

January 1999



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**COMMISSION ON GENETIC RESOURCES FOR FOOD AND
AGRICULTURE**

Eighth Regular Session

Rome, 19 – 23 April 1999

**EXPLORING OPTIONS FOR THE LIST APPROACH WITHIN THE
MULTILATERAL SYSTEM OF FACILITATED GERMPLASM
EXCHANGE WITHIN THE REVISED INTERNATIONAL
UNDERTAKING**

**REPORT OF AN INFORMAL WORKSHOP OF EXPERTS
CONVOKED BY THE 'ISTITUTO AGRONOMO PER
L'OLTREMARE', ON BEHALF OF THE ITALIAN
MINISTRY OF FOREIGN AFFAIRS
FLORENCE, 1-3 OCTOBER 1998**

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Exploring options for the list approach within the multilateral system of facilitated germplasm exchange within the revised International Undertaking

1. Introduction

The Istituto Agronomico per l'Oltremare, on behalf of the Ministry of Foreign Affairs, Italy, organised an informal workshop of experts, in their private capacities (Florence, 1-3 October 1998), to explore, and suggest for the possible consideration of governments negotiating the revision of the International Undertaking on Plant Genetic Resources, within the FAO Commission on Genetic Resources for Food and Agriculture, the issues involved in the development of a list of crops for a future multilateral system of facilitated germplasm exchange. The workshop focused on the technical bases on which a list of crops might be established and options developed.

A series of papers were presented, which will be made available both as volume of proceedings, and as downloadable text files on the IAO's website: <http://www.unifi.it/garr-fi/iao/>.

The workshop agreed, in addition, that the Istituto Agronomico per l'Oltremare should prepare this summary of the discussions, in order to capture the variety of ideas put forward, and the issues and options identified, for the possible consideration of governments in identifying areas of further compromise, during further negotiations. The Italian Government would forward this document to the Commission on Genetic Resources for Food and Agriculture.

2. Listing crops

- It was recognised that it had already been agreed that the scope of the revised International Undertaking would cover all plant genetic resources for food and agriculture.
- Governments may wish to draw up lists to define sub-sets within plant genetic resources for food and agriculture for different agreed access and benefit-sharing arrangements. Such listing, and the contents of the lists, might be dynamic over time.
- Any arrangements under the revised International Undertaking should in any case cover all materials collected before the entry into force of the Convention on Biological Diversity, including the materials in the International Agricultural Research Centres of the Consultative Group on International Agricultural Research.

2.1 Possible reasons for listing crops

- To establish a window within the framework of the Convention on Biological Diversity, and implement a system of facilitated access to plant genetic resources for food and agriculture, and benefit-sharing.
- To minimise transaction costs for the listed crops, to which a regime of facilitated access and benefit-sharing would apply.
- To obviate the need to track individual accessions of these crops.
- To provide an international framework, and minimise the proliferation of differing bilateral agreements, particularly in the case of plant genetic resources for food and agriculture where there is a high degree of interdependence between countries.

2.2 Possible problems in listing crops

- Non-listed crops may in future receive inadequate attention in the context of international collaboration.
- If this happened, scientific work for the improvement of non-listed crops would be seriously affected.
- Crops of regional and local importance are unlikely to be listed, and are therefore likely to be the most seriously affected by such developments.
- It would be necessary to establish, through international negotiation, agreed criteria for designating and monitoring crops.

3. Types of list

3.1 Inclusive lists

By an “inclusive list” is meant identifying individual crops for which specific agreed terms of access and benefit-sharing are established.

- Inclusive listing has the advantage of simplicity, transparency and clarity.
- Inclusive listing would make possible different management of various sub-sets of plant genetic resources for food and agriculture by the international community, within the overall scope of the International Undertaking.
- Inclusive listing would allow prioritisation and focus.
- Inclusive listing would allow either short or comprehensive options.

3.2 Exclusive listing

By an “exclusive list” is meant identifying specific crops which would not be covered by multilateral facilitated access and benefit-sharing.

- A negative list might allow governments to negotiate for the exclusion of specific crops.
- It is likely that an exclusive list would need to include a very large number of crops and other plant species.
- In this context, it would be impossible to list the many potential crops for which information is scarce or non-existent.

3.3 Combining mandatory and optional listing

A possible option was discussed, of having a mandatory core list of crops, and a register of materials voluntarily made available to the multilateral system, in a spirit of reciprocal collaboration and confidence.

- This would allow countries to designate additional materials to the multilateral system in a flexible way that meets their needs.
- It could overcome a number of the problems listed above, particularly with respect to locally and regionally important crops.
- It could facilitate the implementation of the *Global Plan of Action for the Conservation and Sustainable Utilisation of Plant Genetic Resources for Food and Agriculture*, in particular, with regard to under-utilised crops.
- It could help recognise existing arrangements, in particular, with regard to regional and crop-specific networks.

3.4 Recognising existing arrangements

- Existing networks are a major tool for mutually agreed access and benefit-sharing, and the revised International Undertaking should provide a framework for their continued development and effective operations.
- Twelve International Agricultural Research Centres of the Consultative Group on International Agricultural Research have brought their *ex situ* collections into the International Network of *Ex Situ* Collections under the Auspices of FAO, and these should be included in the facilitated access and benefit-sharing arrangements.

4. Criteria for constructing lists

The two criteria that had been used by the negotiators to establish the current *Tentative List of Crops*, namely “(i) their importance for food security at local and global levels, and (ii) countries’ interdependence with respect to plant genetic resources” (*Report of the Fourth Extraordinary Session of the Commission on Genetic Resources for Food and Agriculture*, para. 6), were considered adequate, provided due consideration was given to maintaining intra-specific genetic diversity in the key agricultural crops.

