Report on an ECP/GR meeting of a task force on a *Beta* core collection

held at Cappelle-en-Pévèle (France)

on 30 September, 2000

BACKGROUND

One of the first tasks undertaken by the World *Beta* Network, after it was formed in 1989 as one of the IBPGR crop networks, was the development of an International Database for *Beta* (IDBB). It was felt that the collation, analyses, and dissemination of information through a centralized database was essential in the development of a viable World *Beta* Network (WBN). Since 1989, the BAZ Gene Bank has provided the acting secretariat of the WBN and has managed the IDBB within the framework of the German-Dutch cooperation on plant genetic resources.

In 1995, the BAZ Gene Bank developed a core collection for the genus *Beta* that is composed of accessions from the various national holdings documented in the IDBB – e.g., a "Synthetic *Beta* Core Collection" (SBCC). This core collection, currently, is being used as the working collection within the framework of the EU *Beta* project GENRES CT95 42, which ends on 28 February, 2002. Characterization, evaluation and molecular marker data recorded by project partners will be documented in the IDBB and will be available to analyse the current composition of the SBCC.

At the same time, national curators in the USA, Greece and Russia have started to create their own national core collections, which are not necessarily fully congruent with the core collection developed for the EU project. To maximize the use of an international *Beta* core collection, the development and organization of that collection must be done in conjunction with national collections so that entries from the national collections overlap those of the synthetic core collection.

During the first meeting of the ECP/GR *Beta* working group in Broom's Barn (UK) in 1999, there was a recommendation to establish a task force to review the core collection proposed by the BAZ Gene Bank, to further develop it and bring it into harmony with the various national core collections. Drs. B. Ford-Lloyd (U.K.), L. Frese (Germany), L. Panella (USA) and A. Tan (Turkey) agreed to participate in the task force and to organize a task force meeting in conjunction with the 'Study Group for Breeding and Genetics' of the International Institute of Sugar Beet Research (IIRB).

L. Frese submitted a project proposal to the ECP/GR, which was approved. He was charged by the ECP/GR with the implementation of the meeting on June 30, 2000.

REPORT

The task force members Dr. B. Ford-Lloyd (United Kingdom), Dr. L. Frese (Germany), Dr. L. Panella (USA), and Dr. A. Tan (Turkey) convened at the facilities of the Florimond Desprez, a seed production company, on the morning of September 30, 2000. L. Frese opened the meeting, welcomed the participants, and the draft agenda was accepted. L. Frese agreed to take notes and L. Panella offered to assist in writing the report. L. Frese detailed the task of the group and opened the discussion. The discussion, and this report, was divided into two major themes, the **development** and the **management** of the planned core collection.

CORE COLLECTION DEVELOPMENT

1. Review of the grouping and sampling strategies applied by curators, the structure, and the size of existing core collections

Reports on five *Beta* core collections exist. Detailed information is available on the Synthetic *Beta* Core Collection (SBCC) developed for evaluation purposes, the USDA/ARS *Beta* core collection and the *Beta* core collection of the VIR at Saint Petersburg. The structure of the *Beta* core collection of the Greek Gene Bank is unknown and will be investigated. The Plant Genetic Resources Institute of AARI (Turkey) will develop a *Beta* core collection within a new project.

