

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

Fifth Extraordinary Session

Rome, 8 - 12 June 1998

**TECHNICAL ASPECTS INVOLVED IN DEVELOPING A LIST OF
CROPS FOR THE MULTILATERAL SYSTEM WITHIN THE REVISED
INTERNATIONAL UNDERTAKING**

The Fourth Extraordinary Session of the Commission on Genetic Resources for Food and Agriculture requested the International Plant Genetic Resources Institute (IPGRI), in consultation with the Commission's Secretariat, to prepare a study of the technical aspects of the *Tentative list of crops* annexed to Article 11 of the Consolidated Negotiating Text. This paper, supported by CGRFA-Ex5/98/Inf.1/Annex, which has been issued as a separate document, replies to that request.

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Tentative List of Crops (Extracted from the Annex to the Consolidated Negotiating Text)

TECHNICAL ASPECTS INVOLVED IN DEVELOPING A LIST OF CROPS FOR THE MULTILATERAL SYSTEM WITHIN THE REVISED INTERNATIONAL UNDERTAKING

EXECUTIVE SUMMARY

The Fourth Extraordinary Session of the Commission on Genetic Resources for Food and Agriculture, which met from 1 to 5 December 1997, developed a Tentative List of crops for a multilateral system of germplasm exchange. It was further agreed to request the International Plant Genetic Resources Institute (IPGRI), in consultation with the Commission's Secretariat, to prepare a study of the technical aspects of such a list.

The Tentative List identifies crops by common name and genus. This paper considers how one might specify, in technically acceptable terms, the crops which it is decided to bring within the multilateral system. In this context, it discusses the central role that taxonomy and the gene pool concept can play in identifying the content of crops listed.

Taxonomy provides a complete and effective way of describing plant germplasm which clearly delineates individual crops and provides an effective means of communication about plant genetic resources. There are international procedures and appropriate governing bodies, such as the International Union of Taxonomy, for defining this classification. It can develop to take account of new knowledge, and there are procedures for keeping track of changes and differences of opinion. There is also a considerable body of taxonomic literature in the form of scientifically recognized journals and compendia that permit adequate reference points.

Key units of classification for crop plants are **genus** and **species**. Plants of the same species are usually freely interbreeding and, for crops, the species often includes both the cultivated and, sometimes, the most closely related wild or weedy forms. The genus encompasses a varying number of related species including the crop species and its wild and weedy relatives. A number of considerations, such as the robustness of the classification, the importance of related species in crop improvement and crop plant evolution, indicate that the genus provides a useful basis for describing crop content in the Tentative List. Crop plant genera seldom change and, with a few exceptions, are well circumscribed and independent. There are cases where more than one genus is of relevance to the improvement of a crop, but these are well known and well described in the literature.

The **gene pool concept** allows users to recognize the total pool of genes in a related group of species that are potentially available for improvement of a crop species through hybridization. It reflects actual and potential geneflow in a crop and its botanical relatives. Three gene pools are usually recognized for a crop reflecting the ease with which crosses can be made and hybrids produced (designated primary, secondary and tertiary gene pools).

The gene pool approach describes the biological reality of what can cross with what, or how closely related is a particular wild species or species to the crop in question. It provides a functional way of describing relationships between crop species based on experimental results and takes account of the increasing importance of crop relatives in plant breeding.

Gene pool content is always relative to the crop under consideration and is a tool for identifying current breeding behaviour and inter-crossability. It reflects, in a dynamic way, the complex and interconnected relations between many of our crop species and their evolution from related ancestors. It has been applied to most crops and has proved its value in guiding crop improvement and conservation.

provides a framework for identifying or confirming the range of species to be included within any multilateral system. It provides an important experimental tool for confirming the validity of decisions made and for recognizing where more than one genus is important to the improvement of a crop.

While information on the particular genepools to which taxa belong is often limited, it is increasing all the time and new information can be integrated into existing frameworks of knowledge relatively easily. Furthermore, new information on taxonomic relationships is experimentally verifiable and can be confirmed by other workers.

Any methods developed should be precise, unambiguous, easily interpreted by different users and meet their needs. Updating to take account of new knowledge and changing patterns of use should be an in-built feature of any procedures adopted. A taxonomic framework should provide this and the evidence suggests that a genus-based classification may be the most appropriate. The genepool concept provides a way of confirming the appropriateness of using genus and a basis for extending crop groups beyond the genus in those cases where there is a clearly identified users' need or limiting the group within a genus if the particular genus is very large and varied. 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 and expert review and updating might also be needed.

