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INFORMATION HANDLING SYSTEMS FOR GENEBANK MANAGEMENT

PROCEEDINGS
of a Workshop held at the Nordic Gene Bank
Alnarp, Sweden
21-23 November 1984

J. Konopka and J. Hanson (eds.)

IBPGR Secretariat
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INTRODUCTION

1. Following the endorsement by the IBPGR of a recommendation of the IBPGR Advisory Committee on Seed Storage, a Workshop on Information Handling Systems for Genebank Management was held 21 - 23 November, 1984 at the Nordic Gene Bank, Alnarp, Sweden. The suggestion of the IBPGR was for the first Workshop to be held in Europe, in view of the large number of genebanks in the region. It was felt that the experience would prove useful for organizing other workshops to be held later in other parts of the world. The list of participants is shown in Appendix I.

2. The objective of the Workshop was to raise the standards of genebank management by stimulating the development and implementation of computerized data management systems in order to facilitate seed handling procedures.

3. The programme for the Workshop was designed to allow presentation of short papers about the principles of management of data generated in the course of the day-to-day running of the genebank, to review current systems and to allow ample time for discussion. The programme of the Workshop is shown in Appendix II.

4. The Director of the Nordic Gene Bank, Dr. E. Kjellquist, welcomed participants to the institute and the IBPGR Information Officer, Mr. J. Konopka, welcomed participants on behalf of the IBPGR.

REPORT

5. The papers presented (Appendix IV) emphasized the importance of adequate handling of both seeds and data in genebanks and reviewed examples of several existing systems for handling management data. These papers as requested excluded consideration of data bases solely limited to passport, characterization and evaluation data. However, management data cannot be considered in isolation; for instance, certain passport, characterization and evaluation data are important for decision making with regard to genebank activities such as regeneration. Management data will therefore be an integral part of germplasm documentation in a central genebank documentation system.

6. The Workshop recognized that:

(i) There is a need for high standards of control in the handling of genetic resources samples in genebanks. Without implementing such standards, genebanks will not retain credibility for their work. In this respect, genebank managers will need to use in their management systems clearly defined descriptors. These will enable curators to handle information on such activities as monitoring the inventory of seed stores and viability of seeds in store, and performing regeneration procedures and distribution. The essential feature of better management is to ensure as far as possible that the genetic integrity of each individual accession is maintained and that

the information related to the specific sample remains accurate.

(ii) Although there are basic common data elements in information handling systems for management, each system will be unique because it will reflect the objectives, facilities, manpower and origins of the individual genebank. Such systems, whether computerized or manual, should be reviewed from time to time so that modifications can be made as and when necessary; hence the system should remain flexible.

(iii) Many genebanks have built up substantial holdings without having installed computerized systems for genebank management from the start. In such cases, for a number of years and often due to lack of manpower, there may be an older system running in parallel with a newly installed system. However, every effort must be made to transfer data to the new system.

(iv) Important data for genebank management concern the identity and quantity of seeds, their location in store, and their viability and regeneration. It was further recognized that standards must be maintained during these practical procedures.

(v) Information accompanying samples or provided to users should be provided in a standard format.

7. The Workshop recommended that:

(i) Genebanks should maintain management data in order to allow rapid accessioning of new samples, to monitor the quality and quantity of the samples in store, and to carry out regeneration and distribution. These data may be organized in different blocks or files and will vary according to the system used by each centre. A computerized, rather than a manual, data handling system is a necessity for large collections.

(ii) Through continuous contact with breeders, curators should for each major crop determine and standardize the threshold values for number of seeds per sample in store and the regeneration standard which must be used to ensure proper regeneration, bearing in mind breeding system, patterns of variability and individual seed yield. Advice should be sought from those experienced with conservation and breeding of these specific crops.

(iii) Curators should make themselves aware of available computer software for use in genebank management.

(iv) A limited number of descriptors will be of direct relevance to genebank managers in managing their collections and can be used to form a minimum set of management data. The Workshop defined these descriptors (Appendix III).

The Workshop recorded its appreciation to the Nordic Gene Bank for assistance with making arrangements and for providing facilities for the meeting.

APPENDIX I

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APPENDIX II

WORKSHOP PROGRAMME

Session I:	Principles of Data Handling for Genebank Management	
Chairman:	E. Kjellquist	
Speakers:	R.H. Ellis	Information Required Within Genetic Resources Centres to Maintain and Distribute Seed Accessions
	J. Konopka	Management Data in a Genebank
	F. Yndgaard	Basic Principles for Dataprocessing at Nordic Gene Bank
Session II:	Current Systems of Genebank Management	
Chairman:	E. Kjellquist	
Speakers:	R.D. Smith	The Role of the Computer in the Day to Day Running of the Kew Seed Bank
	D. Astley	Management Systems at the National Vegetable Research Station Gene Bank
Chairman:	R. Schachl	
Speakers:	L. Seidewitz	Management of Data and Information in Genebank Management at the Institute of Crop Science and Plant Breeding of the FAL
	J. Serwinski	Management of Internal Information at the Polish Genebank
	B.L. Tyler	Management of a User-Orientated Genetic Resources Collection
Session III	Demonstration of Management Systems	
Session IV	Conclusions and Recommendations	
Chairman:	D. Astley	

APPENDIX III

MANAGEMENT DESCRIPTORS

A minimum list for use in genebanks

Introduction

The nature of genetic resources collections is such that one accession may be stored as several separate samples. This is because seeds from different regeneration cycles are never mixed and are kept as separate samples within the store, often in a different location. Seeds from the same regeneration cycle may be stored in several containers in addition to being held under different storage conditions; these must also be regarded as separate samples when stored in different locations.

It will be readily apparent that some descriptors relate to general characteristics of the accession and that the states of these descriptors should remain constant for all samples of the same accession. These descriptors therefore apply to all samples of an accession. Other descriptors relate to separate samples of seed stored in each specific location and their states can differ between individual samples. These descriptors apply to each sample separately.

Some descriptors have previously been defined in IBPGR crop descriptor lists, but are included here for clarity and completeness. Their previous designation is noted in brackets after the descriptor name.

ACCESSION DATA

1. ACCESSION NUMBER (Passport descriptor 1.1)

   This number serves as a unique identifier for accessions and is assigned by the curator when the accession is entered into the genebank. Once assigned this number should never be reassigned to another accession in the collection. Even if an accession is lost, its assigned number is not available for re-use

2. DATE OF COLLECTION (Passport descriptor 2.3)

   Date of original collection, expressed numerically (e.g. October = 10, 1978 = 78)

3. ACQUISITION DATE (Passport descriptor 1.7)

   Date when the sample was received by the genebank, expressed numerically

4. PRINCIPLE ATTRIBUTE

Main justification for preservation of the particular accession in the genebank. The states will be defined by individual curators

5. GENETIC STATUS OF SAMPLE

The genetic basis of the material from which this accession was collected

6. LETHALITY/STERILITY PRESENT

Presence of special genes requiring attention during regeneration

7. DISTRIBUTION STATUS

Indicates the availability of seeds of this accession

1 Freely available
2 Limited distribution until regeneration completed
3 Time limit before distribution requested by donor
4 Part of special collection for which there is no agreement to make samples available
5 Other reason specified in NOTES (descriptor 16)

8. DUPLICATION

Information about where this accession can be obtained

8.1 DUPLICATED IN ACTIVE COLLECTIONS

Name of Institutes

8.2 DUPLICATED IN BASE COLLECTIONS

Name of Institutes

SAMPLE DATA

9. SERIAL NUMBER

Number used to identify samples of the same accession number from different regeneration cycles. The states for this descriptor have to be exactly defined by curators depending on the organization of the genebank

10. INITIAL DATE OF STORAGE

Date when this seed sample was placed in storage, expressed numerically

11. LOCATION OF SEEDS WITHIN THE STORE

Indicates the exact location of each container of an accession within the seed store. The states for this descriptor have to be exactly defined by curators depending on the manner in which the seed store is organized

12. VIABILITY TESTING

Note: It is recommended that at an absolute minimum the results of the initial and most recent test be kept

12.1 DATE OF INITIAL SEED TESTING

Date when this seed sample was first tested, expressed numerically

12.2 INITIAL SEED VIABILITY

12.2.1 NUMBER OF SEEDS TESTED

12.2.2 NUMBER OF SEEDS GERMINATED

12.3 DATE OF MOST RECENT TEST

Date when this seed sample was last tested, expressed numerically

12.4 SEED VIABILITY FROM MOST RECENT TEST

The most recent estimate of seed viability expressed numerically

12.4.1 NUMBER OF SEEDS TESTED

12.4.2 NUMBER OF SEEDS GERMINATED

12.5 DATE OF NEXT TEST

Date when this seed sample should next be tested, expressed numerically

12.6 REFERENCE TO COMPLETE VIABILITY TEST DATA

Reference to complete data in either paper or computer files for all seed testing about this accession

13. SEED MOISTURE CONTENT

13.1 ESTIMATE OF SEED MOISTURE CONTENT

Percentage moisture content expressed numerically on a wet

weight basis from the results of determination by a standard method. (Usually this is measured only when seeds are first placed in store, but if change is suspected, e.g. due to leakage of containers, further determination may be necessary.)

13.2 REFERENCE TO MOISTURE CONTENT DETERMINATION DATA

Reference to complete test data on moisture content determination

14. NUMBER OR WEIGHT OF SEEDS IN STORE

Approximate number or weight in grams of seeds in this sample

15. REGENERATION

15.1 NUMBER OF TIMES ACCESSION REGENERATED (Passport descriptor 1.10)

Number of regenerations or multiplications of seeds of this sample since original collection or introduction

15.2 REFERENCE TO COMPLETE DATA

Location of complete data referring to regeneration of this accession

15.3 REGENERATION YEAR

Year when presence of principle attribute last checked

15.4 PRINCIPLE ATTRIBUTE CHECK

A check of whether the main character(s) for which the accession is preserved were maintained during regeneration

16. NOTES

Any specific information regarding maintenance, germination, regeneration behaviour or distribution of this accession

Appendix IV

Information Required Within Genetic Resources Centres to Maintain and Distribute Seed Accessions

by

R.H. Ellis

INTRODUCTION

The balance of activities between maintenance and distribution in a genebank will vary depending upon whether it maintains a base collection, an active collection or a combined base and active collection, but in terms of genebank management the categories of information required are largely the same. Consequently, no attempt is made here to distinguish between the different types of collections. The purpose of this article is to discuss the information required, and the use made of it, to manage the genebank: the points made here apply equally to whether this information is recorded manually on paper or within a computer.

There are four core operations which are performed within a typical genebank:

1. Banking: the incorporation of seed accessions into the seed store and the compilation of inventory lists;

2. Monitoring: ensuring that accessions are maintained according to standards;

3. Regeneration: the production of a fresh stock of seeds from an accession maintained in store; and

4. Distribution: the fulfillment of requests for samples of seeds.

Although these operations are discrete much of the information required is common to several operations, and some is vital to all operations.

INFORMATION ON ACCESSIONS REQUIRED IN ALL CORE OPERATIONS

Accession identification

The accession identification number is obviously required to link the seed accession in the genebank to all the information held on that accession. It is thus essential that a number is allocated as soon as the accession and accompanying information are received. The most

realistic method of ensuring that an accession is identified as soon as it is received is to allot such identifications serially: that is, in the order in which accessions are received. Once allotted the accession number must not be changed.