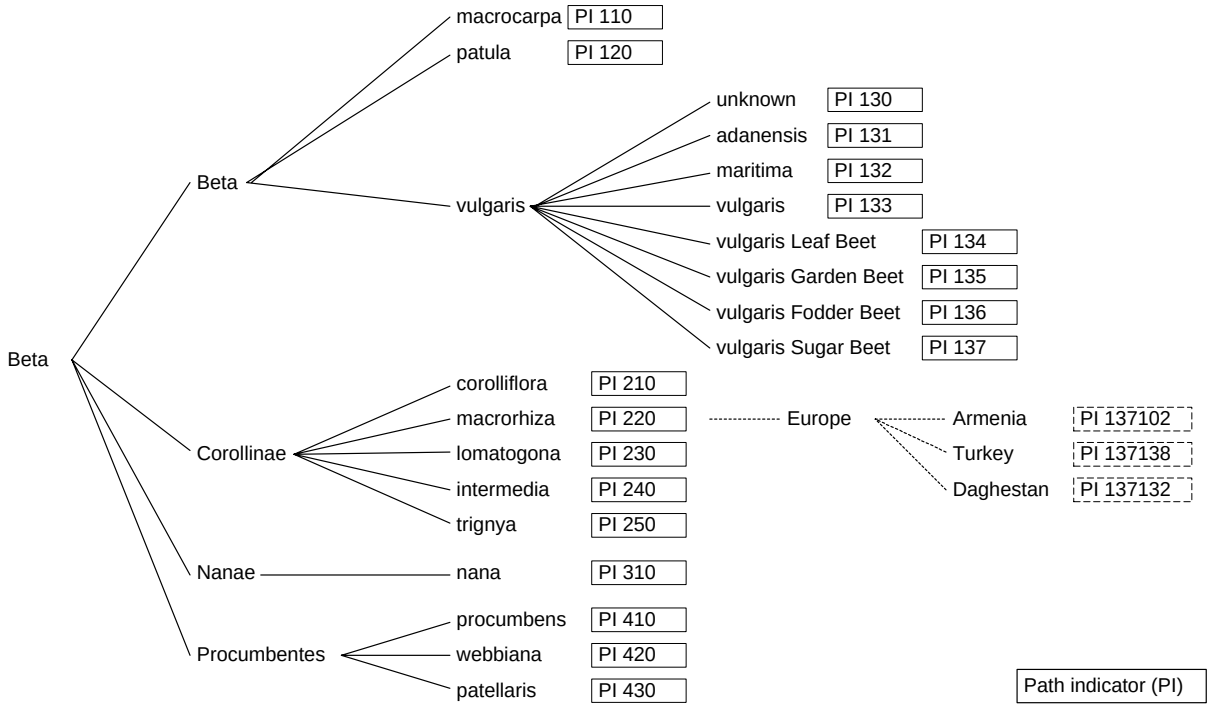
A. Synthetic *Beta* Core Collection

Within a large genetic resources collection it is desirable capture the majority of genetic diversity in a subsample of the entire collection. Frankel (1984) suggested developing core collections that would represent, with minimum repetitiveness, the genetic diversity contained in a collection. Core collections have been developed for many crops to improve the efficiency of germplasm screening procedures (van Hintum, 1999). Molecular Data (RFLP, PCR-based, and DNA sequence), morphological, yield and quality characters have been used to generate cluster analyses of *Beta*. The resulting dendrograms show that the genetic diversity of the genus *Beta* can be described well as an hierarchical tree. Classical taxonomists (e.g. Buttler, 1977) subdivide the genus into four sections, the 'main branches' of the diversity tree. Molecular marker investigations (Jung et al., 1993; Shen et al., 1998) of the genetic relationship among sections are very much in agreement with classical taxonomy. The genetic diversity within each section of the genus *Beta* is organised like side branches of a tree. Wild species in *Beta* section Beta (Letschert, 1993) have been divided into species and subspecies by means of morphological characters and allozymes. Cultivated material in the species, *B. vulgaris*, forms four groups (Lange et al., 1999), within which individual hierarchical classification of accessions is also possible. This is in agreement with studies of Holland (1956) and (Michalik et al., 1998) using morphological traits, yield trait components and RAPD markers. Further divisions into origin region and origin country within an individual side branch produce a more complex diversity tree (as proposed in Figure 1 below). The list of selected Synthetic *Beta* Core Collection accessions is presented in Appendix 1.

B. USDA-ARS National Plant Germplasm System (NPGS) *Beta* Core Collection

In 1999, as a response to the Sugarbeet Crop Germplasm Committee and the other beet researchers in North America, a *Beta* Core Collection was developed from the NPGS Plant Introduction collection as a first attempt to develop a usable subset for evaluation and phylogenetic research purposes. The *Beta* core collection was derived from *Beta vulgaris* ssp. *vulgaris*, and *Beta vulgaris* ssp. *maritima* only, and separate *Beta* core collections were derived, one from each species. In the development of these cores two different sets of selection criteria were used to stratify the accessions within these taxa. Therefore, the USDA/ARS Beta core collection is limited to the species *B. vulgaris* (wild and cultivated types). One hundred and ten accessions (Appendix 2) were selected randomly representing 10 % of the total USDA/ARS *B. vulgaris* holding. By chance, 18 of these accessions match accession numbers contained in the SBCC.

Figure 1. The SBCC was developed based on the "diversity tree" (see Boukema et al., 1997) of the genus *Beta*. Taxonomic and geographic information, as well as curator knowledge (i.e. information on genetic distances among groups of material within a species or information on the occurrence of resistance genes in specific geographic areas) was used to select individual entries from the world *Beta* holding. The SBCC consists of all taxa except for *B. nana* When selecting individual accessions from the world Beta holding a very low weight was given to sugar beet accessions, the target group for base broadening efforts. The final size and structure of the SBCC was determined by the maximum evaluation capacity of project partners charged with screening for disease resistance and the seed availability. The SBCC consists of 805 accessions (Appendix 1). The path indicator method was applied for preliminary analysis of the SBCC. The percentage of accessions represented in the SBCC compared to the total number of accessions present in the world holding varies between 2 % (sugar beet) up to 27 % (*Beta corolliflora*).