TECHNICAL ASPECTS INVOLVED IN DEVELOPING A LIST OF CROPS FOR THE MULTILATERAL SYSTEM WITHIN THE REVISED INTERNATIONAL UNDERTAKING

I. INTRODUCTION

1. At the Fourth Extraordinary Session of the Commission on Genetic Resources for Food and Agriculture, which met from 1 to 5 December 1997, a tentative list of crops was proposed for a multilateral system of germplasm exchange. It was noted that the criteria that had been used to establish the Tentative List of Crops were (i) their importance for food security at local or global levels, and (ii) countries' interdependence with respect to plant genetic resources. It was further noted that "many countries proposed that, in any future development of the tentative list other additional criteria could be used."¹ It was agreed to request the International Plant Genetic Resources Institute (IPGRI), in consultation with the Commission's Secretariat, to prepare a study of the technical aspects of such a list.²

2. The Tentative List identifies crops by common names and genus. This paper considers how one might specify, in technically acceptable ways, the crops which it is decided to bring within a multilateral system of germplasm exchange. The objective is to identify suitable ways of defining the content of the Tentative List with respect to the crops and genera listed which is appropriate for a multilateral system of germplasm exchange (i.e. as applied to crops to which facilitating access will be agreed on the basis of agreed criteria established by the Commission).

3. Various ways of identifying plant groups can be identified which are relevant to the management of plant genetic resources. Initial analysis of different properties of plant genetic resources which might be relevant to determining crop units indicated that two key elements in determining content were taxonomy and the nature of the crop gene pools involved. These can effectively encompass most conservation and use aspects and therefore form the primary focus of this paper. Taxonomy is concerned with the classification of the different crops and the use of formal taxonomy in defining and describing them. The crop gene pool delineates the pool of genetic material potentially available for improvement or alteration of a crop.

4. In developing a list of crops for a multilateral system of germplasm exchange, governments will wish to be precise in the plant groups identified and included. A system is needed which can be easily and unambiguously interpreted, applied and updated. This paper describes how taxonomic knowledge and information on crop gene pools can provide effective procedures for delineating the material to be included under the crops listed. While the Tentative List identifies forages separately, they are considered together with crops, noting any particular factors which need to be considered in their treatment.

5. The primary concern is with procedures based on conventional methods of crop improvement that incorporate genetic material from species related to the crop plants through normal hybridization and selection. The treatment of crops therefore includes their wild relatives, reflecting the increasing use of such materials in crop improvement. The issues involved in the development and use of gene engineering methods lie outside the scope of this analysis.

¹ Report of the Fourth Extraordinary Session of the Commission on Genetic Resources for Food and

II. APPROACHES TO IDENTIFYING CROP CONTENT

II.1. The Taxonomy of Crop Plants

6. In the Tentative List, common names form the basis of crop identification with genera providing a necessary clarification. General descriptive terms and common names of crops can be confusing. It is therefore advisable to use common international procedures, and the taxonomic systems which have been developed using Latin are the most appropriate as they provide international translatability, and thus a common understanding. Indeed, formal taxonomic classification provides a complete and effective way of describing plants at the different levels. It is scientifically verifiable. There are international procedures and appropriate governing bodies, such as the International Union of Taxonomy, for defining this classification, for recording changes and tracking developments. Taxonomy provides an ideal way of communicating, while the literary framework permits researchers to follow changes and developments in the classification of species.

7. Individual groups at any level of taxonomic hierarchy are termed **taxa** and a number of different levels of taxonomic hierarchy can be identified which are relevant to the classification of crop plants. These are:

Family. A category comprising one or more genera or tribes of common phylogenetic origin, more or less separated from other such groups by a marked gap; the principal category between order and tribe (or genus). Thus, the family Leguminosae contains a number of important crops (*e.g.* peanut, chickpea, cowpea, bean, lentil pea, Faba bean, *etc.*) and crop genera.

Genus. A category comprising one or more phylogenetically related, and morphologically similar species; a rank in the hierarchy of taxonomic classification forming the principal category between family and species. A genus usually contains a number of species, for example the genus *Vigna* which includes cowpea and a number of other important crops (*e.g.* mungbean, Bambarra groundnut, black gram, *etc.*).