The identification of species must be verified in order to ensure that within the genebank suitable seed germination test procedures and seed regeneration environments are provided and that the accession is correctly identified on the seed list for distribution purposes, but verification should not delay the banking operations. In some cases, the identification of the accession may need to be altered at some time after the initial receipt of the accession.

Number of (true) seeds

The estimate of the number of seeds within the accession is a vital piece of management information and will determine:

(1) whether the accession can be accepted into long-term storage without prior multiplication (if viability is acceptable);
(2) the distribution policy for the accession;
(3) the number of seeds available for monitoring tests;
(4) how much space is required for the accession within the long-term seed store; and
(5) the date of next regeneration.

The number of seeds will require constant updating to prevent the accession becoming depleted.

In some species empty seeds (where the seed covering structures do not enclose a seed) are a problem. It is necessary for the number of seeds to indicate the true situation, and not the number of seed-like structures present. In Table 1, it is suggested that a purity analysis be carried out after the accession has been cleaned.

The figure for the number of seeds present is likely to be an estimate, since the total accession is unlikely to have been counted; the estimate is likely to be derived from the total weight of seeds divided by an estimate of mean seed weight adjusted by an estimate of purity. The rules of the International Seed Testing Association (ISTA) provide a reliable method for deriving an estimate of 1000 seed weight from which the mean seed weight can be calculated, but in addition good management would ensure that a check is made that the estimated number of seeds remaining is reasonable when accessions are monitored and/or a sample distributed.

Accession location within the store

Locating accessions is essential for all core genebank operations. For various reasons some accessions will be depleted in size (e.g. through distribution) or removed (e.g. discarding duplications): thus spaces will occur within the store; these should be filled to make the most use of the space available. This means that

the location of accessions within the store should be independent of both serial number and/or accession number. In rare cases the location of the accession may need to be altered to make the most efficient use of the storage space available, but this should be done rarely since it would be easy to misplace accessions if these locations were changed frequently.

Viability

The viability of accessions - that is the proportion of true seeds in the accession which are estimated to be alive and capable of producing plants - should be the key factor affecting genebank operation. The viability of the accession will determine whether the accession requires regeneration, whether it can be put on the seed list, the potential storage life of the accession and hence indirectly how frequently accession viability should be monitored. The estimate of accession viability will require periodic updating; it should show the result of the most recent accession viability monitoring test. In addition, it is also useful for some indication of the accuracy of this estimate to be provided; the number of seeds tested to provide the estimate is probably the most useful item of information in this regard. The final point regarding accession viability is that the management of the genebank can have a considerable influence on the maintenance of viability (Ellis, 1984).

INFORMATION ON ACCESSIONS DERIVED DURING THEIR INCORPORATION INTO COLLECTIONS

The objective during this operation should be to incorporate each accession into the long-term seed store as soon as possible in order to reduce to a minimum the loss in viability and reduction in potential seed longevity which can occur during the period preceding incorporation into the long-term store. Before considering what accession management information is required during this operation, it is necessary to determine a sequence of the component activities, for example as shown in Table 1. The accession is placed in the drying room immediately upon receipt and should be entered into the long-term seed store as soon as possible thereafter. When all the information on accession quality is available, the accession is added to the seed list and becomes available for distribution.

The information generated at each stage in this process (Table 1) is largely self-explanatory, but this outline does demonstrate clearly that the gathering of information on the accession is sequential: more information is acquired at each stage. Thus the documentation of this information cannot be considered as an isolated "one-off" function - a single job that is carried out after the accession is in store. Instead the documentation of this information is integral to the whole sequence, with decisions being made at several points depending upon the information documented so far. Consequently whatever system of information management is chosen (manual or computer) it is essential

Table 1. Sequence of component operations to incorporate accessions into collections: example for a grass received as panicles

ACTION	INFORMATION	PRECAUTIONS
RECEIPT	Allocate serial number, Date of receipt.	Insect infestation? Seed treated chemically? Do seeds and documentation match?
VERIFICATION	Despatch all relevant collection information together with herbarium specimens to taxonomist.	
DRYING	Location in drying room.	Open container to allow seeds to dry, but prevent mixing of separate accessions.
THRESHING	Cancel location in drying room, add date of threshing.	Keep discarded material for seed health analyses.
ESTIMATE MOISTURE CONTENT	Record moisture content.	If seeds too moist for long-term storage then return to drying room for further drying.
CLEANING	Provide estimate of number of seeds within accession.	Keep discarded material for seed health analyses.
PURITY	Provide estimate of empty seed fraction, reduce estimate of total seed number.	If too many empty seeds then return for further cleaning.
PACKAGING	No. of containers, type of container, batch no. of containers.	
STORAGE	Date of storage, location in store of all containers.	
ESTIMATE ACCESSION VIABILITY	Record all details of the test(s), Reduce estimate of total seed number by number of seeds removed to estimate viability. Estimate regeneration interval, decide date of first monitoring test.	Sample seeds at random, overcome seed dormancy in germination tests.
ADD TO SEED LIST	Allocate accession number, indicate distribution policy, no. of seeds available for distribution and monitoring and minimum no. of seeds required for regeneration.	Do not add to seed list if insufficient seeds, insufficient viability, verification of species not available, duplicates existing accession or outside remit of the collection.
(DESPATCH SAMPLE FOR DUPLICATION)	Record institute at which accession duplicated, despatch all information with duplicate sample.	

that it enables genebank staff to enter the information sequentially as it is obtained. Some form of error checking is essential to ensure that all information added is ascribed to the correct accession!

To avoid seed deterioration prior to entry into the long-term seed store, one function of genebank management involves monitoring the progress of accessions during incorporation into collections. Some of the information listed in Table 1 is provided for this purpose. If, for example, no date of threshing is provided then the accession remains in the drying room - since it is intended that the accession enters the drying room immediately upon receipt. Similarly if an estimate of the empty seed fraction has been provided but the date of storage and location in store have not been entered then it is assumed that the accession is being packaged. And so on.

It is particularly important that full details of each germination test be recorded. This is to enable subsequent comparison of different germination tests, because the accuracy of the estimate of viability derived from each germination test will be subject to three distinct sources of error, viz: sampling error, where accuracy depends on the method of sampling and the number of seeds sampled; seed dormancy, where the germination of some viable seeds may not be stimulated by the test conditions; and vulnerable seeds, where some viable seeds may die during the germination test due to testing in too harsh an imbibition/germination environment. Table 2 provides an example of the type of information required to set up and then record a germination test. Note the comprehensive specification of dormancy-breaking treatments and the germination test environment, and that the total test period extended over 100 days. The results of the germination test have been recorded in pen every few days or so.

INFORMATION ON MONITORING ACCESSIONS AND THE LONG-TERM SEED STORE

The management of shelf-space within the store interacts with the management of individual accessions. The location of each accession (and if the accession is contained in several containers, the location of all containers) must be documented in such a way that this information is easy to retrieve. It is an important function of management to make full use of all storage space available. Consequently, it is necessary to know where the empty spaces occur on shelves in order that new accessions can be allocated a bank location until every location is occupied.

There are several items which require monitoring from time to time. These are: (1) the location(s) in the store; (2) the number of seeds; (3) the moisture content; and (4) the viability. The frequency with which they are to be monitored must be determined by the curator. It is suggested here that only the date of the next monitoring test of accession viability need be recorded and that accession location and the estimate of number of seeds remaining can be monitored each time a sample is removed.

Table 2. Example of the amount of information generated by, and required to describe, a single seed germination test

Location	Genus	Species	Sub-species	Test date	Accession
12.24.3	Oryza	glaberrima	-	16/02/82	OR7G

1st treatment	HNO_3, pre-applied, 24 hours, 0.1 Normal	1602
2nd treatment	H_2O_2, pre-applied, 24 hours, 0.25 Molar	1702
3rd treatment	Mercaptoethanol, co-applied, 0.01 Molar	1802
4th treatment	Nil	- - - -
Substratum	Top of filter papers (2)	1802
Temperature regime	Alternating, 34°/11°C, 16 hours/8 hours	
Light regime	No special treatment, diffuse light	

Replicate	1	2	3	4	5	6	7	8	9	10	11	12	Total
No. of seeds	33	33	33	33	33	33	35	33	33	33	33	33	398
Date/Days													
2202 4	1	2	-	5	1	1	-	2	2	1	1	4	20
2502 7	2	6	6	7	6	2	7	6	8	6	6	6	88
0103 11	3	3	4	2	3	3	6	4	1	5	4	5	13
0403 14	2	1	5	1	4	3	1	2	3	1	4	1	15
1103 21	7	7	3	6	2	4	3	5	9	9	7	4	22
1503 28	5	2	7	4	5	5	6	5	4	5	6	1	28
2503 35	5	7	1	4	3	5	6	4	1	3	3	5	32
0104 42	2	1	1	1	1	2	1	-	2	-	1	-	33
0504 49	1	-	-	-	1	2	-	1	1	-	-	1	34
1504 56	1	-	1	-	1	-	-	1	-	-	-	-	35
2204 63	1	-	-	1	-	-	-	-	-	-	-	-	35
2904 70	-	-	-	-	-	-	-	-	-	-	-	-	35
0605 77	-	1	-	-	-	-	-	-	-	-	-	-	35
1305 54	-	-	-	-	2	1	-	-	-	-	-	-	35
2705 98	-	1	-	1	-	-	1	1	-	-	-	-	36
Abnormal	2	-	-	-	1	-	-	-	-	-	-	1	4
Fresh	1	2	2	1	3	2	2	2	2	3	1	3	24
Mould/	-	-	3	-	-	3	2	-	-	-	-	2	10
Hard	-	-	-	-	-	-	-	-	-	-	-	-	-
													398

90.5 % germination

There are four topics concerning seed viability which must be covered at this point. Firstly, when monitoring accession viability during storage it is necessary to be able to refer back to the results of all previous tests of viability (e.g. as shown in Table 2) for this accession - and particularly those carried out initially - to ensure that the most suitable conditions for germination and breaking dormancy are provided within the monitoring test. It may be easier to divide this information up, so that - although all the germination test details and results are recorded somewhere - only the details of the most suitable test regime are provided within the (readily accessible) accession management information file.

Secondly, it is necessary for the conditions and the results of this accession viability monitoring test to be recorded (the reasons for this will be covered below) and for the previous estimate of accession viability to be overwritten with the current estimate.

Thirdly, this estimate has been derived for the purpose of making a decision as to whether or not the accession can be maintained in store until the next monitoring test date or whether the accession now requires regeneration. The type of accession viability monitoring test that is chosen will determine the reliability of this decision. Two types of test procedure can be used: fixed sample size tests, or sequential tests. The details, advantages and disadvantages of each procedure have been discussed elsewhere (Ellis and Wetzel, 1983): the principle difference from the point of view of information management is that sequential testing will generate more discrete items of information, but require fewer seeds. Nevertheless within the accession management information file the same information for the monitoring test can be recorded, viz. the total number of seeds germinating and the total number of seeds tested.

Fourthly, the estimate of regeneration interval and the intended monitoring test date must be provided once the result of the initial accession viability test is known and before the accession is added to the seed list. The reason for the imperative here is to avoid the possibility that accessions are added to the seed list with no allowance made by management to ensure their maintenance. There are several ways of determining the intended monitoring test date and it is useful for the source of the estimate to be provided within the accession management information file.