Beta vulgaris* ssp. *maritima

1. Breakdown by ecogeographical region (Table 1).
   A. Mediterranean
   B. Norther European
   C. Transition Zone (France)

2. Random selections were made from each of these regions to achieve the 10% target representation.

Table 1 The *Beta* Core Collection containing *Beta vulgaris* ssp. *maritima* germplasm is made up from the germplasm representing the countries below.

Country	Number of Accessions in NPGS *Beta* collection	Number of Accessions in *Beta* Core collection	Country	Number of Accessions in NPGS *Beta* collection	Number of Accessions in *Beta* Core collection
Belgium	3	1	Israel	1	1
China	1	1	Italy	101	10
Cyprus	1	1	Netherlands	2	1
Denmark	24	2	Poland	1	1
Egypt	26	3	Portugal	6	1
FSU	1	1	Spain	12	1
France	148	15	Tunisia	1	1
Germany	3	1	Turkey	4	1
Greece	50	5	U.K.	115	12
India	1	1	USA	20	2
Ireland	46	5	Yugoslavia	1	1
Total	304	36		264	32

Beta vulgaris* ssp. *vulgaris – *Beta* Core Collection

1. First breakdown was by beet type or use type (Table 2).
   - A. Sugar Beet
   - B. Leaf Beet
   - C. Fodder Beet
   - D. Table Beet

2. Secondly, for those accessions from outside the U.S., within each type, breakdown was by ecogeographical region.
   - A. Mediterranean
   - B. Norther European
   - C. Transition Zone (France)

3. Random selections were made from each of these regions to achieve the 10% target representation.

Table 2 Core collection of *Beta vulgaris* ssp. *vulgaris*. Selected from the NPGS collection at the Western Regional Plant Introduction Station, Pullman, WA.

End Use	Number of Accessions in NPGS Beta collection	Number of Accessions in Beta Core collection
Leaf Vegetable	78	8
Root Vegetable	61	6
Root/leaf Vegetable	24	2
Fodder	105	11
Sugar Extraction	134	13
Biomass	15	2
Total	**417**	**42**

The following countries are represented: Afghanistan, Canada, China, Ethiopia, FSU, India, Iran, Lebanon, Poland, Sweden, Syria, Turkey, U.K., USA, Yugoslavia

Note: A large portion of the collection is composed of germplasm developed by U.S. breeders and deposited into the GRIN system. A coordinated effort is being made to develop a scheme to weight the U.S. gene pool using known pedigree information because this group is heavily represented in the sugar beet germplasm.

C. VIR Beta core collection

The *Beta* collection was grouped into the various taxa and further subdivided into wild, primitive or transient types, landraces, old local varieties and modern varieties. A typical accession of each group was selected as 'base' accession. As there is a high within group variability descriptive data were used for cluster analysis. Within each group accessions were compared to the 'base' accession and selected according to the similarity level. Accessions with very specific characters like cytoplasmic male sterility, monogerm seeds, tetraploid germplasm completed the choice (Burenin, 1999).

The core collection consists of 189 accessions of which 27 accessions belong to the SBCC by chance (Appendix 3, SBCC accessions are indicated by '+').

2. Rational of an International *Beta* Core Collection

The rationale for the need of *Beta* core collections was reviewed. It was decided by the taskforce to pursue and promote the international approach. The taskforce recommends that an 'International *Beta* Core Collection' (IBCC) be developed. We felt that an IBCC would:

- represent the diversity of the genus *Beta* better than any national effort alone could achieve alone.
- improve access to a defined set of entries held within a network of decentralised *Beta* holdings through a central database.
- facilitate and promote the use of genetic resources collections.
- provide the best standard set of entries for biosystematic research.
- improve access to information on core collection accessions through a central database

3. Definition of the domain of an IBCC

The section Beta is the domain in the case of the USDA/ARS core collection, and the cultivated species the domain for the VIR *Beta* core collection. In contrast, the SBCC comprises all species and sections except for section Nanae. The question was raised whether the IBCC should be restricted to section *Beta* (cultivated forms and related wild species) or should encompass the whole genus *Beta*. It was noted that the sections *Corollinae, Nanae* and *Procumbentes* contain valuable genetic variation but, due to technical problems (hard-seeded fruits) and crossing barriers between section *Beta* and sections *Corollinae, Nanae* and *Procumbentes*, utilisation of the germplasm is still difficult. Furthermore, breeders only

recently have started to fully exploit section *Beta* for broadening the genetic base of the sugar beet crop. The participants suggested that section *Beta* should be the priority domain of the IBCC. This does exclude the development of a small core collection of sections *Corollinae, Nanae* and *Procumbentes* for research purposes.