4.1 Food security

- It was recognised that there is already an internationally agreed definition of food security, in para. 1 of the *World Food Summit Plan of Action*, where food security is considered at

“the individual, household, national, regional and global levels. Food security exists when all people, at all times, have physical and economic access to sufficient, safe and nutritious food to meet their dietary needs and food preferences for an active and healthy life”.

- Any listing should facilitate the achievement, over time, of food security in all its aspects.
- In the context of listing for food security, agricultural production and consumption needs are of particular importance.
- In this context, the construction of any list should contribute to sustainable agricultural development throughout the world.
- Possible qualitative and quantitative indicators of key aspects of food security are:
 - world food production and consumption, and value,
 - nutritional needs, including for protein and macro- and micro-nutrients,
 - regional and local dietary habits and needs.

4.2 Interdependence

In using the concept of interdependence to construct a list or lists, its many components should be adequately covered, such as:

- the large interdependence of all countries on foreign genes for their agricultural production and food security,
- countries’ reliance on non-indigenous crops for sustainable production and consumption,
- the multiple sources of intra-specific genetic diversity that are used in developing cultivars, drawing on many regions and countries, as can be shown in cultivar genealogies,
- the many types of germplasm (advanced cultivars, breeding lines, local cultivars and wild relatives) used in developing cultivars.

4.3 Other possible criteria

Other possible criteria that might be taken into account included:

- the existence of centres of diversity of a crop in more than one country, or region,
- the economic importance of a crop,
- the importance of germplasm in meeting internationally agreed development needs, (such as salinity tolerance, in the context of the United Nations Convention to Combat Desertification),
- genetic erosion.

5. Defining the unit for listing

After detailed technical consideration, the conclusions of the documents that had been prepared by the International Plant Genetic Resources Institute (IPGRI) and the FAO, at the request of the Commission on Genetic Resources for Food and Agriculture, and submitted to its Fifth Extraordinary Session (CGRFA-Ex5/98/Inf.1, *Technical Aspects Involved in Developing a List of Crops for the Multilateral System within the Revised Undertaking*, and CGRFA-Ex5/98/Inf.1/Annex, *Relative Characteristics of the Crops and Genera in the Tentative List of Crops Annexed to Article 11 Of the Undertaking*) were supported:

- *Taxonomy provides a satisfactory basis for defining crop content.*
- *The genus is the most suitable taxonomic unit for most crops.*
- *The genepool concept provides an effective complement to taxonomy, and can be used to identify crops where more than one genus should be included (for example, wheat, brassica crops, and potato)*
- *Any procedures should be able to evolve to reflect new knowledge and practices.*

The paper presented to the workshop, entitled *An In-depth Study of Wheat, Related to the Definition of the Crop, and its Implications for the Sustainable Use of Wheat Genetic Resources*, was considered to be an important practical demonstration of these principles, and it was recommended that it be made available to the Commission on Genetic Resources for Food and Agriculture as an information document.

6. Criteria and mechanisms for up-dating the list or lists

- The list or lists, and their contents, should be dynamic, and updated according to agreed procedures and criteria, incorporated in the International Undertaking.

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- Systems would need to be developed to facilitate such updating, on the basis of agreed scientific procedures, and of a monitoring the effects of implementing the International Undertaking, particularly on the use of materials, including of non-listed crops.

In-depth study of wheat, related to the definition of the crop, and its implication for the sustainable use of wheat genetic resources

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The aim of this paper is to demonstrate a possible dependence of an in-depth study and sustainable use of wheat genetic resources on the alternative concepts of the crop definition, suggested in the FAO Background Paper CGRFA-Ex5/98/Inf.1. An attention is paid to the following topics: (a) a definition of wheat as the crop; (b) an in-depth study of world wheat diversity; (c) the availability of genetic resources for wheat breeding depending on the crop definition.

The definition of wheat as the crop

It is quite difficult to explain the technical meaning of the word "wheat". It is especially difficult to do when this word becomes a part of an important international document. The final wheat definition should mark the conditions and fullness of access to genetic resources necessary for successful breeding of this major food crop.

The FAO Background Paper prepared by IPGRI represents detailed generalisation concerning the technical aspects of developing a list of crops for the revised International Undertaking (CGRFA-Ex5/98/Inf.1). This paper can serve as a good basis for working out the principles of the crop definition. Its essential statements can be listed in the following 10 theses:

1. Common names of crops can be confusing.
2. The formal taxonomy provides a clear and effective way of identifying plant groups.
3. A species constitutes the basic unit of biological classification.
4. At species level and below a classification can frequently differ according to different authors.
5. The genus is the most appropriate level of operation for any descriptive system.
6. The gene pool (GP1, GP2, GP3) concept complements formal taxonomy.
7. The gene pool designation provides a practical way of determining taxa potential and utility.
8. Crop wild relatives belonging to GP1, GP2, GP3 are increasingly being used in crop improvement.
9. The gene pool description remains informal and to some extent subjective.
10. It is likely that crop-based expertise will be needed to determine the appropriate treatment for at least some of the more important or taxonomically complex groups.

These statements are quite reasonable and do not have any other more acceptable alternative. At the same time, it is necessary to pay attention to existing problems. The history of wheat taxonomy counts more than two centuries. However, we have no

generally accepted point of view on classifications of wheat species, genus *Triticum*, and even – the tribe *Triticeae*. Scientific disputes concern, mainly, the boundaries of genera and principles of an intrageneric grouping, which determine, in turn, the number of recognised taxa. Thus, the number of species in the genus *Triticum* varies from 5 (Mac Key, 1968) up to 27 (Dorofeev et al., 1979). In some classifications this genus includes only species of wheat while in others – species of wheat and *Aegilops* (Bowden, 1959; Morris and Sears, 1967, etc.). The number of genera in the tribe *Triticeae* varies from 16 up to 25 (Miller, 1987). In recent classifications one can find rather radical changes in numbers and nomenclature of taxa. It is often necessary to have a quite long list of synonyms to understand some of scientific publications. The report of the 1st IWGS Taxonomy Workshop comments upon this uneasy situation in the following way: “The present state of taxonomy and nomenclature in *Triticum* is confusing for people who collect germplasm, for people who maintain genebanks, and for wheat breeders and geneticists who use the seed held by these genebanks” (Morrison, 1998).