INFORMATION ON ACCESSIONS REQUIRED FOR AND DERIVED DURING REGENERATION/MULTIPLICATION

Accessions require regeneration as a result of low viability or insufficient number of seeds. Thus the information which triggers regeneration is either the estimate of viability or the estimate of the number of seeds remaining in store. The first action must be to indicate the temporary unavailability of the accession on the seed list. As a second step, it is necessary to consider the possible

alternatives to regeneration, since regeneration is a costly and risky procedure. Thus it is necessary to check if the accession has been duplicated within another genebank for safe keeping and, if so, to ask for a check on the status of that duplicate (thus the location of the institute in which the duplicate is stored is required on the accession management information file), and to check whether a fresh collection of the accession could be made more cheaply (by contacting the original collectors or suppliers, who also should be noted on the accession management information file). If it is decided that regeneration is essential then the primary evaluation data must be consulted to determine the environment, pollination and isolation requirements for regeneration and any information on seed health and insect infestation must also be consulted to ascertain whether any diseases or pests might inadvertently be introduced to the regeneration site during the regeneration of the accession, and thus whether special precautions should be taken. After consulting this information it may be decided that the accession can only be regenerated in another institute, in which case the regeneration institute must be noted on the accession management information file. The number of seeds remaining in store must be decreased by the number of seeds sampled for regeneration, but care must be taken not to exhaust seed stocks in order to enable further attempts at regeneration if the first attempt fails. To produce the required number of seeds during regeneration, the number of seeds sown will need to be calculated on the basis of the multiplication factor for the accession.

INFORMATION REQUIRED FOR DISTRIBUTION ON ACCESSIONS AND ON CUSTOMERS

When a request is received for seed samples it is obvious that the name and address of the customer must be recorded, together with a list of accessions requested. A decision must then be made as to whether each request can be satisfied and, if so, how many seeds should be supplied. This depends largely upon the degree of genetic variation within the accession, the number of seeds within the accession available for distribution, and possibly accession viability. It is helpful for the accession management information file to denote the distribution policy for each accession since in some cases e.g. narcotics - this may have to be restricted, and to specify how many seeds should be sampled to satisfy any one request. A permanent record of the accessions distributed to each customer is also suggested to avoid abuse of the collection through particular accessions being depleted as a result of repeated requests from one customer within a short period.

A good deal of the information within the accession management information file should be distributed together with the sample from the accession to the customer, viz. accession viability, the proportion of empty, dormant and hard seeds, and the suggested procedure for obtaining maximal germination together with the primary evaluation data and any information available on seed health and insect infestations. Finally the genebank may wish to request information gained during evaluation by the customer.

GENEBANK PERFORMANCE

An important function of genebank management is to monitor and report on the operation of the genebank. There are several obvious performance criteria which a genebank manager will record in annual reports of the operation of the genebank. For example:

- Total number of accessions in the bank;
- Total number of accessions available for distribution (with details for each species etc.);
- Number of accessions deleted from the seed list in the past year;
- Number of accessions added to the seed list in the past year; and
- Number of samples distributed in the past year.

RELATIVE PRIORITY OF GENEBANK MANAGEMENT OBJECTIVES

Genetic resources conservation by seed storage is a long-term activity. Consequently when responding to short-term problems it is important to avoid introducing long-term problems. Each genebank activity should have a priority assigned. It is suggested here that the first priority of genebank management is to incorporate accessions into the store as soon as possible and the second priority is to ensure the maintenance of accessions by monitoring.

These priorities are suggested because:

(a) delaying the incorporation of accessions into the long-term store will increase genebank operating costs in the longer term; and

(b) failure to maintain good quality accessions within the collection will result in a decline in the value of the collection for distribution and may limit its future utilization.

ACKNOWLEDGEMENTS

The author of this paper is grateful to Professor E.H. Roberts, Chairman of the IBPGR Seed Storage Committee, Mr. S. Linington and Mr. R.D. Smith of the Royal Botanic Gardens Kew, Wakehurst Place, for helpful discussions prior to preparing this manuscript, and to the International Board for Plant Genetic Resources for financial support.

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Appendix IV (cont'd.)

Management Data in a Genebank

by

J. Konopka and J. Hanson

INTRODUCTION

The information maintained by a genebank can be of several types:

1. Data related to sample characteristics (passport, characterization and evaluation data)

   These describe the origin and characteristics of accessions and have both a large internal and external value because the information is disseminated from the genebank in different forms, whether accompanying the actual material or not. This type of data has received a considerable amount of attention and, in order to facilitate standardization of data, lists of descriptors have already been developed by the IBPGR for many of the major crops. The management of this type of data has been discussed extensively and need not be considered further here except to note that ideally a relational data base management system is needed to manage special sub sets of data.

2. Management data

   These relate to the practical maintenance of the germplasm and its distribution to users. Much of the data relating to maintenance have only internal value and are of concern primarily to the curator in making decisions about the management of the seed store. However, some of the data such as those relating to the history of the sample within the store and to the regeneration methods are very pertinent to users and also have considerable external value.

3. Bibliographic data

   The amount of bibliographic data varies from genebank to genebank. Literature referring to accessions may amplify the passport, characterization and evaluation data and justify the inclusion of particular samples into the genebank, for example a breeder's line that has been a landmark in breeding or has special genetic characteristics.

GENEBANK ACTIVITIES

The genebank curator carries out many tasks in order to properly conserve and distribute the germplasm. Data are generated in the course of these activities and these data must be stored and utilized in planning for efficient management. The major activities of a curator are:

1. Introduction of germplasm

Germplasm enters a genebank from many sources. Some material is sought on an exchange basis or is obtained from field collecting missions, while other material is sent to the genebank without its being requested. There are two major approaches to handling this material: Firstly, the sample may be immediately assigned an accession number and entered into the genebank. This is usually the case with material from known sources, or which has been requested and which arrives in the genebank in visibly good condition. Samples which are found to be duplicates or have poor viability and cannot be maintained will later be eliminated from the genebank. Alternatively, a provisional number and status could be assigned and only if both seed quality and quantity are satisfactory and the sample is considered not be a duplicate of accessions already in the genebank, then registration of the sample will proceed and the sample will be assigned an accession number. This latter situation typically occurs when material has not been solicited or is of uncertain origin. When an accession number has been assigned and the sample is fully accepted into the genebank, the data accompanying the sample will be incorporated into the main data base of the genebank.

In some genebanks accessions which are very heterogeneous are subdivided into sub-samples of different morphotypes and these may later be re combined in an attempt to again form the original population. It is obvious that the genetic constitution of the samples will differ both between samples and from the original population and all samples cannot be given one accession number. It is possible that each morphotype could be recognized as a separate sample but since the relationship between these samples cannot be disregarded, data should then be recorded as if each were a separate accession.

2. Maintenance

The three inter-related aspects involved in the maintenance of samples, namely storage, monitoring and regeneration, should have relevant data stored in a suitable data management system which can be used to aid decision making in running the genebank.

The storage of the accessions provides data important for management, e.g. number and location of separate samples of the same accession, type of container used for each and information on where duplicate samples are stored in other genebanks. It may also be helpful to know where accessions are duplicated in active collections

in order to redirect seed requests or to reintroduce accessions which have been lost. Standards for adequate storage conditions in genebanks have been defined by the IBPGR Advisory Committee on Seed Storage (IBPGR, 1985).

Seed viability should be monitored during storage to detect declines in viability and to schedule regeneration of accessions. The period between monitoring tests depends on the normal storage characteristics of the species, the quality of the seeds at the start of the storage period and the storage conditions employed. The number of test results included in a data base should be limited to keep the data manageable. As a minimum the results of both the initial and most recent test should be recorded and if further information is required for special cases it could be sought from the original paper data files.

When viability begins to decline or seed quantity falls below a critical level the accession is usually regenerated. A regeneration standard, i.e. the percentage germination at which regeneration is necessary, should be set for each crop using information about the usual longevity period and effects of deterioration on genetic change for that species. The IBPGR Advisory Committee on Seed Storage has recommended that a regeneration standard should be agreed for each species, although genebanks are expected to obtain advice from experts on individual crops in order to make decisions. A regeneration standard at 85% true viability has been taken as an acceptable level for the majority of species of crop plants (Hanson, Williams and Freund, 1984).

The environment for the regeneration must be chosen with care to minimize selection pressure during the process and maximize quantity and quality of seeds obtained. The most suitable technique for a particular species will also depend on the breeding system and population characteristics of the original accession. Each time the accession is regenerated a new sample of that accession is considered to have been formed; it should not be mixed with other samples and a complete set of data specifically referring to it becomes available.

3. Distribution

Seed samples are distributed to users only from active collections (i.e., not base collections). When the accession is available only from a base collection, the accession is usually regenerated before supply to the user. Data regarding the accession numbers provided, quantity, recipient and purpose for the distribution is usually stored for reference in order to determine where and for what purpose the material is used and to allow statistical reports to be prepared about the operation of the genebank. It may also prove to be important to know where an accession has been distributed so that in case of loss the accession can be reintroduced into the genebank.

Information on the origin and characteristics of the accessions and technical data on germination procedure and regeneration should be extracted from the data base and accompany the germplasm. Feedback from the recipient regarding either the condition of the seeds or the

characteristics of the accession should also be entered into the data base. These data should be stored in a way that relates them to the other data on the same accession. Distribution files, however, are usually kept separately because of their large size.

4. Characterization and evaluation

Characterization and evaluation of the germplasm are important for the proper utilization by scientists and plant breeders. While these data are particularly important for the user and for the management and regeneration of the germplasm, they are perhaps the least important for day to day running of the seed store. The data are used for preparing lists of those accessions which have been or will be grown out, following assignment of priorities by the curator. They are also referred to before attempting regeneration, in order to select the most appropriate method and conditions. Computer programs are also available to print these data in field books and in the lists for planting.

MANAGEMENT DESCRIPTORS

Data generated daily in the genebank are not all of equal importance, either internally or externally; thus to keep the amount to a manageable quantity it is useful to pinpoint certain pieces of information which are the most important for the curator and to develop management descriptors. These descriptors are not crop-specific and should be of considerable value in the control and management of all plant germplasm.

The need for management descriptors has also been recognized by a Working Group (on barley) of the UNDP/IBPGR European Cooperative Programme for Conservation and Exchange of Crop Genetic Resources. Considering that accessions can differ in their requirements for successful maintenance and regeneration, it was recommended that appropriate management descriptors be developed (UNDP/IBPGR, 1983).

The following is a list of descriptors prepared by the authors as a basis for discussion at this Workshop:1/

> Note: One accession may be stored as several separate samples. Seeds from different regeneration cycles are never mixed and each is kept separately within the store, usually in a different location. Seeds from the same regeneration cycle may also be stored under different storage conditions and these must also be regarded as separate samples. The descriptor states, therefore, relate directly to each sample of the seeds stored in each specific location.

1/ After considerable discussion by the participants of the Workshop, a more comprehensive list of management descriptors was agreed upon (see Appendix II).