Species. A group of organisms formally recognized as distinct from other groups. Below genus in the system of classification it constitutes the basic unit of biological classification. It is normally used to define a group of fully interbreeding individuals. Thus, *Oryza sativa* (Asian rice) constitutes a species.

8. Below species are further levels of taxonomic classification of which the most important in describing and differentiating between different crops and different groups within a crop are Subspecies, and Variety.

9. Crop plants occur in different families, some of which contain many useful species while others contain only a few. The *Poaceae* (grass family) are especially important and include *Saccharum* (sugarcane), *Sorghum bicolor* (sorghum), *Oryza sativa* (rice), *Zea mays* (maize), *Triticum* spp. (wheat) and many more. Similarly, some genera contain many crop species, such as the genus *Brassica* (cabbages, rape and mustard), whereas others consist of only one crop, *e.g.* *Lens* (lentil) and *Cocos* (coconut). Of course, both families and genera may contain a large number of useful plant species which are not grown as crops but are important as medicinal species, for firewood, construction and many other purposes.

10. Crop plants are often classified taxonomically as species (*e.g.* *Pennisetum glaucum*, pearl millet; *Vigna unguiculata*, cowpea) but they are also sometimes classified as subspecies (*e.g.* *Zea mays* ssp. *mays*, maize) or even as varieties (*e.g.* *Brassica oleracea* L. var. *italica*, broccoli or calabrese). Thus in any list of crops one may find oneself operating at different taxonomic levels (*e.g.* see Box 1) and the genus usually provides the most convenient encompassing mechanism.

11. There is an increasing acceptance that the species should include all those taxa which are fully interfertile (the biological species concept). This has yet to be fully adopted in classifying crop plants, where wild and weedy taxa are often recognized as species even where they are fully fertile with the crop (*e.g.* *Lens culinaris* - lentil and its wild relative *Lens orientalis*). The importance of gene exchange is recognized in this approach to classification,

12. A frequently cited concern with taxonomy is that there are some groups of species, particularly cultivated ones, which have presented substantial difficulties in reaching an agreed and satisfactory classification. This is particularly apparent at the species level and below, and where crop plants are present in the taxa concerned. However, while it would be wrong not to recognize the complexities involved in classifying cultivated plants (see Box 1 - wheats), it should be emphasized that these largely occur at species level or below. The consensus of taxonomists today would be that appropriate taxonomic classifications can be reached, with the assistance of modern molecular and other methods.

Box 1: The taxonomy of different crops

Coconut: A crop that constitutes the only species in the genus			
Family: Palmae	Cultivated species: <i>Cocos nucifera</i> L.		
Exists in a wide range of wild and cultivated forms. The most likely region for domestication is Malaysia, on the coasts and islands between Southeast Asia and the Western Pacific.			
Chickpea: A crop with interfertile species in the same genus			
Family: Leguminosae	Cultivated species: <i>Cicer arietinum</i> L.		
The genus contains approximately 40 species. <i>C. reticulatum</i> was first found in SE Turkey in 1974 and is fully interfertile with the crop. While they are currently both given species rank, they may be the same biological species. Crosses between the crop and <i>C. echinospermum</i> are also possible. Other cross fertile groups exist within genus and many of the species possess potentially useful characters.			
Wheats: Crops in closely related species with a complex and related origin			
Family: Poaceae	Cultivated species ¹ :	hexaploid:	<i>Triticum aestivum</i> - bread wheat
		Tetraploid:	<i>T. turgidum</i> - durum wheat, emmer and others <i>T. timopheevi</i>
		Diploid:	<i>T. monococcum</i> - eikorn
Wild forms of diploid and tetraploid wheats occur and have been extensively used in breeding. The crops are taxonomically designated as varieties of the species. Three genomes (designated A, B and D) have been involved in the origin of bread wheats from both the <i>Triticum</i> and <i>Aegilops</i> genera. There are close relationships with a number of other genera (<i>Agropyron</i>, <i>Hordeum</i>, <i>Secale</i>, etc. which have been important in breeding and research.			