We can also find different versions of the gene pools concept. Developing ideas of Harlan and De Wet (1971), first Smartt (1980) then Konarev et al. (1986) have suggested to increase the number of gene pools for cultivated plants from three up to four, associating them accordingly with populations, species, genera and tribes.

The rapid progress of molecular biology renders new changes in classifications of cultivated plants. With reference to wheat and its relatives, the available methods allow to carry out rather objective determining the genomic structure and relationships of analysed taxa. They can supplement and concretise the taxonomic approach and concept of gene pools to define wheat as the crop in multilateral system of access to PGR.

The relevant information about wheat and its relatives is represented in Figure 1. We have used the Latin names and genomic structure of *Triticum* species from classification of Dorofeev et al. (1979) that reflects biological and economic characteristics of cultivated wheats. In some other major classifications (Bowden, 1959; Morris and Sears, 1967; Mackey, 1966, etc.) *T.aestivum* includes the majority of hexaploid wheats while almost all tetraploids enter in the taxon *T.turgidum*. We can find *T.monococcum* L. in all classifications although in one cases it includes cultivated and wild *Eincorns*, but in others (as by Dorofeev et al. 1979) - only cultivated.

The new genomic compositions were found in the *Triticeae* species in 19980s-1990s and genomic classifications were modified. Considering these changes, we have included in our scheme the genome designations for *Triticeae* genera from the recent CIMMYT report on wide hybridisation (Mujeeb-Kazi & Hettel, 1995).

Figure 1 reflects the possible versions of wheat definition. The final one will depend on completeness of access to wheat genetic resources expecting in revised International Undertaking on PGR. As we can see, all these versions are within the limits of tribe *Trticeae*. In our days, researches are thinking about examining the possibilities of even wider hybrids, such as crossing wheat with maize, millet, sorghum, teosinte, and *Tripsacum*. (Mujeeb-Kazi & Hettel, 1995). There are no doubts that further progress in gene engineering methods will allow using in wheat breeding a genetic material of more remote genera of botanical family *Poaceae* Barnh. However I support the IPGRI point of view that these methods should lie outside the scope of crop definition.

In my opinion, Figure 1 provides, in compact form, the necessary information for wheat definition, “which can be easily and ambiguously interpreted, applied and updated”,

as it is underlined in FAO Background Paper CGRFA-Ex5/98/Inf.1. For practical using the data of Figure 1 it is possible to accept the following assumptions:

- (a) Primary gene pool corresponds to the concept of the biological species;
- (b) Secondary gene pool includes all species of genus;
- (c) Tertiary gene pool covers related genera of the tribe;
- (d) Specific technical names correspond approximately to the level of species or sub-species.

Basing on these assumptions and Figure 1, we can consider three main versions of wheat definition: (1) as a common or technical name and botanical species (~ GP1); (2) as a common name and genus (~ GP1-GP2); (3) as a common name, genus and related genera of tribe (Gp1-GP3).

The study of the world wheat diversity

The comprehensive study of the collected wheat diversity is important part of researches for providing the sustainable use of wheat genetic resources. At the N.I. Vavilov All-Russian Institute of Plant Industry (VIR) we try to solve in this work the following tasks:

1. To obtain the versatile information about biological peculiarities and economically important characteristics of accessions;
2. To clarify their place in the variability system of botanical species and genera;
3. To search and develop the promising initial material for solving traditional and new problems of wheat breeding.

Figure 2 represents the basic scheme of wheat study in the VIR's system. It includes a characterisation and evaluation of accessions in the experimental network and laboratories of the Institute.

Field study is carried out in regions where subsequent use of the selected materials in breeding is planned, as well as at a number of locations providing the most favourable conditions for testing such characters as draught and heat resistance, winter hardiness, resistance to various diseases and pests, etc. All this work is performed with using uniform procedures. The study of each accession includes its botanical description, determination of resistance to major diseases and unfavourable abiotic stresses, as well as assessment of productivity and some others agronomic characters. The best accessions selected in course of field studies undergo further in-depth evaluation in the research departments of the Institute, such as departments of molecular biology, plant pathology, physiology, industrial qualities, biochemistry, genetics. (Figure 2).

Basing on results of the field and laboratory study, we carry out the cataloguing of new samples, replenish the computer database, form the active collection, allocate the sources and donors of valuable characters, and establish genetic collection of accessions with identified genes. All these activities provide the breeders, research institutes and universities with the necessary seeds and information (Figure 2).

The eminent expert in plant genetic resources Prof. John Hawkes (1985) defines the in-depth evaluation as *to some extent open-ended and largely concerned with laboratory*

or glasshouse screening for pest and disease resistance and for adaptation to extreme environments. Today plant breeders wish to know more about phenotypically superior accessions. It is thus necessary to look for approaches that allow us to obtain complete and objective information of **long-term value**. The data obtained by methods of classical and molecular genetics meet these requirements in the best way.

In recent years a considerable amount of work has been done to study the genotypic peculiarities of accessions possessing the highest mean values for major valuable characters. Nevertheless, the determination of genetic nature of many accessions with desirable phenotypic characteristics is not practicable. In our opinion, a way out of this situation is to apply a systematic approach in studying the intraspecific diversity of plants (Merezhko, 1994, 1998). Figure 3 represents the main stages of this systematic approach.