1. ACCESSION NUMBER

This number serves as a unique identifier for accessions and is assigned by the curator when the accession is entered into the genebank. Once assigned this number should never be reassigned to another accession in the collection. Even if an accession is lost, its assigned number is not available for re-use

2. LOCATION OF SEEDS WITHIN THE STORE

Indicates the exact location of each container of an accession within the seed store. The states for this descriptor have to be exactly defined by curators depending on the manner in which the seed store is organized

3. DATE OF RECEIPT OF SAMPLE

The month and year expressed numerically when the sample was received by the genebank (e.g. October = 10; 1978 = 78)

3.1 Month

3.2 Year

4. INITIAL DATE OF STORAGE

The month and year expressed numerically when this seed sample was placed in storage

4.1 Month

4.2 Year

5. VIABILITY TESTING

Note: It is recommended that as an absolute minimum the results of the initial and most recent test be kept

5.1 DATE OF INITIAL SEED TESTING

The month and year expressed numerically when this seed sample was first tested

5.1.1 Month

5.1.2 Year

5.2 INITIAL SEED VIABILITY

Percentage viability expressed numerically from the results of an initial standard germination test relating to the date above

5.3 DATE OF MOST RECENT TEST

The month and year expressed numerically when this seed sample was last tested

5.3.1 Month

5.3.2 Year

5.4 SEED VIABILITY FROM MOST RECENT TEST

Percentage viability expressed numerically from the results of a standard germination test relating to the date above

5.5 DATE OF NEXT TEST

The month and year expressed numerically when this seed sample should next be tested

5.5.1 Month

5.5.2 Year

6. SEED MOISTURE CONTENT

Percentage moisture content expressed numerically on a wet weight basis from the results of determination by a standard method. (Usually this is measured only when seeds are first placed in store, but if change is suspected, e.g. due to leakage of containers, further determination may be necessary.)

7. STORAGE CONTAINER

Code used to indicate the type of container used for this sample when various containers are used in the genebank. The states for this descriptor must be defined by the curator depending on the containers used

8. NUMBER OR WEIGHT OF SEEDS IN STORE

Approximate number or weight in grams of seeds in this sample

9. THOUSAND SEED WEIGHT

Note: Used for inter-conversion of seed number and seed weight

10. REGENERATION

10.1 NUMBER OF TIMES ACCESSION REGENERATED

Number of regenerations or multiplications of seeds of this sample since original collection or introduction

10.2 DATE OF REGENERATION

Month and year expressed numerically when sample regenerated

10.2.1 Month

10.2.2 Year

10.3 SITE OF REGENERATION

Name of site

10.4 REGENERATION METHOD

10.4.1 REGENERATION METHOD RECOMMENDED

The method of regeneration recommended for this accession

10.4.2 REGENERATION METHOD USED

Regeneration method used, if the procedure differs from the above

11. DISTRIBUTION STATUS

Indicates the availability of seeds of this sample

1 Freely available
2 Limited distribution until regeneration completed
3 Time limit imposed before distribution is permitted (at donor request)
4 Part of special collection for which there is no agreement to make samples available
5 Other reason specified in NOTES (descriptor 13)

12. DUPLICATION

Other institutes where this sample can be obtained

12.1 DUPLICATED IN ACTIVE COLLECTIONS

Name of institutes

12.2 DUPLICATED IN BASE COLLECTIONS

Name of institutes

13. NOTES

Any specific information regarding maintenance, germination, regeneration behaviour or distribution of this sample

DOCUMENTATION OF MANAGEMENT DATA

As outlined above, the daily operation of a genebank generates a large amount of management data which must be maintained for future reference. Although management data are in many instances retrieved independently to other types of data, they should be considered an integral part of a genebank documentation system. All records which are pertinent to the particular accession and for the particular application should therefore be closely linked.

The most advanced concept of properly maintaining data is the use of a data base viewed as a common resource for different applications. Although different models of data bases are theoretically workable, relational data bases seem to be the most appropriate for genebanks. The data base system maintains the necessary link between data entering the system at different times and by different people. The relationships between sets of data may change whenever new data are added, but this is handled by the system itself. The software which takes care of the location of data in the storage unit and provides the interface to the application programs is called the Data Base Management System (DBMS).

Whenever the data base and the DBMS are available at the genebank the problem of incorporacion of management data to the data base is simplified. Once the exact definitions of the new data are provided the system automatically conducts storage and retrieval of data. If, as is often the case in practice, the system software offers only file handling features, the linkages between different files will need be built up and maintained by the data base manager The file with management data will be one of these and the descriptor linking the majority of files will be the accession number.

If the software used at the genebank does not permit files to be easily linked, the management data have to be incorporated into one of the existing files. The file with passport data is probably the most appropriate one for this; however, the number of management descriptors will likely be limited. Some management data, such as data on distribution of samples, can still be kept as separate files. The absence of links to other files will obviously limit the usage of these data, but computerized systems for data processing will nonetheless be more efficient in comparison to manual systems.

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Appendix IV (cont'd.)

The Role of the Computer in the Day to Day Running of the Kew Seed Bank

by

R.D. Smith, S.H. Linington and D.J. Fox

INTRODUCTION

Genebanks are long-term investments and genebank managers should adopt highly efficient working practices to hold annual costs to acceptable levels. This paper describes the current level of computer integration into the day-to-day running of the Kew Seed Bank (Royal Botanic Gardens, Wakehurst Place, Ardingly, UK). The system aims to eliminate the duplication of effort spent in handling the basic data as well as monitoring the progress of accessions into the bank and the distribution of seeds from it.

CONSTRAINTS DURING PROGRAMME DEVELOPMENT

When the project started, only the central facilities of the Ministry of Agriculture mainframe computer located some 65 km from the Seed Bank at Wakehurst Place were available. Data were collated onto specially designed forms and then sent by post to the computing centre for data entry and subsequent processing. The data for each collection was divided between two paper records: the Primary data form (GB1) which covered all the collecting (passport) data and could be completed on the seed's arrival; the Secondary data form (GB3) designed to record the information produced as each stage of seed processing was completed and the seed placed into long-term storage. These two forms are presented as Figures 1 and 2. For completion, Figure 3 shows the regeneration data form (GB2) which replaces the Primary data form when the material being accessioned has undergone regeneration. As the management data recorded is the same for both types of material and regeneration is infrequent, no further reference is made to form GB2.

At this stage of the development, the prospects for integrating the computer into the day-to-day management of the bank were recognized. The use of the computer in this role demands that:

1. The flow of material into and out of the genebank conforms to a clearly defined series of procedures from which no deviation will occur; and

2. Access to the computer is available both continuously and locally.

GENE BANK - PRIMARY DATA FORM ROYAL BOTANIC GARDENS - WAKEHURST PLACE

INDICATIVE DATA
1. Data type (last box - enter 1 for Kew or W.P., 2 for via others) 1
2. Serial number (plus check digit)
3. Accession number (plus century code)
4. Processing indicator (1 = insert, 2 = amend, 4 = delete)
5. Data indicator (1 = complete, 2 = incomplete)

IDENTIFICATION
6. Date collected Day Month Year
7. Collectors (coded)
8. Collection number
9. Date donated Day Month Year
10. Organisation identifier (donor)

LOCATION
11. Geographical code
12. Local situation
13. Latitude
14. Longitude
15. Altitude

ECOLOGY
16. Nature of habitat (coded)
17. Nature of habitat
18. Other modifying factors

TAXONOMY
19. Division or order
20. Family
21. Genus
22. Species
23. Sub-species

COLLECTION DATA
24. Material collected
25. No. of plants sampled
26. No. of plants found
27. Herbarium voucher
28. Where lodged
29. Further data available
30. I.U.C.N. category
31. Distribution policy
32.
33.

GB 1 (Rev. 1979)

79-2804

Figure 1. Primary data form (Royal Botanic Gardens)

GENE BANK – SECONDARY DATA FORM ROYAL BOTANIC GARDENS -- WAKEHURST PLACE

INDICATIVE DATA
1. Data type (last box - enter 1 for field source, 2 for regenerated) 3
2. Serial number (plus check digit)
3. Accession number (plus century code)
4. Processing indicator (2 = amend, 3 = transfer to history)
5. Data indicator (1 = complete, 2 = incomplete)

RECEPTION
6. Number of seeds
7. Date banked (Day Month Year)
8. Bank number
9. Storage temperature (degree K)
10. Storage container (No. of containers)
11. Moisture content
12. Gaseous atmosphere

GERMINATION
13. Date tested (Day Month Year)
14. Scarification (type code/amount)
15. Conditioning treatment 1 (type code/temperature/days)
16. Conditioning treatment 2 (type code/temperature/days)
17. Germination temperature
18. Alternate night temperature (day hrs/night hrs/temperature)
19. Chemical treatment (type code/units code/amount)
20. Other treatment
21. Number sown
22. Number germinated
23. Germination result code
24. Distribution policy
25. In Seed List (year)

VERIFICATION
26. Verification code
27. Date verified (Month Year)
28. Material verified
29. Where lodged
30. Verifier
31. Verifier's institute

TAXONOMY
32. Division or Order
33. Family
34. Genus
35. Species
36. Sub-species

CONSERVATION
37. Location of duplicate collections
38. Local frequency
39. Global frequency
40. I.U.C.N. category

STORAGE
41. Projected storage life (years)
42. Source of estimate
43. Monitoring policy

HISTORY
44. Reason for transfer to history
45.
46.

GB 3 (Rev. 1979) 792806

Figure 2. Secondary data form (Royal Botanic Gardens)

GENE BANK – REGENERATION DATA FORM ROYAL BOTANIC GARDENS – WAKEHURST PLACE

INDICATIVE DATA

1. Data type (last box - enter 1 for Kew or W.P., 2 for via others) 2
2. Serial number (plus check digit)
3. Accession number (plus century code)
4. Processing indicator (1 = insert, 2 = amend, 4 delete)
5. Data indicator (1 = complete, 2 = incomplete)

PARENTAL DATA

IDENTIFICATION

6. Serial number (plus check digit)
7. Accession number (plus century code)
8. Number of seeds
9. Date collected Day Month Year
10. Collectors (coded)
11. Collection number
12. Date donated Day Month Year
13. Organisation identifier (donor)

LOCATION

14. Geographical code
15. Local situation
16. Latitude
17. Longitude
18. Altitude (– 1,000 to 10,000 metres)

ECOLOGY

19. Nature of habitat (coded)
20. Nature of habitat
21. Other modifying factors

TAXONOMY

22. Division or Order
23. Family
24. Genus
25. Species
26. Sub-species

COLLECTION DATA

27. Material collected
28. No. of plants sampled
29. No. of plants found
30. Herbarium voucher
31. Where lodged
32. Further data available
33. I.U.C.N. category

SIBLING DATA

34. Relationship to Parent Collection
35. No. of seeds sown
36. No. of plants harvested
37. Date seed harvested Day Month Year
38. Isolation techniques employed
39. Where regenerated
40. Herbarium voucher
41. Distribution policy
42. Date received by Gene Bank Day Month Year
43.
44.

GB 2 (Rev. 1979)

432/82

Figure 3. Regeneration data form (Royal Botanic Gardens)

The second condition did not, at the time, accord with Ministry of Agriculture policy. The Physiology Section at Wakehurst Place was allowed to purchase a Data General Nova 3 minicomputer with its own funds. The purchase of commercially available software was not possible; therefore, all programs had to be written by our own staff. To overcome the lack of expertise amongst Seed Bank staff, computer science students were offered placements, working at Wakehurst Place during their industrial training period. A number of discreet programs have resulted, each reflecting the contribution of a student. These programs are combined to form the complete system. The various programs and their inter-relationships are shown in Figure 4.