13. The taxonomy of crop plants becomes more robust and less problematic at higher taxonomic levels. For useful crop and forage species, the genus may be a particularly appropriate level of taxonomic hierarchy for describing the content of the crops which it is agreed to bring within the multilateral system. Crop plant genera very seldom change in the process of taxonomic revision and, where this has occurred recently (*e.g. Vigna*), it has made

no functional difference to the crop plants involved. In some cases, a genus includes a number of different crops (*e.g.* *Brassica* - oilseeds, vegetables and forage crops; *Allium* - onions, leeks, garlic, chives, *etc.*): these are often mutually important sources of useful characters and the whole genus provides a resource for workers on specific crops - a feature that is often reflected in the determination of gene pools.

14. There are a number of cases in which more than one genus is of relevance to the improvement of a crop but these are fairly circumscribed, easily identified and well known. Examples include the genus *Aegilops* which is a major contributor of useful genes to wheat (see also Box 1), the genus *Solanum* which has been used in tomato breeding and the Cruciferae genera (*Brassica*, *Raphanus*, *Sinapis*, *Eruca*, *etc.*) which have been intercrossed for crop improvement. In fact, in these cases, the genus is probably the appropriate functional level at which to operate, since utility and crossing relationships are generally reflected by the genus as much as by any individual pair of species.

15. Considerable taxonomic information exists on many temperate forage species, such as *Lolium* spp. (ryegrasses) and *Trifolium repens* (white clover), *Medicago sativa* (lucerne) and *Dactylis glomerata* (cocksfoot), but information and theory concerning tropical forages are only beginning to emerge. In fact, forage grasses have some unresolved taxonomic difficulties. There is large genetic variability within species and poor separation between species. In tropical grasses, this is reflected in considerable numbers of species occurring in a few genera. From a breeding and crop improvement point of view this is most useful, as it offers immense scope for further selection from natural populations, and relations between genera (as well as within them) will be important.

16. There are crops for which substantial taxonomic studies are still required (*e.g.* chicory, *Cichorium* spp.), but many of the major crops are well defined taxonomically, although molecular information will undoubtedly clarify a number of remaining difficulties. This is likely to be particularly true for clonally propagated species such as cassava and yams, which require better taxonomic definition and more studies on species relationships and intercrossability.

17. Different taxonomists do treat material differently, and over time classifications do change and evolve. There has been a tendency, in many cases, to reduce the number of recognized species (*e.g.* in *Sorghum*) and to combine crop species and their interfertile wild or weedy relatives into a single species. While it would be wrong to underestimate the taxonomic problems of some species groups, it is important to recognize that within taxonomy as a discipline, there are ways of dealing with these problems. Procedures exist for reaching international agreement and making accepted revisions. The system is such that changes in the classification can be followed, and accepted synonyms can be identified. Authorities and sources can be quoted to ensure clarity with respect to exchange of information and materials.

18. Broadly speaking, formal taxonomy provides a clear and effective way of identifying plant groups in ways that can be used in determining the content of the crops in any list. A scientific framework of study and description exists and ways of identifying and taking account of differences have been developed. There are a number of advantages in exploring whether the genus is the most appropriate level of operation for any descriptive system. It is fairly stable, encompasses most useful groupings and, where further definition is needed, this can often also be most usefully done at the genus level. However, it does not always fully reflect crossing relationships between plant groups that constitute crops and their useful relatives.