In dependence on breeding goals, accessions with high or low mean value of character are of practical interest. The best accessions based on phenotype can be included in the first group of sub-collection – **first stage** (Figure 3). The average level of character envisioned for the new varieties defines the criteria for the choice.

The world practice shows unequal breeding value of accessions selected based on phenotype. For this reason it is important in the **second stage** of research (Figure 3) to determine the degree of genetic similarity of the best accessions, selected based on phenotype. When they have identical alleles of the same genes, forms that have other useful properties should be included in crosses. If an identical phenotype in several accessions is controlled by alleles of different genes, the most effective of them should be chosen for breeding. Three approaches are recommended for determining the degree of genetic differences among the phenotypically superior accessions:

- (1) Study the accessions in contrasting environments;
- (2) Analyse their parentage;
- (3) Cross the best accessions among themselves and studying the inheritance of the character in first, second, and, sometimes, later generations.

Revealing non-allelic differences among investigated accessions provides an opportunity to select in segregating generations of test crosses the recombinant genotypes with a new mean value of a character under study. This creates a basis for progress of breeding in a definite direction.

It is very important to understand the genetic system of intraspecific variability for a given character - **third stage** (Figure 3). In applying standard or specially designed genetic procedures, it is necessary:

- (1) To determine which level of character is dominant and which is recessive;
- (2) To clarify an influence of genetic background, cytoplasm, and environments on the character;
- (3) To get an idea of the number of genes responsible for intraspecific diversity of the character;
- (4) To study the effects of the most important genes and their interactions;
- (5) To identify the major genes for the character in test crosses;
- (6) To determine a possible association of these genes with known genetic markers.

Genetic collections of accessions with identified genes are created for characters well studied genetically - **forth stage** (Figure 3). It is also important to transfer these genes through backcrossing into a common genetic background in the process of developing near-isogenic lines. Sets of such lines for different useful characters are of unique value for researchers. Testing near-isogenic lines in various agroclimatic conditions allows determining the ecological value of individual alleles and their different combinations.

The obtained information serves as a basis for revealing in collection and developing donors of useful characters - **fifth stage** (Figure 3). Developing new donors is achieved through backcrossing. Valuable alleles are transferred into the genetic background of the varieties with well-known combining ability. A breeder can purposefully use this valuable material in crosses to solve the stated tasks (Figure 3).

Implementation of the proposed approach permits to quickly input all data accumulated in the world on different characters. All this together provides adequate information necessary for understanding the system of intraspecific variability of useful characters and organising on this basis a way of a «phenogenetic screening» the wheat diversity. By studying a limited number of specially selected accessions, the genetic potential of a species can be determined, and genes that play a particularly important role in controlling useful characters can be identified and included in breeding programmes.

The system approach promotes more intensive introduction of genetics in germplasm evaluating and developing new initial breeding material. Quite promising potentialities are open with modern methods of molecular biology. They can be very helpful in organising the marker-based introduction, screening and breeding.

Our approaches to the in-depth study of wheat genetic resources are based, first of all, on analysing the intraspecific variability of biological and the most economically important characters. From the point of view of mathematical statistics, the Linnean species could be considered as a general infinite population. Well-organised collection of plant genetic resources, belonging to this species, must be a representative sample from the general population. If we do not find necessary variability within the limits of an investigated species, we search for it among accessions of other *Triticum* species or other genera of tribe *Triticeae*.

Thus, the main conclusion important for our workshop is as follows: for the effective study of wheat genetic resources, focused on breeder demands, scientists need unlimited access to all global diversity of wheat species (*Triticum* ssp.) and related genera of tribe *Triticeae* (Figure 1). It, in turn, imposes the appropriate requirements to completeness of wheat definition as the crop in multilateral system of access to PGR.

The availability of genetic resources for wheat breeding depending on the crop definition

The contribution of genetic resources in wheat breeding is evident in the high yield increases and improvement industrial and nutritive value of wheat products, which have produced millions in profits. Only a few citations in the literature evaluate this impact in terms of money. However, the available estimates are rather impressive. The successful use of Japanese semidwarf wheat Norin 10 in world breeding is widely known (Borlaug, 1968; Reitz and Salmon, 1968; Sims, 1968 and others). Using genetic diversity from all

continents, CIMMYT's Wheat Program initiated a real revolution in world grain production. According to Hawkes (1985), in 1962-85 there were 319 named bread wheat cultivars and 250 named durum wheat cultivars developed from CIMMYT or CIMMYT-related materials through different national programmes. The additional grain production, obtained due to these cultivars is estimated at US\$ 1.2 billion per year.

Another example of remarkable impact of plant genetic resources on world wheat breeding is developing the winter bread wheat Bezostaya 1. At the beginning of this century Italian breeder Nazareno Strampelli used the semidwarf Japanese wheat Akakomugi in crosses and developed a number of cultivars, including – Ardito. Ernst Klein used it in hybridisation in Argentina to develop cultivar Klein 33. Russian breeder Pavel Lukyanenko crossed this cultivar with local wheat and created new variety Bezostaya 1. The latter became world famous for its extraordinary ecological plasticity and as a popular parental form for crosses, especially in Europe. For decades cultivation of Bezostaya 1 in Russia has provided an annual income more than 30 times greater than the annual investment in the entire National Plant Genetic Resources Programme that was rather expensive.

Both these examples demonstrate the necessity for breeders to have the maximally wide access to the global wheat diversity. It can serve a perfect example of interdependence of countries with respect of plant genetic resources. The germplasm from many regions of globe is used in developing wheat cultivars playing the most substantial role in world grain production.