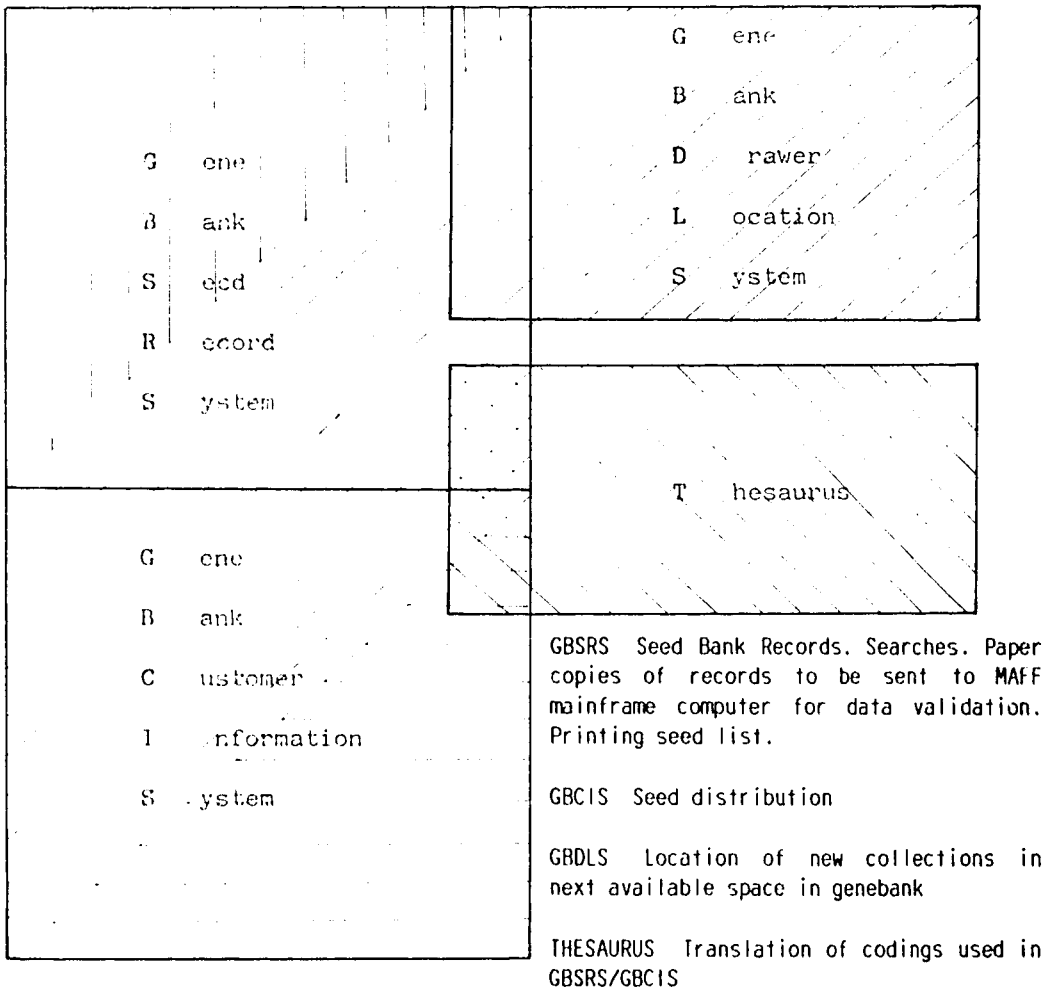

Figure 4. Inter-relation of GBSRS, GBDLS, GBCIS and Thesaurus (Royal Botanic Gardens)

THE CURRENT SYSTEM

The Genebank Seed Record System (GBSRS) stores, retrieves and sorts the passport and secondary data held on the two forms. Only the information recorded when the seed is first processed into the genebank is held in this system.

A reduced version of this record including those fields which (a) are important for stock control, (b) are liable to change through the seeds' storage life or (c) specify germination conditions and test results, are then written over into the Genebank Customer Information System (GBCIS). The details of customers (users) and the records of their previous requests are also recorded in this system.

The Genebank Draw Location System (GBDLS) is a small program designed to find and allocate the first available space in the cold room to a collection of known size and thus prevent inefficient use of the cold room facilities.

The Thesaurus Program translates back into words the various codings used within GBSRS and GBCIS. Numerical codings were adopted wherever possible in order to keep computer processing time to a minimum, as well as exploiting a logical hierarchy within the codes to speed searches.

DATA FIELDS TO FACILITATE EFFICIENT BANK PROCEDURES

Serial number and check digit (GB1/2)

The serial number, once assigned, is unique to the sample. If the processing indicator (GB1/4) is set to one for insertion then validation checks run to ensure that the serial number has not been previously allocated. The check digit is derived from the serial number to minimize clerical error. Mis-keying errors are most damaging when records are being subsequently amended or updated and misalignment would result in two records being corrupted, the intended form remaining unchanged whilst the erroneously identified record is inappropriately amended.

Accession number (GB1/3)

The possibility of misidentification of the collection is further reduced by the allocation of a three part accession number, a practice extant within the Royal Botanic Gardens Kew at the time of the establishment of the Seed Bank. The elements of the accession number are as follows. The first, fifth and sixth digits are the century, decade and unit of the year of accession i.e. 1984 becomes 984. The numbers are split because the century indicator was added later to allow for the long lifespans expected under genebank conditions. Digits 2, 3 and 4 specify the batch of seeds (all seed made on one collecting mission being given the same, batch number). These two

elements allow a "folk memory" amongst bank personnel of the appropriate accession number against the collecting mission. The final digits specify each collection within the batch.

Validation checks are made on subsequent processing of any data to ensure that the accession number entered is that already known.

If material is regenerated the serial number will change but the accession number will remain the same, allowing any relationship between the collections to be easily identified.

Once a collection has been accessioned into the system, the record is not lost even though seeds of that collection are no longer available for reasons such as seed predation by insects in the field, the field collection of incompetent empty seeds, loss of viability, depletion of seed stocks, etc. Where viable seed is no longer available, the record is transferred from the original data base into an historical file. In this way, the accumulation of records with no corresponding seeds is prevented. These would unnecessarily increase the search time of the data for which seeds were available. The value of the history file is two fold. Firstly, the genebank manager will be able to examine and analyze the discarded collections for illuminating correlations, such as short genebank life with container type, or collecting location with low initial viability, or species with heavy insect seed predation in the field. Such observations will, hopefully, lead to improvements in germplasm collecting and conservation. Secondly, a genebank may no longer have the seed within its collection, yet their progeny may be available elsewhere. Thus the data held in the computer will still have value.

Deletion of records from the whole system (Code GB1/4) is used only to correct gross errors in accessioning, i.e. where collecting data is received without any seed. In a well managed genebank such errors would be detected before rather than after accessioning.

Data indicator (GB1/5)

Unfortunately, some collections are still made without full passport data being recorded. This field allows collections with poor data and little prospect of obtaining the missing data to be coded as practically complete. Thus further effort spent in trying to obtain the unobtainable can be avoided. Consideration of this field by anyone using the data base will enable them to fully interpret what they find.

Further data available (GB1/29)

Collecting notes often include collectors' subjective comments for which no formal data fields have been allocated and on which no useful data searches can be made because of the vagaries of free textural comment. This element allows the bank manager to ascribe the subject matter of the comment to its appropriate areas, e.g. I = identification, L = location, T = taxonomy, etc. In this way, the

existence of comments is recorded in an easily sorted manner rather than the comment itself. Should at any stage the comment be required, the original collecting notes will be consulted.

Distribution policy (GB1/31)

This data field allows managers to identify those collections which will follow the normal distribution procedures and those which require special consideration for distribution, e.g. duplicate collections. An opportunity to amend this designation is offered in the secondary data form (GB3/24), once seed numbers, viability levels and verified identity are known. Where collections are classified as not available, the computer prevents attempts to list this seed for distribution.

Verification data (GB3/26-31)

Within the unique interests of the Kew Seed Bank, accurate identification is perhaps all that can be done as regards description of accessions. Identification is a matter of taxonomic opinion. Emphasis is therefore placed on recording the material identified, where it is located, the certainty of the opinion, who gave it and their institute. In such a way, anyone wishing to take issue with the identification can readily locate the material and identify it for themselves.

MONITORING THE PROCESSES OF SEED ENTERING THE GENEBANK

Monitoring seed entry can only be achieved if there is a clearly defined and unwaiving relationship between the physical acts of seed processing and the completion of the various data elements. Figure 5 shows the scheme of activities adopted at Wakehurst Place.

DATA USED IN RUNNING GERMINATION TESTS AND EVALUATING THEIR RESULTS

One of the greatest savings of time and effort gained by recording data on the computer has stemmed from its ability to provide germination test sheets (Figure 6). The risks of transcription error inherent in any manual system are considerably reduced and much time is saved. In turn, the test sheet can be used as some form of credibility check on the computer record.

The harvest date, date donated, country of origin and collector's identity recalled from the passport data are useful in considering the test results when coupled with the date when the material enters the genebank. If too much time is spent between harvest and receipt at the seed bank then loss of viability in the field can be expected and an early confirmation of this by tetrazolium testing sought. "How long is too long" is greatly influenced by the country of collection. In warm humid tropics, significant losses of viability can be expected within a

Seed Processing	Data Processing	Searches Possible and Management Inferences Which Can Be Drawn
Collection received. Serial number and accession number allocated and attached to seed bag. Seed collections placed in the dry room (15% RH ±15°C) until manpower is available to clean the seed	Indicative data and passport data entered onto computer. (Serial number, check, digit, accession number and date donated are the management descriptors)	If date donated completed but seed number incomplete, then seed awaiting cleaning. Possible to arrange these in chronological order so that a minimum time is spent awaiting cleaning.
Seed cleaned and a sample checked by X-ray to ensure all seeds are full. If not, seed is recleaned until empty seeds are removed. Rarely this is not possible, then the proportion of empty seeds is determined. Seed number estimated.	Number of seeds (GB3/6)	If number of seeds is completed but date entering genebank incomplete, then seeds are undergoing final drying. Simple programs noting the date on which the number of seeds was completed allow drying to be monitored and managed.
Cleaned seeds are further dried for 4 weeks at 15% RH ±15°C to ensure the moisture content falls to 5-7% mc.		
Total collection volume determined and seeds placed in appropriate containers. Genebank location allocated by GBDLS	Date entered in bank (GB/7), Genebank number (GB3/8) and storage container type and numbers (GB3/10) entered	GBDLS automatically updated when GB3/8 and GB3/10 completed
Seed held at -20°C and 5% mc in genebank until manpower is free to execute the germination tests.		If date entering genebank is completed but date tested incomplete, then the collection is waiting to be tested. These records can be further sorted by family, genus, or species to allow testing to be more efficiently organized. This will be especially true where incubators are in short supply and all the test conditions cannot be provided simultaneously. When the germination test sheet is printed the identifier of the collection is deleted from the file. Thus, if a collection with an incomplete test date is not found in the file, testing is in progress.
Germination test carried out	Date tested (GB3/13) Germination result code (GB3/23) Distribution policy (GB3/24) (GB3/43)	If germination result code is acceptable and distribution policy state does not prevent exchange, records can be sorted to produce seed list

Figure 5. Processes of seed entering the genebank (Royal Botanic Gardens)

TEST SHEET

WILD COLLECTION

SERIAL NO 0030038 FAMILY LEGUMINOSAE

ACC NO 96858311527 GENUS Sesbania

VERIFY CODE SPECIES

GEOGRAHICAL CODE SOMALIA

COLLECTORS Linington S. Wickens G. Aronson J.