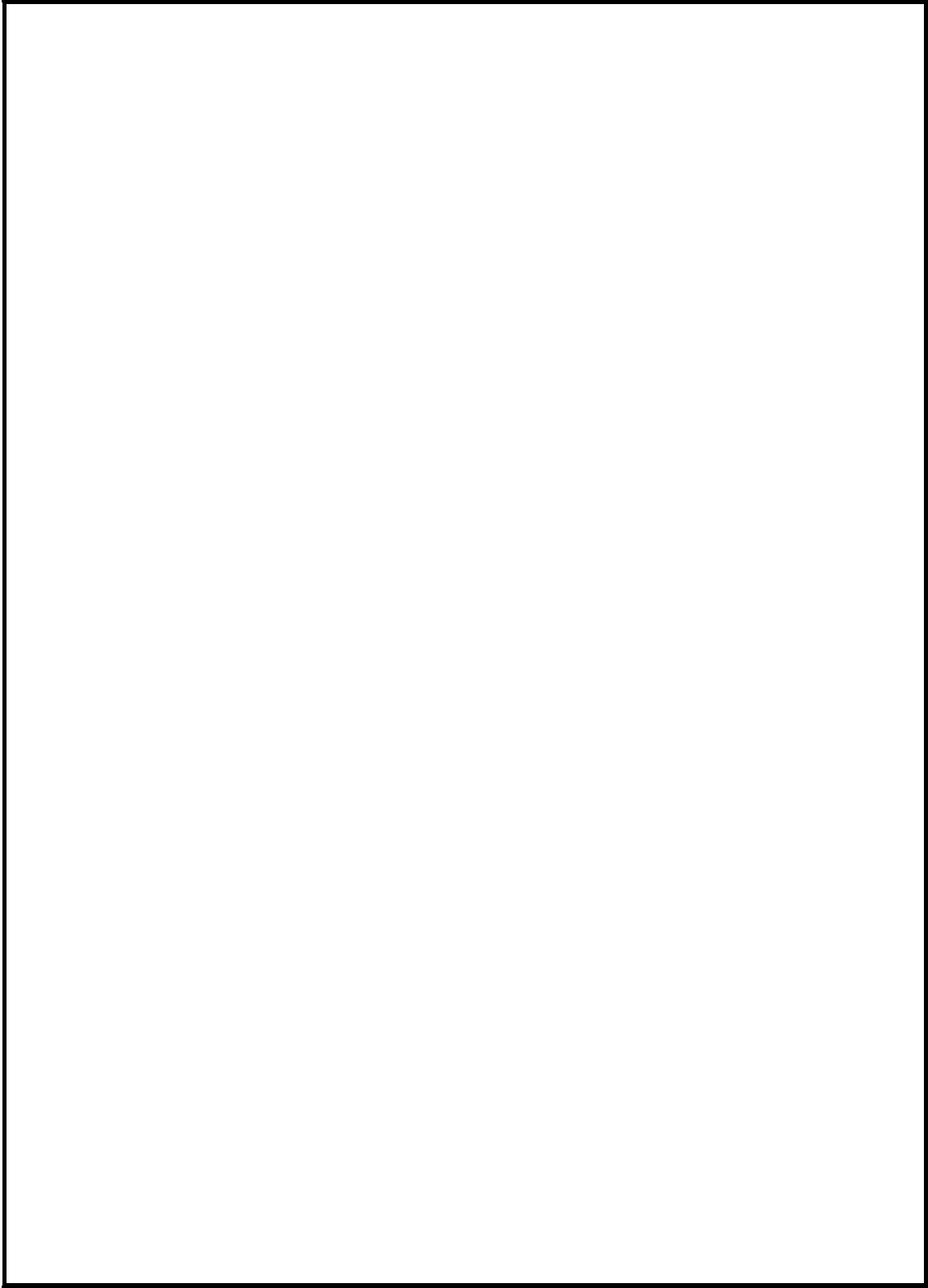
19. The genepool concept as developed by Harlan and de Wet¹ has found wide acceptance and application in plant genetic resources management. It complements formal taxonomy, allowing users to recognize the total pool of genes in a related group of species that are potentially available for improvement of a crop species through inter-taxa hybridization. Harlan and de Wet divided a crop's genepool into three categories: primary, secondary and tertiary, depending on the ease of natural (sexual) gene exchange.

The *primary genepool* (GP1) consists of the domesticated species plus those wild forms that are fully inter-fertile and hybridize readily with the domesticated species. The primary genepool corresponds to the traditional concept of the biological species. Within it hybrids are usually fertile, and gene transfer is easy.

The *secondary genepool* (GP2) consists of those biological species that can be crossed with the domesticated species using conventional breeding methods, to produce at least some fertile progeny. Gene transfer is possible but less easy, as many hybrids are sterile or difficult to bring to maturity.

The *tertiary genepool* (GP3) consists of those species that can be crossed with use of special techniques, such as embryo culture or tissue culture. Hybrids are usually completely sterile or non-viable, but gene transfer may be achieved or new amphidiploid species created.

20. The genepool approach has proved to be a remarkably effective and useful way of grouping related species and has been applied to nearly all crops. It describes the biological reality of what can cross with what, or how closely related is a particular wild species to the crop in question. It focuses on the potential for gene flow between related taxa and provides a functional way of describing relationships between crop species based on experimental results. In fact, a key feature of applying the genepool concept is that the results are experimentally verifiable and can therefore be confirmed by other workers. Thus, if a new species is used in crosses with a crop and progeny obtained, its genepool status is determined and can be independently verified. The crop genepool which incorporates the crop and its wild relatives has become an accepted focus for management and use of plant genetic resources which takes account of the increasing importance of crop relatives in plant breeding (see Box 2 for examples).