Article 6bis of consolidated negotiating text for revision of the International Undertaking includes the measures to provide the sustainable utilisation of PGRFA. At least, four of them are directly associated with plant breeding. Table 1 represents the levels of wheat germplasm diversity necessary for performance of these measures. Strengthening researches that enhance biological diversity by maximising intra- and inter-specific variation (*the measure 'b'*) includes utilisation of gene pools Gp1 and Gp2 already by definition. These two gene pools can also provide the expanded use of local and locally adapted crops, varieties and underutilized species (*the measure 'e'*). The developing varieties adapted to conditions of marginal areas (*the measure 'c'*) and broadening the genetic base of crops (*the measure 'd'*) require also the involvement of other *Triticeae* genera in the breeding process. We can thus see that the Article 6bis of International Undertaking assumes the maximally wide interpretation of crop definition for the sustainable use of PGR.

In conclusion, it will be demonstrated the availability of genetic resources for bread wheat breeding depending on the alternative crop definitions in accordance with figure 1.

The definition I - as a common or technical name and botanical species (~ GP1):

wheat (*T.aestivum* L.), GP1 or bread wheat (*T.aestivum* L.), GP1

According to this definition, only accessions of bread wheat would be included in system of multilateral access to genetic resources. Even in this case we can still have rather large chances for breeding. The intraspecific variability of bread wheat *T.aestivum* L., concentrated in genebanks of the world, has been used in crosses only partially. It has been poorly investigated genetically. Properly studied, the available diversity can provide multiple solutions for many traditional and new breeding problems. Nevertheless, the existing reserves of intraspecific variability of bread wheat on some characters are almost exhausted. It is especially evident concerning resistance and tolerance to many biotic and some abiotic stresses. The modern breeding of this species requires an introgression of novel variability from more remote taxa. It, in turn, requires wider definition of wheat as the crop in revised International Undertaking.

The definition II - as a common name and genus (~ GP1-GP2):

wheat (*Triticum* ssp.), GP1-GP2

This version of wheat definition implies including the diversity of all species of genus *Triticum* in system of multilateral access to PGR. It considerably expands the resources of bread wheat breeding, especially for resistance to numerous diseases. According to McIntosh et al., (1993), the genes of resistance to powdery mildew – Pm4b, Pm5, Pm16, to stem rust - Sr21, Sr22, Sr35, Sr36, Sr37, Sr40, and to yellow rust - Yr15 were transferred into *T.aestivum* L. from various other species of genus *Triticum* L. (Figure 4).

The most significant results have been achieved through hybridisation of bread wheat with *T.durum* Desf., *T.dicoccum* (Schrank) Schuebl. and *T.timopheevii* Zhuk. The use of the *Emmer* wheats Khapli (India) and Vernal (Russia) in crosses by USA breeders has allowed to produce a number of varieties that have played the important role in control of destructive stem rust epidemics (Loegering et al., 1967; Dorofeev et al., 1987). One of these varieties - Hope was the extremely popular parental form in world wheat breeding during a long time.

Though the large reserves of hereditary variability of the *Triticum* ssp. are yet not used in plant breeding, the breeders pay more and more attention to different genera of tribe *Triticeae* for solving existing problems. It, in turn, requires such definition of wheat as the crop that would ensure access to the tertiary gene pool GP3.

The definition III - as a common name, genus and related genera of tribe (Gp1-GP3):

wheat (*Triticum* ssp.) and related genera of Triticeae, GP1-GP3

This is the widest definition of wheat as the crop. In case of its acceptance, the system of multilateral access to genetic resources will allow to breeders the maximally

effective using the existing germplasm. The genera of tribe Triticeae provide a large potential source of new genes for economically important traits for cultivated wheats.

The richest diversity of species, belonging to *Aegilops*, will have especially important role in future breeding of bread wheat. A number of varieties and breeding lines of *T.aestivum* L. have received many genes of resistance to diseases and pests from this genera: to powdery mildew - Pm12, Pm13, Pm19; to leaf rust - Lr21, Lr22a, Lr28, Lr32, Lr36, Lr41, Lr42, Lr43; to stem rust - Sr32, Sr33, Sr34, Sr38, Sr39; to yellow rust - Yr8; to Russian aphid *Diuraphis noxia* - Dn3; to Hessian fly - H13; to root rot nematode - *Rkn*; to cereal cyst nematode - Cre2, Cre3, and others (McIntosh et al., 1993; McIntosh, 1998) – Figure 4. According to Mujeeb-Kazi & Hettel (1995), accessions of *Ae.tauschii* have a wide range of resistances and tolerances to various biotic and abiotic stresses, such as Karnal bunt, scab, spot blotch, leaf rust, stripe rust, salinity, drought, improved bread-making quality. CIMMYT has produced more than 500 synthetic hexaploids - most involving a unique *Ae.tauschii* accessions (Mujeeb-Kazi & Hettel, 1994.). These synthetics can be easily crossed with bread wheat.

Rye is a valuable source of useful genes for bread wheat. Among them are the genes of resistance to powdery mildew - Pm7, to leaf rust - Lr25, to stem rust - Sr27, Sr31, to yellow rust - Yr9, to copper deficiency - Ce (McIntosh et al., 1993) – Figure 4. The world sounding event in bread wheat breeding is the use of wheat-rye translocations 1BL/1RS, 1AL/1RS. According to Rabinovich (1998), 330 cultivars and lines were created on this basis in 35 countries. They have high productivity, wide adaptation and high disease and pest resistance. Varieties with wheat-rye spontaneous translocation 1BL/1RS occupy more than 5 million hectares (Mujeeb-Kazi & Hettel, 1994.). The valuable source of rye genes is triticale.

The perennial genera of *Triticeae* bring also an essential contribution into bread wheat breeding. They have tolerances to toxic levels of aluminum and salt, copper deficiency, *Septoria tritici*, wheat curl mite (the vector of wheat streak mosaic virus), and Russian wheat aphid (Mujeeb-Kazi & Hettel, 1994; Thomas et al., 1998). The genes of resistance to leaf rust - Lr19, Lr24, Lr29, Lr38 and to stem rust - Sr24, Sr25, Sr26 were introgressed from species of genus *Thinopyrum* (syn.: *Elytrigia*) (McIntosh et al., 1993) – Figure 4. All genomes of the perennial *Triticeae* have been combined, with the A, B, and D genomes of bread wheat (Mujeeb-Kazi & Hettel, 1995).