BANK NO	1033703	HARV DATE	12/10/1983
CONTAINER	02		
CONT NO	002	RECD DATE	15/11/1983
SEED NO	0019210		
USABLE	2881	BANK DATE	08/02/1984

A. GERMINATION DATA

TEST NO	PRE-TREAT	OTHER TREAT	GERM TEMP	TEST TYPE	DATE STARTED

										FRESH	HULLED	EMPTY
DAY												
REP A												
REP B												
REP C												
REP D												
REP E												
CUMULATIVE TOT												

TOT GERM → TOTAL → GERM % [ ]

TEST NO	PRE-TREAT	OTHER TREAT	GERM TEMP	TEST TYPE	DATE STARTED

										FRESH	HULLED	EMPTY
DAY												
REP A												
REP B												
REP C												
REP D												
REP E												
CUMULATIVE TOT												

TOT GERM → TOTAL → GERM % [ ]

Figure 6. Germination test sheet (Royal Botanic Gardens)

week. In hot arid climates similar losses can take several weeks. If, however, the time taken between harvest and banking is short then the likelihood of dormancy can be expected. In such cases the application of a range of dormancy-breaking treatments in the first series of tests would be the most efficient use of manpower.

Managers need to exercise some control over the number of seeds consumed in germination tests. Where the number of seeds available is large, the number of seeds needed to define the appropriate test conditions and estimate viability will be a small proportion of the total number. Regrettably, this is not true where collections are smaller than 1000 seeds. Use of full ISTA tests would seriously delete seed numbers, leaving barely enough seeds to ensure proper regeneration, bearing in mind the uncertainty of this process. At Kew, the allowable maximum number of seeds which can be used in germination tests has been set arbitrarily for all collections at 15%. This figure is calculated by the computer and presented on the germination test sheet so that bank personnel can quickly make proper decisions in the allocation of the available seeds to various tests.

The location in the genebank is necessary to allow the seed to be found and withdrawn, whilst the number of containers and their type allow inventory checks to be made at the same time.

In order to keep the size of an individual record within reason, only the accepted test is entered on to the computer. All test sheets are held in a manual system organized by family, genus and species. Analysis of this paper record lead to the development of the germination schemes or algorithms currently in use. The verification status of the collection is shown in order to assist in the subsequent curation of this manual system.

MONITORING SEED VIABILITY

A combined electronic and paper record is used to prevent areas of little used computer space being allocated to record the results of the periodic tests which monitor viability. The results of the initial seed test and conditions are held in GBSRS and do not change. At the outset, this result and the germination conditions are copied over to the abbreviated seed record held in GBCIS. The data in GBCIS is overwritten when a 10-year viability test is carried out. This process of overwriting GBCIS is repeated each time a viability test is executed. Holding the latest retest result on GBCIS ensures that all users receive the latest available information. The complete record of all viability tests will be held as a paper record. Initially, the monitoring policy will be to repeat tests every 10 years. A simple program involving test date, monitoring policy and calendar date can then be written to list those collections in need of retesting in any year.

When sufficient results have been obtained, the storage life of

that seed lot before the regeneration level is reached can be estimated by probit analysis. Once such a prediction has been made, the retest period can then be adjusted so that tests are carried out when 1/2, 1/4, 1/8th and 1/6th of the lifespan remains. A similar approach can be adopted much earlier for those species with known seed viability constants and where the sample size used in the initial test is sufficient for storage life to have been reasonably estimated.

MONITORING SEED STOCKS

As in the monitoring of viability, the number of seeds (copied over from GBSRS to GBCIS) is amended when samples are distributed. Incorporated into this system are indicators that seed numbers have fallen to various critical values at which the distribution policy will need to be amended. Using such techniques, it is possible to operate the active and base elements of a single collection within one container, provided the inital estimate of numbers was correct.

Where multiples of containers have been used to hold one collection, so maximizing the use of the cold room space, then exhaustion of seed stocks from one container must be recorded in order to update GBDLS.

PRODUCTION OF SEED LIST

The distribution policy descriptor (GB1/31) is the first field considered in the computer-aided production of the seed list so that only the seeds which are freely available are offered. All the other descriptors used are taken from the Passport data.

MONITORING SEED DISTRIBUTION

In view of the relatively high cost of collecting, processing and conserving germplasm collections, monitoring is necessary to ensure the proper use of germplasm. When a request for seed is made by a user, a file is created recording the user, his address and the serial numbers of the seeds requested. When further requests are made, the user's file is scanned to see whether any of the collections currently required have been despatched over the past 5 years. Request for accessions which have not been previously distributed are accepted, the seed number amended and the request recorded. The conditions used in the most recent germination test are provided with seeds in order to help the user to produce the required plants. Some collections contain a high proportion of incompetent (empty) seeds which cannot be separated in cleaning. Genebank staff are alerted to the need to increase the size of the sample so that the proper number of viable seeds are sent. Passport data are also provided where requested. Where previous requests have been made the material is withheld at the manager's discretion. The user is then asked to offer his explanation

for the need of the repeat donation. Anyone making proper use of the material has no difficulty in satisfying this check. Anyone using germplasm collections merely because of their convenience are likely to be deterred and improper use of the material can be avoided.

ANNUAL CHECKS OF GENEBANK EFFICIENCY

The difference between the date of donation and the date of entering the genebank for each collection processed in any one year can easily be calculated. Comparing the average time of processing against the total number of samples processed in any one year can be looked at to ensure that throughput is acceptable. Similar comparisons can be done to determine whether or not the difference between the date of banking and testing is acceptable.

FURTHER POSSIBLE ENHANCEMENTS OF THE SYSTEM

Areas for future improvement of the management function of the computer appear to be:

(i) Storing the germination schemes/algorithms at present being developed for a wide range of plant families by Royal Botanic Gardens, Kew/Reading University. The computer would then be able to print the test sheet with the initial germination suggestions of the appropriate scheme already completed.

(ii) Storing ISTA germination requirements for use as in (i).

(iii) Storing requirements of the universal type of test suggested for rice by Ellis et al. (1983) for use as in (i)

(iv) Programming the computer to decide whether regeneration is necessary or unnecessary on the basis of sequential testing.

(v) Using probit analysis on a series of retest results through time to estimate the longevity of that seed lot under bank storage conditions.

(vi) Calculating the minimum number of seeds necessary to give uniform accuracy in moisture content determinations.

(vii) Processing the results of gravimetric determination of seed numbers to ensure that overestimation is avoided.

(ix) Interfacing with an electronic balance for the immediate recording and calculation of moisture content and seed number determinations.

Whether the availability of such information is of value will

depend on the range of material for which the genebank is responsible. Where genebanks are responsible for only one species, then standard answers to these problems will be more appropriate and need not be held on the computer.

THE APPLICATION OF THIS APPROACH

The unique nature of the seed bank at Wakehurst Place is often cited as a reason why the system described here has little general applicability. However, most of the management descriptors used are common to the other genebank systems, either extant or proposed, which are described at this workshop. Close consideration of the system described in this paper shows that these are the descriptors which form the basis for the management system. In genebanks responsible for a restricted range of species, then the need for an elaboration of the germination conditions may be equally restricted and could be recorded more simply. Indeed, "testing in accordance with ISTA rules" would appear to remove any need to record germination conditions. Yet within ISTA rules, there are six alternative dormancy-breaking treatments which can be acceptably applied to barley seed lots and three alternative, yet acceptable, temperature regimes at which to test rice seed. Surely if any of these alternatives are used in testing, then any user of the seed will need to be informed before the conditions necessary for their germination can be provided. Bank managers should be aware that most users are unlikely to be familiar with ISTA's rules.

Adopting the less ambiguous conditions of the universal tests of Ellis et al. (1983) would do much to overcome the problem of alternatives but not the problem of a user's ignorance of the temperature and chemical treatments involved. The provision of both seeds and the necessary germination conditions will help prevent the waste of genetic resources and the user's efforts in rediscovering what the seed bank already knows.

ACKNOWLEDGEMENTS

The work of A. Black, C. Ward, O. Peterken and D. Trimnell, students of the Lanchester Polytechnic Coventry is gratefully acknowledged.

REFERENCE

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Appendix IV (cont'd.)

Management Systems at the National Vegetable Research Station Gene Bank

by

D. Astley

The Gene Bank, established in 1981, has a remit for the long-term conservation of small-seeded vegetables. The site of the Gene Bank at the National Vegetable Research Station (NVRS), Wellesbourne, UK ensures that a wide spectrum of scientific expertise is available for consultation. The management system for the Gene Bank has evolved through numerous changes attempting to simplify the daily working routines. The organization of the various steps of the genebank process, culminating in a coordinated sequence of events and well-documented, stored germplasm is the essence of the genebank curator's work. Essentially this entails the acquisition, storage and documentation of new material; the monitoring and maintenance of extant collections and the dissemination of information and germplasm to users. The system as described below represents one point along the ever-changing continuum of the NVRS programme.

The basis of the management system is a combination of various manual data handling techniques and a computer program for data storage and manipulation. The Agricultural and Food Research Council provides a computing service to all its institutes in England and Wales through a network of distributed multi-user minicomputers (AGRENET) from the Digital Equipment Corporation VAX range. The NVRS and the Genebank are serviced by the NVRS node of AGRENET. The NVRS VAX 11/750 has 40 terminals, 3 MB internal memory and 454 MB Winchester user disks, services approximately 180 users. The Gene Bank houses one terminal.

For historical reasons the Gene Bank uses INFO, a pseudo-relational database management system, rather than DATATRIEVE, the VAX native file handling package. INFO uses a conversational language allowing the user to create and maintain information in an easily accessible format. Five general areas of use can be defined: Data Entry, Data Update, Querying, Report Writing and Programming.

Data preparation for input to the database has been via a paper input form (Figure 7). This step raises some questions:

1. Is direct data entry more efficient?
   We have found the collation of data from many sources onto one form per accession for a single direct entry has suited <u>our</u> needs.

2. Once data in the database change (i.e. addition) is the original

NVRS GENE BANK PASSPORT/STOCK DATA FORM

Accession Number NVRS _ _ , _ _ _ _ _ _

Genus _ _ _ _ _ _ _ _ _ _
Species _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ Subspecies _ _ _ _ _ _ _ _ _ _ _ _ _ _ _
Varietal Name _
Common Name _
Donor _
Donor Number _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _

Additional sample identifier and number:

_ _

Collectors name or institution _
Collectors sample number _ _ _ _ _ _ _ _ _ _ _ Date of collection _ _ / _ _ / _ _
Country of collection _ _ _ Region of collection _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _

Precise location of collection site: _
_ _

Altitude _ _ _ _ _ m. Latitude _ _ _ _ _ Longitude _ _ _ _ _
Cultivar name _ _ _ _ _ _ _ _ _ _ _ _ _ _ _

Donor Status:
1-Collector 2-Plant Breeder 3-Farmer/Grower
4-Seed Firm 5-Gene Bank 6-Institution
7-Other _ _ _ _ _ _ _ _ _ _ _ _
_ _ _ _ _ _ _ _

Genetic Status of Sample:
1-Wild 2-Weed 3-Landrace
4-Breeders material 5-Cultivar
6-Other _ _ _ _ _ _ _ _ _ _ _ _
_ _ _ _ _ _ _ _

Collection Source:
1-Natural vegetation 2-Farmer/Grower
3-Plant Breeder 4-Market
5-Seed Firm 6-Gene bank
7-Other _

Types of Sample:
1-Seed 2-Vegetative

Status of Sample:
1-Pure line 2-Population

Number of plants sample _ _ _ Size of sample, seed _ _ _ Size of sample, vegetative _ _ _

Extra notes _
_ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _

Rack number _ _ Shelf letter _ Box number _ _

Number of sample packets (10g) _ _ _ (5g) _ _ (0.5g) _ _

Total seed weight _ _ _ _ . _ _ g. Minimum seed weight emergency level _ _ g.

Germination test percentage-initial _ _ _ % Germination test percentage-latest _ _ _ %

Date of last germination test _ _ / _ _ / _ _ Germination test interval in years _ _

Year of last regeneration/multiplication _ _

Figure 7. NVRS Gene Bank passport/stock data form

sheet defunct?
We maintain original input sheets for passport data. Obviously updated accession information is available on hard copy.