Genepool designation is complementary to taxonomic description. In part, this reflects the fact that crops are often classified at different levels (species, subspecies, variety). Generally the three genepools are included within the genus. Where this is not the case, the genepool description becomes particularly valuable in identifying where a genus-based designation of crop content will result in difficulties for users (as in the case of the intercrossability of some *Solanum* and *Lycopersicon* species).

22. By comparison with taxonomic classifications, the genepool description remains informal and to some extent subjective. Different authors vary with respect to the precise limits they put on different genepools, and GP3, in particular, is flexible defining the outer limits of genetic reach in breeding a crop. Current developments in biotechnology have provided for a major expansion in GP3 through the use of embryo rescue for interspecific hybrids. However, it remains an important way of identifying useful species with affinities to individual crops, which are of the first importance in crop improvement work.

23. The primary genepool of a crop includes the crop itself and those taxa with which it is fully inter-fertile. Gene flow between the crop and its close wild and weedy relatives often continues naturally (e.g. between pearl millet and its wild relatives and between maize and teosinte). A number of authorities regard this process as important in providing new sources of variation for local cultivars. As noted below, wild relatives of the primary genepool are also a major resource for plant breeders.

24. Genepool content is always relative to the crop under consideration. The species identified as belonging to the primary, secondary or tertiary genepool depend on the crop specified. Thus, wild *Secale cereale* forms part of the primary genepool of rye and the tertiary genepool of wheat. In practice, this is unlikely to cause difficulties so long as the point of reference is specified and the aim is to support effective use of the materials. It reflects the complex and interconnected relations between many of our crop species and their evolution from related ancestors under the management of farmers over many generations throughout the world. In this aspect, a description of the genepool content of a particular crop provides the additional information needed to complement a taxonomic description.

25. Genepool identities primarily reflect biological relatedness between taxa. However, they also depend on the nature of reproductive barriers between different taxa. These are usually broadly congruent, but significant differences may be observed between some genera or families. Thus, it has proved extremely difficult (if not impossible) to cross different *Vigna* species, even though they appear to be taxonomically rather closely related. In contrast, within the Cruciferae, species from different genera such as *Brassica* and *Raphanus* may be crossed relatively easily. Similarly, genepool descriptions do not necessarily fully capture evolutionary relationships between species and the complex aspects of hybridization and speciation that are part of crop plant evolution. Thus, the genepool concept complements rather than replaces taxonomic methods and evolutionary studies.¹

26. For many crops, reliable information about the content of the different genepools is limited. Often we have only a poor knowledge of the species that should be included within GPs 2 and 3 and, in a few cases, even our knowledge of GP1 is limited. This has limited practical significance in the context of the development of a multilateral system, provided that there is adequate provision to reflect our expanding knowledge. In fact, in this sense, one advantage of using the genepool concept to complement taxonomy is that it is based on experimentally documented results and that it can reflect the development of new knowledge and needs.

27. Lack of knowledge of the extent and content of different genepools is especially the case for forage species. The cultivars of tropical forage legumes are often ecotypes, which have been either collected from wild populations of the same species or derived from a breeding programme based on such collections. However, there are a number of cases where

¹ Molecular studies are adding substantial new information on these aspects, by allowing us to identify

information on gene pools exists and complements a taxonomic approach based on genera (as in the case of *Lolium* and *Festuca* crosses). A number of forage species and genera constitute part of the gene pools of arable crop plants and *vice versa* (e.g. *Agropyron* and wheat) and consistency in any listing is required to reflect this.

28. Crop wild relatives belonging to GP1, GP2 and GP3 are increasingly being used in crop improvement. Nearly all our major crops now include genes obtained from wild species and molecular genetic techniques are likely to facilitate the processes of identifying and transferring useful characters. Key characters obtained from wild relatives include many disease-resistance genes present in today's tomato cultivars, resistance to grassy stunt virus in rice (from *Oryza nivara* a GP1 relative of rice), nematode resistance in potato, disease resistance and protein quality in wheat and many more (Box 3).

29. In determining the content of any crop list, a reference to crop gene pools therefore provides an important framework for identifying the range of species that might be included. It provides an experimental tool for confirming the validity of decisions made, and a way of cross-referencing between crops to prevent limitations in availability that would run counter to the objectives of a multilateral system. It complements and informs taxonomic approaches, providing a practical way of determining taxa potential and utility.