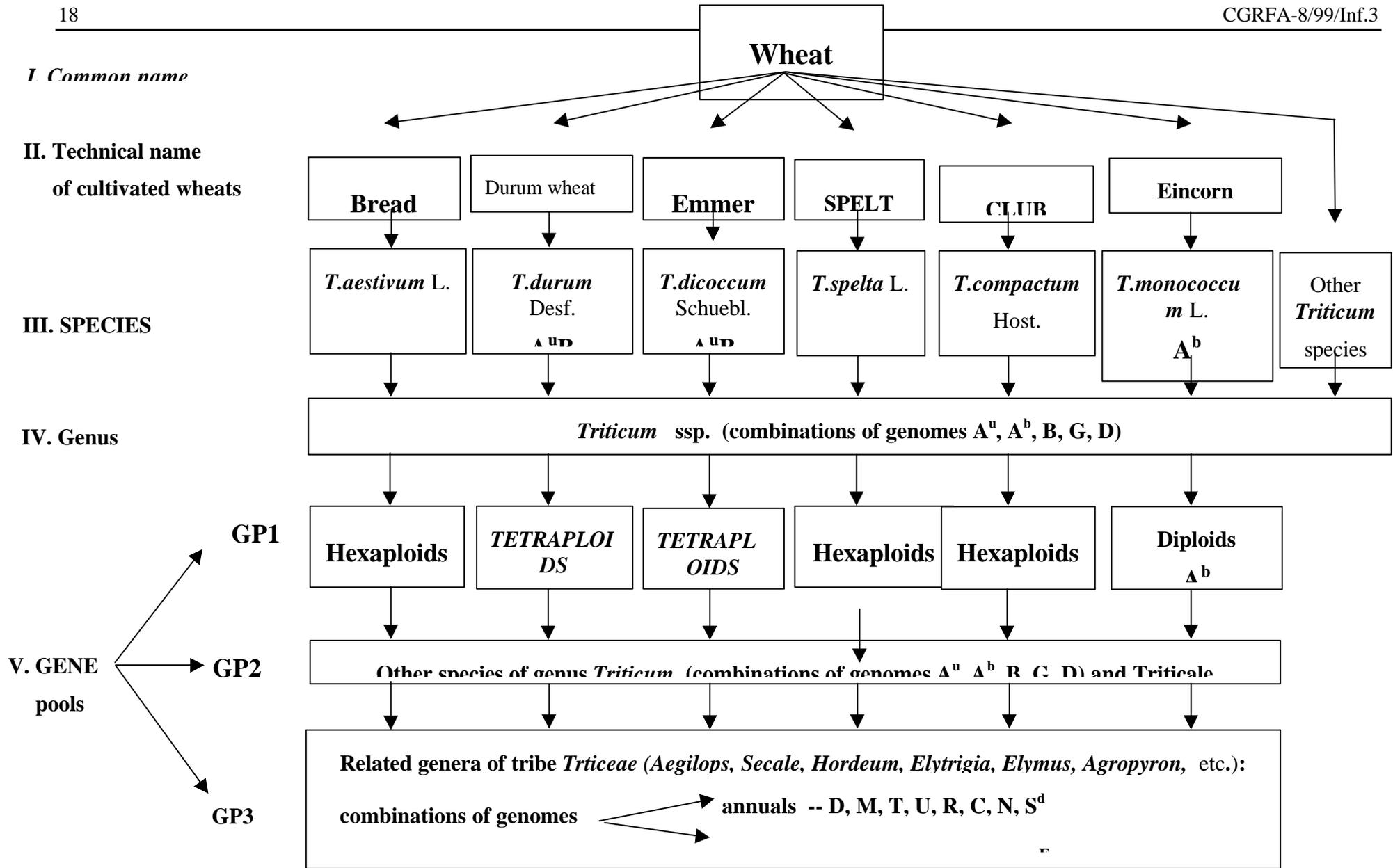
Conclusion

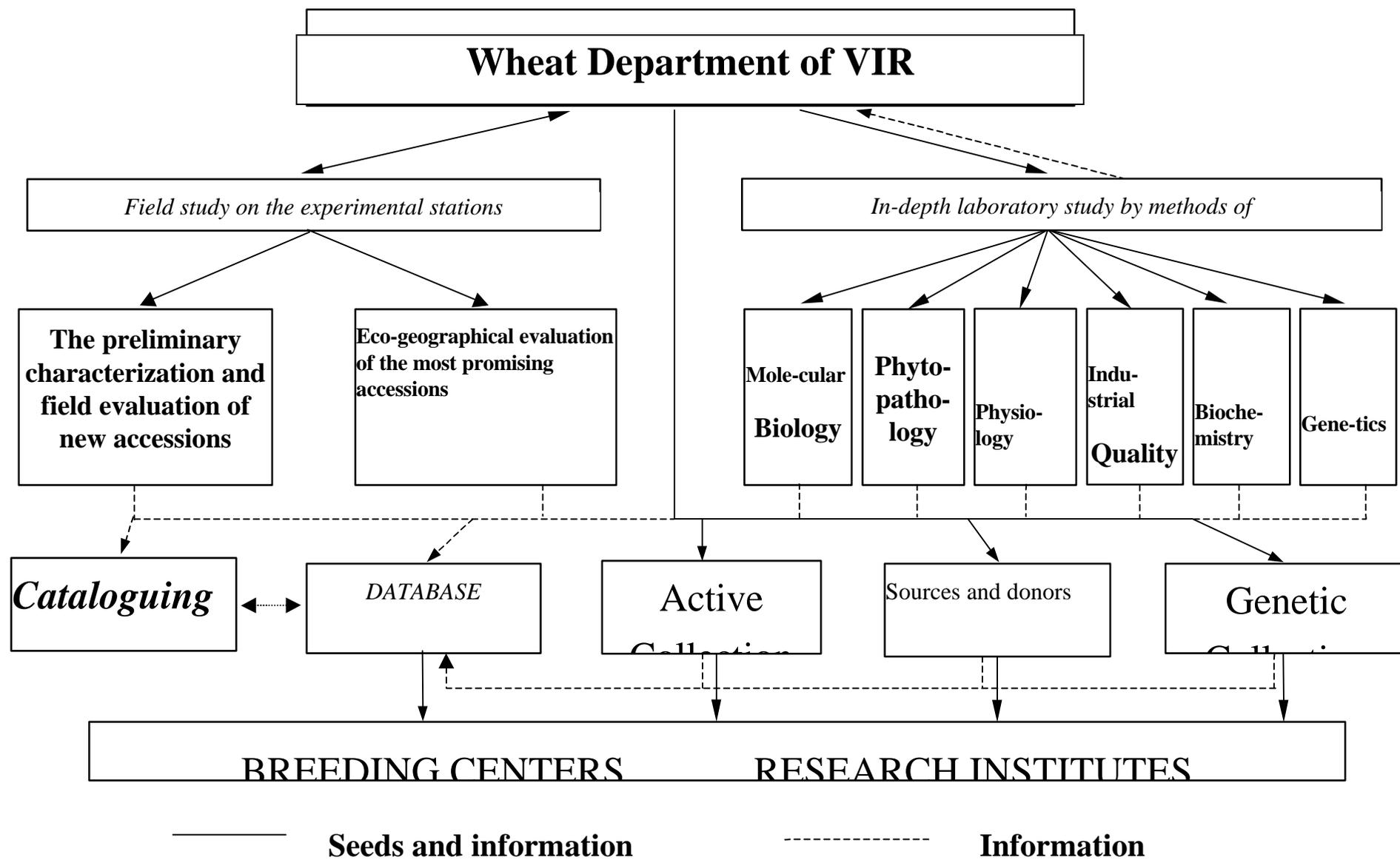
Thus, the modern wheat breeding ensuring sustainable the utilisation of plant genetic resources can not be limited only by the boundaries of one species or even genus. The access to all diversity of wheat and its relatives (wild and cultivated) is