The fact that the Gene Bank is responsible for a number of small-seeded vegetable crops governs the definition of the database file structure (Figure 8). Passport and stock data are common to all crops while characterization and evaluation data are crop specific. In

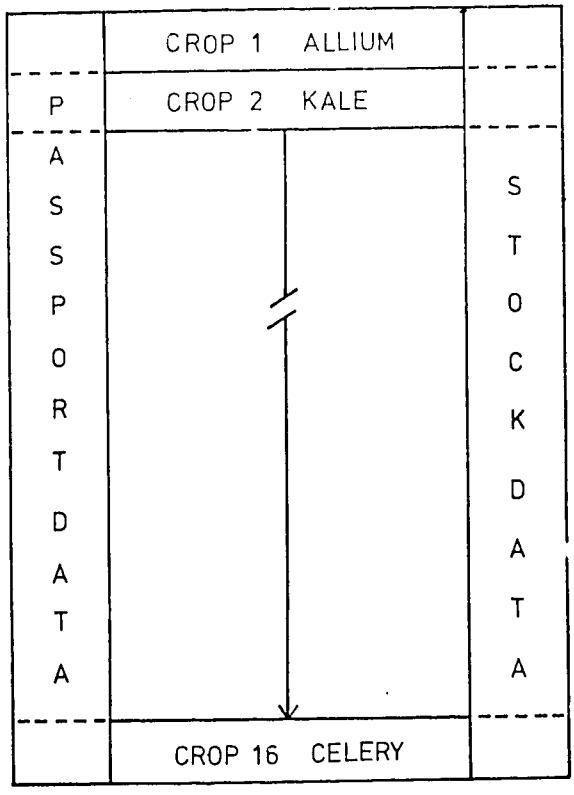

Figure 8. NVRS Gene Bank file structure

INFO, files can be related allowing simultaneous manipulation of all data relevant to a single accession, e.g. passport data related with stock data.

The need for non-computing staff to use the database requires that the system be 'user friendly'. To achieve this, a series of INFO programs was written to provide a simple menu driven system. The various facilities provided by the menu (Figure 9) are a culmination of what were thought to be necessary and what in practice has been desirable subsequently.

(A) Data entry (Figures 10 to 11)

The data entry mechanism is also menu driven. The screen response offers a choice of four options (Figure 10), three crops defined by IBPGR descriptors and a non-descriptor crop category. For example, the

```
09:23:43        NVRS GENE BANK DATABASE MANAGEMENT SYSTEM          8/11/1984
                              MASTER MENU

Data Entry:                                   Catalog/stock-update
    (A)   Data entry menu                          (D)  produce catalog
                                                   (E)  variety list
                                                   (F)  embargo expiry

Reports:                                      Hard Copies:
    (G)  Database status report                    (J)  print accessions
    (H)  Seed weight report                        (K)  full accession report
    (I)  Crop status report                        (L)  print data

Other options:
    (M)  sort data files                           (Q)   Diary
    (N)  exit to INFO                              (R)   Auto Return  [ ON  ]
    (P)  set output file

 please enter your selection:
```

Figure 9. Master menu (NVRS)

selection of 'A' initiates the Allium data input form (Figure 10) giving the list of pages available. At this point there is validation of the crop code and accession number uniqueness. A numerical check digit was envisaged as a valuable security feature but, as yet, has not been introduced. Pages can be selected in any order with the fields available per page being displayed (Figure 11). For characterization fields, the available descriptor states for each descriptor field are displayed as the cursor moves down the page (Figure 12 and 13).

```
                    menu
                    ====
                    (A)     Allium accessions
                    (B)     Beet accessions
                    (C)     Brassica accessions
                    (N)     NONDESC accessions

                    enter your option ->

09:38:48                ALLIUM DATA INPUT FORM                  8/11/1984
                        -----------------------

     PAGE       CONTENTS                  PAGE       CONTENTS
     ----       --------                  ----       --------
      1         Stock Data                 8         Disease Resistance
      2         Accession Data             9         Bacteria
      3         Collection Data           10         Virus
      4         Seed Sample Data          11         Full Evaluation
      5         Characterisation          12         Full Evaluation
      6         Characterisation          99         HELP
      7         Pest Resistance         RETURN       Start a new Accession

Please enter Accession Number:
                Check Digit:
```

Figure 10. Allium data input form (NVRS)

```
IS THIS RECORD ACCEPTABLE (Y,N,Q OR L) >

                    P A S S P O R T   D A T A          Page 2
                    -------------------------        Accession Data

GENUS          Allium
SPECIES        cepa
SUBSPECIES

VARIETAL NAME     WHITE GLOBE
COMMON NAME       BULB ONION

DONOR             BDDNVRS
DONOR NUMBER      AC123456

ADDITIONAL SAMPLE IDENTIFIER AND NUMBER
```

Figure 11. Allium cepa passport data (NVRS)

```
                    C H A R A C T E R I S A T I O N        Page 5
                    -------------------------------

NATURE OF THE STORAGE ORGAN
OTHER                                          MENU
PLACE OF MULT/REGENERATION                     ----
LIFE SPAN                                  1   BULB SINGLE LARGE
LEAF LAMINA                                2   BULB SEVERAL SMALL
ABILITY TO FLOWER                          3   RHIZOMES
GENERAL FERTILITY                          4   CLOVES
SIZE OF UMBEL                              5   FOLIAGE LEAF BASES
FLOWER COLOUR                              6   OTHER (SPECIFY)
OTHER
PRESENCE OF BULBILS (TOPSETS)
MODE OF REPRODUCTION
BULB SHAPE
OTHER
UNIFORMITY OF BULB SHAPE
BULB SKIN COLOUR
OTHER
FOLIAGE COLOUR          OTHER
PRIMARY CROP USAGE      OTHER
```

Figure 12. Characterization data (NVRS)

```
                    C H A R A C T E R I S A T I O N        Page 5
                    -------------------------------

NATURE OF THE STORAGE ORGAN  1
OTHER                                          MENU
PLACE OF MULT/REGENERATION NVRS                ----
LIFE SPAN   2                              1   WHITE
LEAF LAMINA                                2   YELLOW
ABILITY TO FLOWER  +                       3   LIGHT BROWN
GENERAL FERTILITY  1                       4   BROWN
SIZE OF UMBEL   2                          5   DARK BROWN
FLOWER COLOUR   1                          6   RED
OTHER                                      7   CHARTREUSE GREEN
PRESENCE OF BULBILS (TOPSETS)  0           8   MIXED POPULATION
MODE OF REPRODUCTION   3                   9   OTHER (SPECIFY)
BULB SHAPE   4
OTHER
UNIFORMITY OF BULB SHAPE   1
BULB SKIN COLOUR
OTHER
FOLIAGE COLOUR          OTHER
PRIMARY CROP USAGE      OTHER
```

Figure 13. Characterization data (NVRS)

The stock input page (Figure 14) defines the fields available but also illustrates certain practical points in the management system.

1. The position in the -20°C cold room of any accession can be pinpointed by a 5 digit code, e.g. Rack Number 12, Shelf Blockletter B, Box Number 21.

2. Each accession is divided into base and active collections (Figure 15). One 5 g sample per accession is double packed in foil laminate pouches and stored as the base collection. It is convenient to standardize by weight, although a wide variation is evident between crops in the numbers of seeds stored as a base collection. The active collection seed are packed into 10 g pouches, any remaining seed are divided into 0.5 g lots, the latter samples being used for distribution and germination tests.

3. A compulsory field, EMBARGO, was introduced to define the availability of an accession. Dead or embargoed accessions are rejected in the searches for the production of catalogues. A seed embargo is against the general ethos of freely available genetic resources, but in certain instances agreeing to an embargo has been the only method of obtaining material.

```
IS THIS RECORD ACCEPTABLE (Y,N,O OR L) >

                              S   T   O   C   K                    Page 1
                              ---------------

RACK NUMBER    12
SHELF LETTER   B
BOX NUMBER     21
NUMBER OF SAMPLE PACKETS- 10g   4  5g  1  0.5g  6
TOTAL SEED WT.        48.00
MINIMUM SEED WT. EMERGENCY LEVEL     5.00
GERMINATION TEST % (INITIAL)        99.0
GERMINATION TEST % (LATEST)
DATE OF LAST GERMINATION TEST       8/ 6/1984
GERMINATION TEST INTERVAL IN YEARS       4
YEAR OF LAST REGEN./MULTIPLICATION
EMBARGO (A,D or E)       A
EMBARGO YEAR
```

Figure 14. Stock input form (NVRS)

(H) Seed weight report (Figure 16)

Initially designed as an aid to the regeneration programme to list all accessions where total seed weight is less than or equal to 5 g, there was an obvious flaw, i.e. it is possible to have 100 g of low quality seed. The search parameters were redefined to eliminate embargo material from the search and then extract all accessions where total seed weight is less than or equal to 5 g or the most recent

NVRS Vegetable Gene Bank Seed Storage
For a sample of 31.5g

	Packet weight	Number of packets	Single/Double packet
Base	5g	1	D
Active	10g	2	S
	0.5g	13	S

Sample for - germination test
- distribution sample

Figure 15. Example of accession divided into base and active collections (NVRS)

germination test (i.e. initial or last) is below 50%. The data in Figure 16 are fictional from the demonstration file, hence all store locations equal 12A12. The search parameters can be redefined as the quality of stored material is improved by regeneration.

(I) Crop status report (Table 3)

This report details the numbers of accessions held in the database for the various crops. The code refers to a two digit crop-code prefix in the accession number.

8/11/84 PAGE 1

Seed Wts. Below Emergency Level

Acc-No	Common Name	Weight	Init%	Last%	Locn
1000017	BULB ONION	1.60	81.0		12A12
1000027	BULB ONION	4.52	81.0		12A12
1000033	BULB ONION	1.60	81.0		12A12
1000038	BULB ONION	25.20	2.0		12A12
6000051	BRUSSELS SPROUT	85.10	18.0		12A12
6000054	BRUSSELS SPROUT	27.10	39.0		12A12
6000058	BRUSSELS SPROUT	27.50	31.0		12A12
6000066	BRUSSELS SPROUT	1.40	81.0		12A12
6000073	BRUSSELS SPROUT	4.00	98.0		12A12
6000086	BRUSSELS SPROUT	25.00	25.0		12A12
6000090	BRUSSELS SPROUT	10.20	18.0		12A12
6000099	BRUSSELS SPROUT	29.10	40.0		12A12
10000167	LETTUCE	17.00	97.0	14.3	12A12
10000180	LETTUCE	65.00	84.0	49.0	12A12
10000203	LETTUCE	16.50	81.0	34.0	12A12
1000208	SHALLOT	58.50	35.0		11B22

MORE?

Figure 16. Seed weight report (NVRS)

(D) Produce catalogue (Tables 4 and 5)

This program produces crop catalogues by an initial selection on the crop-code and subsequent selection on embargo, seed weight and germination percentage. The product of each search is ordered and printed. The field to be ordered is determined by the crop-code, two formats for the final print being possible; single crops are ordered on variety (Table 4) while multiple crop groups, e.g. "08 Brassica others", are ordered on Latin names and on variety within each species (Table 5). The selection criteria are predetermined to ensure that quality seed are available for distribution. Only the first accession of each variety meeting the requirements is selected for inclusion in the catalogue. The crop catalogues are the main mechanism for information distribution; more specific information can be produced upon request.