Box 3: The use of the tomato gene pool

All gene pools have been used to improved cultivated tomatoes. Some of the major species used and characters they possess are:	
<u>Primary Gene pool</u>	
<i>L. pimpinellifolium</i> :	Resistance to the pathogens including <i>Fusarium oxysporum</i> ; <i>Cladosporium fulvum</i> , <i>Pseudomonas spp.</i> and <i>Verticillium datiliae</i> ; high fruit soluble solids and Vitamin C content; tolerance of high temperature.
<i>L. cheesmanii</i> :	Change to the pedicel (stalk of the individual fruit) for mechanical harvesting; thick skin, for transportation; tolerance to salinity from a wild tomato found on the shores of the Galapagos Islands.
<u>Secondary Gene pool</u>	
<i>L. hirsutum</i> :	Resistance to pathogens including Tobacco Mosaic Virus and <i>Cladosporium fulvum</i> ; more intense internal and external colour; higher beta-carotene (provitamin A) content; resistance to low temperatures.
<i>L. chmielewskii</i> :	Increased soluble solids.
<u>Tertiary Gene pool</u>	
<i>L. peruvianum</i> :	Resistance to pathogens such as <i>Fusarium oxysporum</i> , <i>Meloidogyne spp.</i> and <i>Cladosporium fulvum</i> ; higher vitamin C content; drought resistance.
<i>Solanum lycopersicoides</i>	Resistance to low temperatures.

III. CONCLUSIONS

30. This paper has reviewed some of the issues involved in using formal taxonomy and the gene pool concept in specifying the crops for a multilateral system of germplasm exchange in a technically acceptable way. It has been suggested that these two elements are of greatest direct relevance to the definition of crops, and that other aspects such as conservation

method, germplasm use patterns or other methods of classifying plant genetic resources can be effectively integrated into a framework based on them.¹

31. Taxonomic procedures provide an effective and internationally accepted way of describing crops and their relatives. While different experts may have very different views on specific classifications, there is a clear framework for expressing, considering and ultimately resolving any differences. Taxonomic classification to the level of *Genus* is robust and easy to apply in the context of the Tentative List. *Variety* and *species* may change and their classification can differ according to different authors. But, at the genus level changes are not common and, even when they do occur, can be effectively integrated into existing practices². The genus level of classification may therefore be particularly useful for specifying crops in a technically acceptable way. It also allows the importance of interspecific gene flow to be fully reflected.

32. The genepool concept provides a valuable and practical way of describing the related groups of taxa that may be useful for improving a crop. It complements but does not replace formal taxonomy. Information on the particular genepools to which taxa belong is often limited but is increasing all the time and new information can be integrated into existing practices relatively easily. Furthermore, new information on taxa relationships is experimentally verifiable and can be confirmed by other workers.

33. There is an increasing use of the total genepool in crop improvement and this is likely to continue. Already GP3 species have donated essential characters in crops such as tomato and wheat. It has to be concluded that an inclusive approach is likely to be increasingly important to maintaining rates of yield increase and ensuring food security. It is also clear that prediction of the source of future useful traits is very uncertain. There is good reason to include all potentially useful germplasm as part of the crop, as has been amply demonstrated from past crop improvement work.

34. Taking into account the biological and technical aspects of identifying the content of the crop units, the Commission may wish to establish a series of general principles that can be used to define the crop units. From the information presented in this paper it is suggested that these principles should involve the use of a taxonomic approach, focusing on an identification of genera to be included for a multilateral system, complemented by a use of genepools to ensure the inclusion of taxa identified as coming within GP1, GP2 and GP3. It is likely that technical experts in various crops will be needed to develop the appropriate detailed descriptions. They should also be able to advise on the few cases where more than one genus should be considered (*e.g. Triticum* and *Aegilops* in the case of wheat). An examination of congruence between forage and arable crop genera listed would also be required (*e.g. Vicia* crop and forage species).

35. It is essential to recognize that any system developed needs to be able to be modified as knowledge improves and as technologies and patterns of use change. Crop-based expertise may be needed to review developments on an occasional basis to take account of new molecular genetic information and new needs for specific production characteristics. While the nature and problems of defining crop units are many and various, they are not insoluble and procedures can be developed which are flexible and evolving, and based on available biological knowledge.

