag leaf glaucosity	10. Resistance to leaf rust
11. Tillering capacity	11. Resistance to stem rust
12. Anther coloration	12. Resistance to powder mildew
13. Ear glaucosity	13. Resistance to fusarium
14. Culm glaucosity	14. No. of spikelets/ear
15. Straw-pith in cross section	15. No. of sterile spikes/ear
16. Ear coloration	16. Ear weight
17. Awns or scurs length	17. Biomass weight/m ²
18. Ear shape in profile	18. Harvest index
19. Apical rachis segment hairiness of convex surface	19. No. of grain/spike
20. Lower glume - shoulder width	20. Kernel weight/spike
21. Lower glume - shoulder shape	21. Spike index
22. Lower glume - beak length	22. 1000-kernel weight
23. Lower glume - beak shape	23. Grain yield
24. Lower glume - extent of internal hairs	24. Flour yield
25. Lowest lemma - beak shape	25. Sedimentation value
26. Grain coloration	26. Protein content
27. Grain coloration with phenol	
28. Seasonal type	

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