4. Improvement of existing core collections

A. Use of characterisation and evaluation data

A Large characterisation data set has been recorded on the US *Beta* collection and is available documented in the GRIN (Genetic Resources Information Network) database. Similar data were also taken on the collection of the BAZ Gene Bank and on the SBCC accessions used in the GENRES CT95 42 project. Additional data may exist in other national documentation systems and these data should be collated in the central crop database, the IDBB. L. Frese related to the group that the BAZ database manager, C. Germeier, recently visited the USDA-ARS station in Beltsville, MD, where the GRIN database is maintained. They discussed the issue of data transfer from GRIN to the IDBB. C. Germeier also noted that the final, consolidated sets of GENRES evaluation data will be sent by project partners to the IDBB in late 2001. Once the data are received, the SBCC can be analysed statistically to characterize the structure of genetic diversity present. Based on the results of the analyses, the size and structure of an IBCC can be recommended. It was suggested to develop the IBCC by applying the diversity tree concept. In the case of the SBCC, the end points of the diversity tree described by path indicators culminate at the level of collection sites. Breaking points determined by the sample status (landrace, variety, breeding line, etc.) could help refine the core collection.

B. Use of molecular marker data

Molecular markers have been used by several researchers (for example Jung et al. 1993, Letschert 1993, Kraft et al. 1997, Shen et al. 1998, McGrath et al. 1999). Only Michalik and co-workers (1998) recorded molecular marker data together with agronomic characters and made suggestions for a 'Garden Beet' core collection based on both sets of characters. B. Ford-Lloyd noted that new AFLP data are currently generated within the framework of the GENRES CT95 42 project on nomenclature duplicates; the duplicate group itself is sometimes represented by its 'most original accession' in the SBCC. He suggested to use the AFLP data for the enhancement of the SBCC. Of particular interest for the decision making process is knowledge on the within accession variability in relation to the between accession variability in beet species. B. Ford-Lloyd noted that a population of *B. vulgaris* subsp. *maritima* growing in southern England is known to represent the majority of all genetic diversity occurring in English populations. If it can be assumed that a large fraction of genes and alleles present in an individual accession also are shared by many accessions, there would be important implications for the design of the IBCC. Instead of the 805 accessions selected for the SBCC, a limited set of accessions might suffice to represent most of the genetic diversity present in an out-crossing *Beta* species. However, sufficient and detailed information is still lacking, and investigations of the *Beta* species with molecular markers will certainly help to elucidate the structures of genetic diversity. A research project perhaps could be submitted within the 5th framework programme of the EU (deadline mid February, 2001). The preparation of the 6th framework programme has started recently and very probably will allow research on biodiversity aspects.

It was also reiterated that the IBCC should not be developed from scratch but the SBCC used as a starting point. There should be a stepwise improvement as more characterisation, evaluation and molecular marker data become available through the GENRES CT95 42 project initially and other evaluation projects of accessions in other genebanks. It was recommended that the improvement of the core collection be considered a dynamic process, which underscores the need for continued communication among curators and gene bank managers.

C. Use of pedigree data

It was noted that little is known about the existence of pedigree data. Some information is perhaps available in the USDA/ARS system. Where it is available, it can be useful in predicting the genetic relationships among accessions representing germplasm that has undergone some level of commercial genetic improvement.

D. Use of curators knowledge

L. Frese and L. Panella brought up the important role in the decision making process that the curators knowledge could play in helping to determine entries for a core collection. If still available, knowledge on the breeding history of landraces and early open-pollinated varieties could also be used. A. Tan reported that, in Turkey, narrative on the local use of germplasm is being collected and documented. This knowledge can be invaluable in the development and improvement of a core collection.

CORE COLLECTION MANAGEMENT

1. Recommendation for technical management procedures

The structure of the *Beta* core collection of the Greek Gene Bank is unknown and will be investigated.

The task force recommends that an 'International Beta Core Collection' (IBCC) be developed.