necessary. Considering the mentioned above reasons, I offer the following definition of wheat as the crop in the annex to Article 11 of revised International Undertaking on PGRFA: **“Wheat (*Triticum* spp.) with related genera of tribe Triticeae.”**

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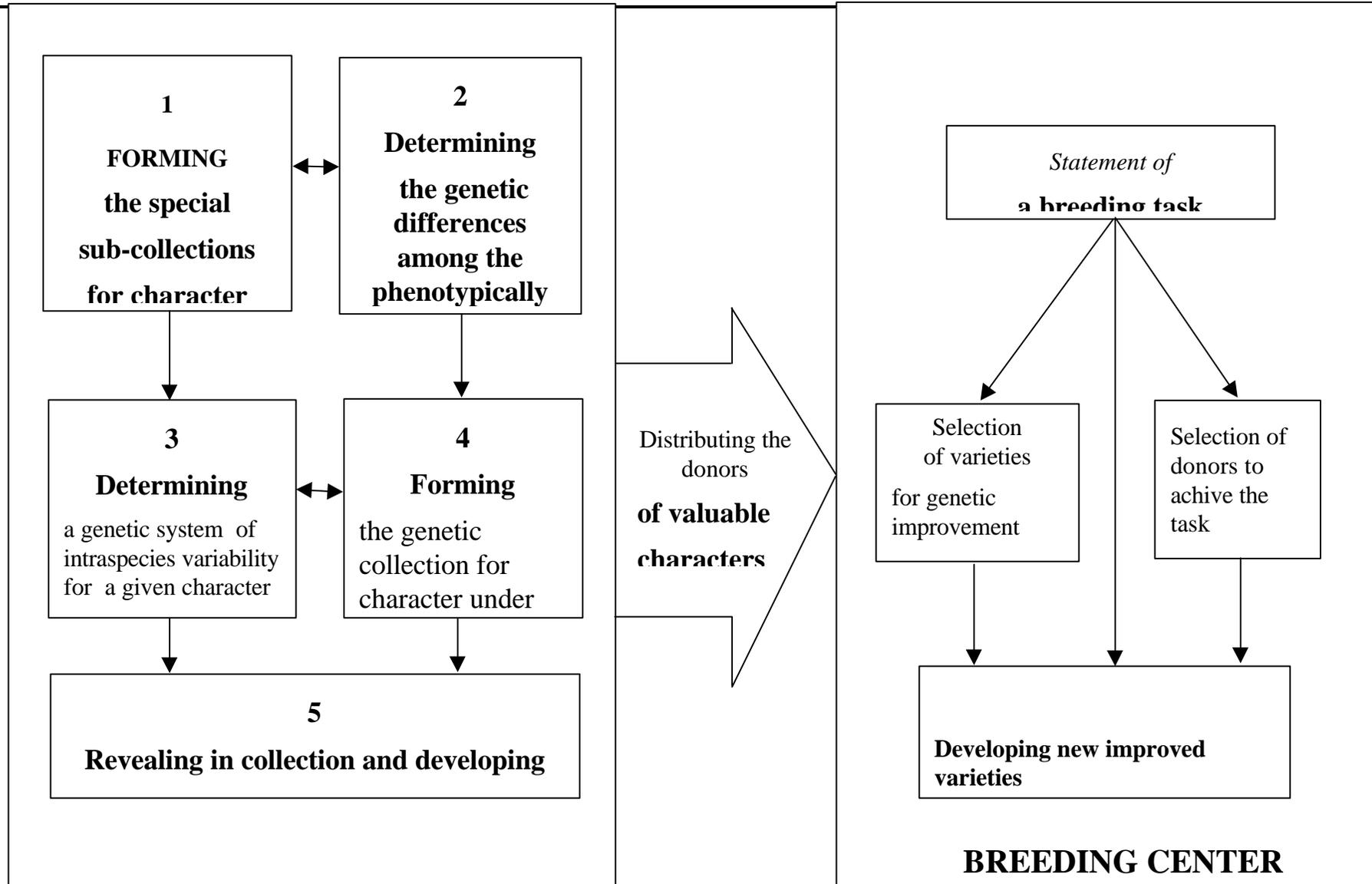