¹ Some account may need to be taken of other features such as species rarity: thus, endangered species may be subject to restrictions, as a result of national legislation or CITES regulations limiting movement. These will be fairly uncommon and are probably best dealt with on an individual case-by-case basis.

² A recent example involves the redesignation of the genus *Vigna* by Marechal in 1978.

APPENDIX

Tentative List of Crops (Extracted from the Annex to the Consolidated Negotiating Text)¹

<u>Common name</u>	<u>Genus</u> ²	<u>Common name</u>	<u>Genus</u> ²
Rice	<i>Oryza</i>		<i>Agrostis</i>
Oats	<i>Avena</i>		<i>Alopecurus</i>
Rye	<i>Secale</i>		<i>Andropogon</i>
Barley	<i>Hordeum</i>		<i>Arrhenatherum</i>
Millets	<i>Pennisetum</i>		<i>Axonopus</i>
	<i>Setaria</i>		<i>Brachiaria</i>
	<i>Panicum</i>		<i>Bromus</i>
	<i>Eleusine</i>		<i>Bothriochloa</i>
	<i>Digitaria</i>		<i>Cenchrus</i>
Maize	<i>Zea</i>		<i>Chloris</i>
Sorghum	<i>Sorghum</i>		<i>Cynodon</i>
Wheat	<i>Triticum</i>		<i>Dactylis</i>
Peanut	<i>Arachis</i>		<i>Elymus</i>
Cowpea	<i>Vigna</i>		<i>Festuca</i>
Pea	<i>Pisum</i>		<i>Hyparrhenia</i>
Beans	<i>Phaseolus</i>		<i>Ischaemum</i>
Lentils	<i>Lens</i>		<i>Lolium</i>
Soybean	<i>Glycine</i>		<i>Melinis</i>
Potato	<i>Solanum</i>		<i>Panicum</i>
Sweet potato	<i>Ipomoea</i>		<i>Paspalum</i>
Yams	<i>Dioscorea</i>		<i>Pennisetum</i>
Cassava	<i>Manihot</i>		<i>Phalaris</i>
Bananas, plantains	<i>Musa</i>		<i>Phleum</i>
Citrus	<i>Citrus</i>		<i>Poa</i>
Sugarcane	<i>Saccharum</i>		<i>Schizachyrium</i>
Beet	<i>Beta</i>		<i>Setaria</i>
Pumpkins, squashes	<i>Cucurbita</i>		<i>Themeda</i>
Tomato	<i>Lycopersicon</i>	Legumes (<i>Leguminosae</i>)	
Coconut	<i>Cocos</i>		<i>Aeschynomene</i>
			<i>Alysicarpus</i>
Tannia	<i>Xanthosoma</i>		<i>Arachis</i>
Taro	<i>Colocasia</i>		<i>Bauhinia</i>
Cabbages, rape, mustards	<i>Brassica</i>		<i>Calopogonium</i>
Onion, leek, garlic	<i>Allium</i>		<i>Canavalia</i>
Chickpea	<i>Cicer</i>		<i>Centrosema</i>
Faba bean	<i>Vicia</i>		<i>Clitoria</i>
Pigeon pea	<i>Cajanus</i>		<i>Coronilla</i>
Melons	<i>Cucumis</i>		<i>Desmodium</i>
Flax	<i>Linum</i>		<i>Dioclea</i>
Sunflower	<i>Helianthus</i>		<i>Galactia</i>
			<i>Indigofera</i>
Cotton	<i>Gossypium</i>		<i>Lablab</i>
Oil palm	<i>Elaeis</i>		<i>Lathyrus</i>
			<i>Lespedeza</i>
Forages			<i>Leucaena</i>
Grasses (<i>Gramineae</i>)			<i>Lotus</i>
	<i>Agropyron</i>		<i>Lupinus</i>

¹ Reproduced from the Report of the Commission on Genetic Resources for Food and Agriculture, Fourth Extraordinary Session, Rome, Italy, 1-5 December 1997.

² Genera are indicated only to clarify to which genus a particular crop belongs.

Macropitium
Medicago
Melilotus
Neonotonia
Onobrychis
Pueraria
Stizolobium
Stylosanthes
Teramnus
Tephrosia
Trifolium
Trigonella
Vetiveria
Zornia