A. Maintenance

L. Panella noted how critical this matter is and suggested that it be discussed during the next ECP/GR *Beta* working group and World *Beta* Network meeting. Because seed samples of the international *Beta* core collection will be maintained in a network of decentralized *Beta* germplasm holdings, curators of these individual holdings need to guarantee sufficient seed stock, unrestricted access to these entries, and seed shipment within a reasonable time period after receipt of a users request. In addition, a core collection is not expected to remain static over time. Accessions may be removed from or added to the core collection, it is crucial that evaluation data be shared to help in these decisions. For these reasons it is crucial that the genebanks involved be willing to cooperate, and, therefore, one of the first steps needs to be getting agreement from the curators of collections involved that they are willing and able to participate. If they are not, then duplicate samples can be obtained and maintained by one of the other participating genebanks.

L. Frese noted that the ECP/GR *Beta* working group recommended the development of a system of sharing of responsibilities for conservation and suggested that the responsibility for maintenance of core collection entries could be linked to it. He further explained that

all SBCC samples have already been earmarked within the IDBB. Therefore, the IDBB can serve as a central technical management tool. Since it is not possible to charge a single institution/genebank with the maintenance and distribution of core collection samples the work load must be shared. L. Panella noted seed multiplication capacity could be found in the USA for such an important project and offered to assist curators in maintaining IBCC accessions.

Also noted was that, in some countries, the genus *Beta* is not a priority species, though the country itself forms an important part of the natural distribution area and is sheltering a high diversity of cultivated and wild types (for instance, the Iberian peninsula and the Canary Islands). How, under such circumstances, maintenance of wild and cultivated germplasm (the international interest) can compete with the national priority crops still remains to be answered.

The question of whether we should try to maintain a core collection similar to the barley core collection in parallel to the original collection was raised again. The group voted against this concept since it would reduce variability within core collection entries and would increase maintenance work considerably. Members of the taskforce pointed out that self-pollinated crop species and cross-pollinated species must be handled differently.

A quite interesting discussion ensued on the maintenance of core collection entries of sections *Corollinae, Nanae* and *Procumbentes*. Of particular interest are the species of section *Corollinae* and *Nanae*, which are not at all adapted to the climate in Central Europe or in the USA. If grown in an alien environment, a strong selection pressure might very well favour genotypes most adapted to genebank management practices rather than maintain the population's natural diversity. For these species, *in situ* management of the species really would complement *ex situ* management practices (which guarantee ready access to germplasm for research purposes).

To underline the importance and function of *in situ* management programmes it was suggested to add a database module for *in situ* managed populations / sites of *Corollinae, Nanae* and *Procumbentes* species to the IDBB, and to earmark the accessions as core collection entries. Hopefully, this would strengthen national *in situ* programmes because the international user community would stress the concern for genetic resources maintenance and the scientific and economic need for *in situ* management of species and specific populations. A. Tan supported this idea and recommended using official channels to approach the institutions, local communities, or persons involved in *in situ* management of *Beta* species or of sites sustaining *Beta* populations.

B. Information management and access to IBCC entries

The dynamic nature of the core collection requires that functional information exchange mechanisms be established among curators responsible for entries from their national collections that are part of the international synthetic core collection. Data on IBCC entries needs to be provided by national genebanks to the IDBB. Through this focal point, information any user will have access to IBCC seed and the data linked with it. The IDBB and IBCC manager will function as an information and germplasm broker. Through routine inquiries the IDBB/ IBCC manager will update information on seed availability.

C. Duplication backup of IBCC

The taskforce felt that it would be a good idea to backup the entire IBCC as a unit. This should probably be done at two locations because any one location that would act as a backup would also probably have a portion of the collection from their genebank. Lee Panella offer the USDA – ARS National Seed Storage Laboratory as available for backup.

Recommendations for follow-up and assignment of tasks

- Initiate discussion on the need for *in situ* management programmes for sections *Corollinae, Nanae* and *Procumbentes*. Where possible link existing programmes with the in situ / on farm management of wild and cultivated material of section *Beta*.

- Organise supporting letters from IPGRI and the IIRB and inform co-ordinators of national genetic resources programmes on the need for specific *in situ* management activities in I. Refer to the GPA and the Bern convention (in the case of *Nanae* and *Procumbentes*).

- Find a mechanism to help encourage users to return characterisation and evaluation data to national genebanks.

- Acquire data from national genebanks and, if appropriate, analyse them together with GENRES CT95 42 data. Exploit data to improve the IBCC.

- Provide national genebanks through the national focal points with the complete list of IBCC entries ordered by origin country.

- Contact curators of national *Beta* collections and inform them on the existence and function of the IBCC.

- Ask curators whether they are prepared and able to accept maintenance responsibility for IBCC entries.

- Inform curators that the number of seed requests for IBCC entries may increase and make sure that the IBCC accessions are maintained using the best practices.

- Stress the importance of base and safety duplicate samples.

7. Closing of the meeting

The meeting was closed at 12.30 h.

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