Figure 3. The search, development and use of donors of valuable characters

Levels of wheat germplasm diversity for providing the sustainable use of wheat GRFA

<p align="center">THE MEASURES TO PROVIDE THE SUSTAINABLE USE OF PGRFA (CGRFA/IUND/CNT: article 6bis)</p>	<p align="center">LEVELS OF WHEAT GERMPLASM DIVERSITY</p>		
	<p align="center">Species Gp1</p>	<p align="center">Genus (<i>Triticum</i> ssp.) GP2</p>	<p align="center">Related genera of tribe <i>Triticeae</i> GP3</p>
<p>(b) Strengthening research which enhances biological diversity by maximizing intra- and inter-specific variation ...</p>	+	+	
<p>(c) Promoting plant breeding efforts ...to develop varieties adapted to the various ... conditions, including in marginal areas</p>	+	+	+
<p>(d) Broadening the genetic base of crops and increasing the range of genetic diversity available to farmers</p>	+	+	+
<p>(e) Promoting the expanded use of local and locally adapted crops, varieties and underutilized species</p>	+	+	

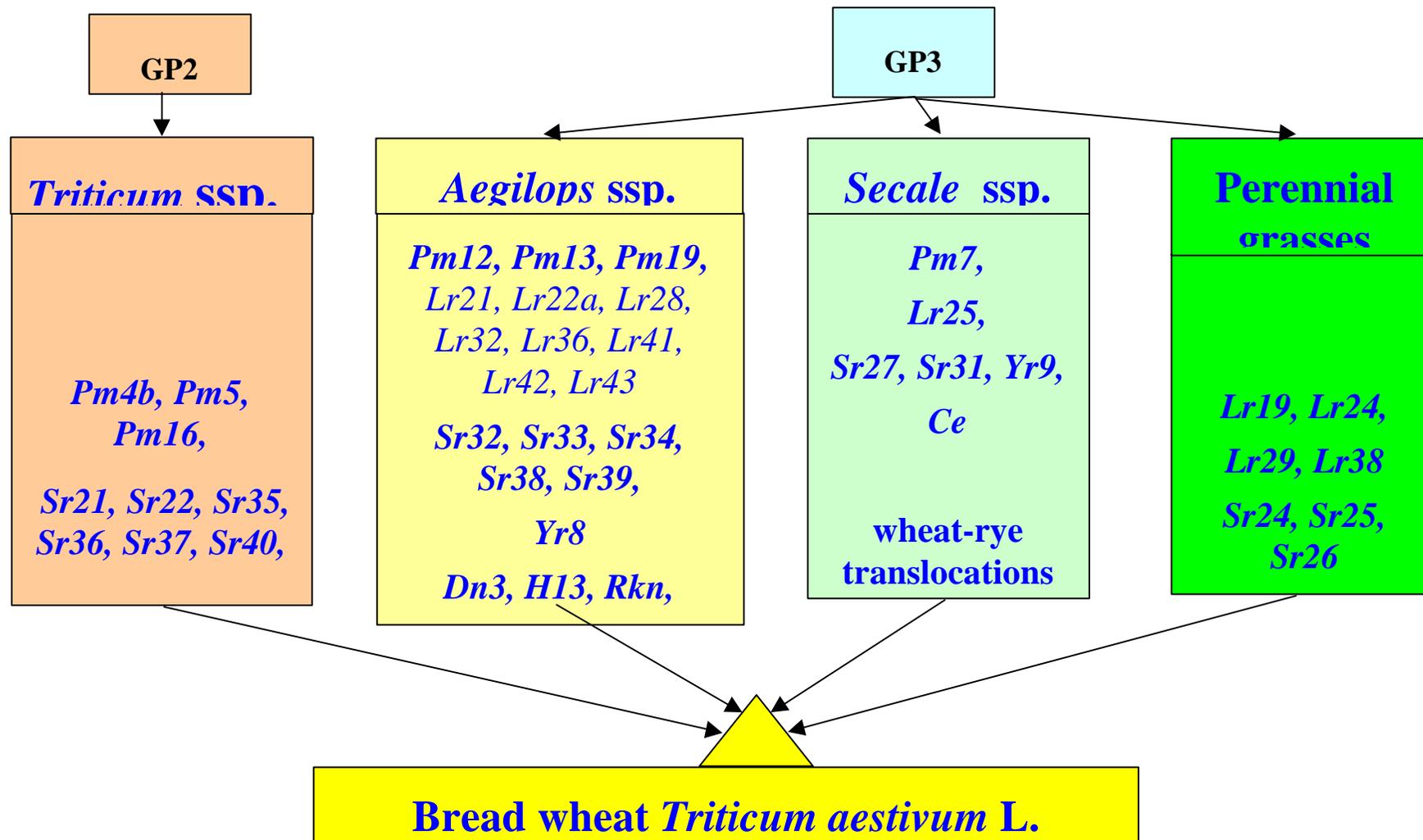


Figure 4. The genes introgressed in the bread wheat *Triticum aestivum* L.