Table 3. Crop status report (NVRS)

CODE	CROP	TOTAL
1	ALLIUM	827
2	KALE	73
3	CAULIFLOWER	367
4	BROCCOLI	170
5	CABBAGE	684
6	BRUSSELS SPROUT	935
7	KOHL RABI	30
8	BRASSICA OTHERS	446
9	RAPHANUS	456
10	LETTUCE	1208
11	VICIA BEAN	0
12	PHASEOLUS BEAN	0
13	CARROT	219
14	BEET	36
15	PARSNIP	0
16	CELERY	21

Table 4. Example of crop catalogue (single crop) (NVRS)

NVRS VEGETABLE GENE BANK
****

CROP: - CARROT

VGB NO	VARIETY	VGB NO	VARIETY
005592	ADORNO RS	003970	AMSTEL
003981	AMSTERDAM 5564	005477	AMSTERDAM FORCING
005120	AMSTERDAM FORCING-ASMER *	003942	AMSTERDAM GRACE
003943	AMSTERDAM INDIA	003944	AMSTERDAM MASTER
005590	AMSTERDAM NINICOR RS	003967	AMSTERDAM OUTDOOR
003935	AMSTERDAMMER BAK	003963	AMTOU
004009	ANNUAL RED RAWALPINDI	005117	ASMER BABY CAN
003848	AUTUMN KING	003958	AUTUMN KING LAROS
003895	AUTUMN KING ORIGINAL	003897	AUTUMN KING SELECTED
005118	AUTUMN KING-ASMER KINGSTON	003949	BANTA
005116	BERLICUM-ASMER BERLICUM *	005119	BERLICUM-ASMER BERLINDA
005593	BERLIKUMER BERCORO RS	003990	BLANCHE A COLLET VERT ...
003923	BLANCHE A COLLET VERT...	003919	BLANCHE DEMI-LONGUE
003991	CARENTAN	003938	CENTURY
003971	CHAMPION SCARLET HORN	005090	CHANTENAY LONG
003928	CHANTENAY RED CORED	005588	CHANTENAY RED CORED CHANSON
005115	CHANTENAY RED CORED CLUSEED *	005589	CHANTENAY REX RS
003883	CHANTENAY SUPREME	005585	CLAIRON RS
003830	CLUCAS'NEW MODEL RED CORED	003898	CLUSEED NEW MODEL
003986	CRUISSY	003950	CYLINDRA AMSTERDAMER
005595	DANVERS DANKO RS	005128	DANVERS RED CORED
003899	EARLY GIANT	003964	EARLY MARKET
003886	EARLY NANTES	003969	EARLY SPARTAN
005591	EDJORA RS	003834	FLAKKEE FRENCH STRAIN
005594	FLAKKESE FLACORO RS	003961	FLAKKO
003905	G 1958	003894	GIANT IMPROVED
005127	GOLD KING	003885	GOLD PAK
005475	IDEAL RED	003891	IMPERATOR 407
003907	IMPERATOR 408	003892	IMPERATOR 58
003979	IMPERIAL LONG SCARLET	003926	JAUNE OBTUSE DU DOURS
003972	KINKO CHANTENAY 4 INCH	003974	KINKO CHANTENAY 6 INCH
003975	KINKO CHANTENAY 8 INCH	003977	KURODA CHANTENAY
003965	LITTLE FINGER	003924	LOBBERICHER
003902	LONG CHANTENAY	003896	LONG CHANTENAY RED CORED
003916	LONG IMPERATOR 1	003917	LONG IMPERATOR 58
004079	MACBETH	003952	NANTA
003945	NANTES DUKE	003946	NANTES EXPRESS
003947	NANTES FANCY	005584	NANTES FORTO RS
003948	NANTES KIKMA	003957	NANTES NARKO
005582	NANTES PRODUCO RS	005583	NANTES SLENDERO RS
003890	NANTES STRONG TOP	005586	NEVESTA
003976	NEW KING CHANTENAY 3 INCH	003978	NEW KURODA
003940	OKANZA	003966	PARIS FORCING
005596	PARIS MARKET	003937	PERFECTA
003968	PRIMA (TOUCHON)	003953	PRIME NANTES
003900	RED CORED CHANTENAY	003835	RED GIANT
003954	REDO	003941	REGULUS IMPERIAL
004014	R.Y	005126	ROYAL CHANTENAY
003925	ROYAL CHANTENAY ELITE 275	003989	ROYAL CHANTENAY RED CORED
003914	SCARLA	005125	SCARLET NANTES
003901	SHIN KURODA WASUN	004013	SHIRAZ
004011	SHIRAZ H.O.	003856	SPALDING RED CORED IMPROVED
004010	SPEERS NORLEK GIANT	003929	ST. VALERY
003951	SWEET HEART	003986	TABOR
005587	TAMINO RS	003992	TANGAR

Table 5. Example of crop catalogue (multiple crop groups) (NVRS)

NVRS VEGETABLE GENE BANK
****

CROP:- BRASSICA OTHERS

GENUS	SPECIES	VARIETY	VGB NO
Brassica	campestris	SNOWBALL	004087
		SNOWBALL SELECTED	003446
		SPRINTER	003442
		TARONDA	003371
		TEUTOBURGER	004060
		THE BRUCE	004061
		THE WALLACE	004062
		TYFON	003341
		VEITCH'S RED GLOBE	003445
		VOBRA	003342
		WESELER	004063
		WHITE GLOBE	004035
		WONG BOK	005168
		YELLOW TANKARD	004064
		YUMANG	003135
Brassica	carinata	ADDIS ACEB	002485
		KARATE	004264
		TAMU TEXEL GREENS	004669
Brassica	chinensis	CHOI SUM	005103
Brassica	juncea	COMMON GREEN	005157
		GIANT TAISAI	005159
		KAI CHOI	005105
		KAI CHOI(CHIU CHAU)	005104
		KAI CHOY	002487
		KOMATSUNA	004682
		LATE KOMATSUNA	005163
		NAMFONG LOOSE LEAVED	005158
		NDAKUPUKA	004286
		SANTOH FRILLED	005162
		SANTOW ROUND LEAVED	005161
		SHIRONA	005164
		TAISAI	004681
		TSUNGA	004313
Brassica	napus	ACME	004038
		ASHGROVE	003267
		AUGBINY GREEN TOP	003469
		BALMORAL	003276
		BANGHOLM	004026
		BEST OF ALL	003457
		BISHOP	003308
		BROAD LEAF ESSEX	003333
		CANARD	003301
		CHAMPION	004039
		CHIGNECTO	003468
		CONQUEROR	003279
		CONQUEROR BRONZE GREEN TOP	003470
		CRACK	003354
		CRIFFEL	003318
		DANESTONE	003280
		DEVON CHAMPION	003367
		DOON MAJOR	004040

(E) Variety List (Figure 17)

The problems of duplication are not easy to solve but the Variety List program provides a starting point. Given a unique-number (equivalent to accession number in the ordered main file) the program will select other accessions with identical crop-code and varietal name. The resulting print out provides a range of stock control data and the donor name. At present all accessions of out-pollinating crops are being maintained separately, hence in Figure 17 variety Avoncross exhibits five accessions, all from East Craigs.

(F) Embargo enquiry

This program screens the embargo field for embargo accessions and checks the embargo end date against current date. Any accession resulting from this screen can be removed from the embargo category and made available.

Outside of the menu driven system the query language in INFO permits direct manipulation of the data (Figure 18). Selection of the passport file provides a data set which can be reduced in size by reselection using relational operators on combinations of fields. Reselection for crop-code 01 will provide a sub-set of all Allium accessions which can be further reselected, e.g. country of collection. Data from selected fields can be displayed and hard copy output obtained. Data from associated files, e.g. stock can be displayed or printed by relating files.

Additional facilities are provided by the EPSON HX20 microcomputer and FX80 dot-matrix printer. At present this equipment is used to

CROP:- BRUSSELS SPROUT
VARIETY:- AIRES

ACC-NO	DONOR	INITIAL TEST %	LATEST TEST %	TOTAL SEED WT	PACKETS 10	5	0.5	STORE LOCATION
6000055	EAST CRAIGS	80.0		0.10	0	1	6	01A09

PLEASE ENTER UNIQUE-NO
65

CROP:- BRUSSELS SPROUT
VARIETY:- AVONCROSS

ACC-NO	DONOR	INITIAL TEST %	LATEST TEST %	TOTAL SEED WT	PACKETS 10	5	0.5	STORE LOCATION
6000063	EAST CRAIGS	92.0		55.00	5	1	0	01A09
6000064	EAST CRAIGS	98.0		65.00	6	1	0	01A09
6000065	EAST CRAIGS	98.0		45.30	4	1	0	01A09
6000066	EAST CRAIGS	81.0		1.40	0	0	3	12A12
6000067	EAST CRAIGS	98.0		55.00	5	1	0	01A09

PLEASE ENTER UNIQUE-NO

Figure 17. Sample of variety list (NVRS)

```
ENTER COMMAND >SEL PASSPORT
   5652 RECORD(S) SELECTED

ENTER COMMAND >RES FOR CROP-CODE = 01
    827 RECORD(S) SELECTED

ENTER COMMAND >RES FOR SPECIES = 'cepa'
    584 RECORD(S) SELECTED

ENTER COMMAND >RES FOR VARIETY CN 'RED'
     31 RECORD(S) SELECTED

ENTER COMMAND >RES FOR COUNTRY-OF-COLL = 'SDN'
      6 RECORD(S) SELECTED

ENTER COMMAND >DIS ACC-NO,SPECIES,VARIETY,COUNTRY-OF-COLL
 1004102 cepa            HUDEIBA RED                    SDN
 1004103 cepa            WAD RAMLY RED                  SDN
 1005534 cepa            RED ONION                      SDN
 1005535 cepa            RED ONION                      SDN
 1005536 cepa            RED ONION                      SDN
 1005537 cepa            RED ONION                      SDN

ENTER COMMAND >
```

Figure 18. Query language permits direct manipulation of data (NVRS)

print self-adhesive labels for the foil pouches stored at -20°C. Simple BASIC programs produce labels with accession number, Latin binomial, etc. with or without sequential packet numbers. The micro is used in simple repetitious calculations such as moisture determination.

The potential value of this equipment is very broad, e.g.:

- production and reading of bar codes;
- direct links to electronic balances;
- data logging with direct transfer to VAX;
- production of glasshouse and field labels; and
- address/mailing lists.

Finally, there are routines at the NVRS Gene Bank which are recorded manually for convenience. All germination test information is logged onto data sheets with only the final percentage being entered to the computer, although the data sheets from all germination tests are stored for future consultation.

In the regeneration programme, plants in outbreeding populations are treated as individuals from germination to new seed, including growing, harvesting and threshing; the 'new' population being a mixture of equal seed weights from all plants. The coordination of this complex annual scheme is entirely manual.

There is the need always to be efficient but not at the expense of accuracy. The stages of genetic resources work are labour-intensive so new methodology must be investigated. In looking for improvements we have investigated various technological innovations for performance with small seeds. Thus far, seed counters, vacuum stations for germination tests, mini threshing machines and automated packaging machines have all proved less successful than dextrous assistants.

Management systems do not have to be complex, but they do have to reflect various constraints, e.g.:

- available resources;
- available staff;
- number of collections;
- number of crops; and
- crop types - inbreeder/outbreeder/vegetative.

Obviously the extant management system at any site will be a reflection of these constraints.

Appendix IV (cont'd.)

Management of Data and Information in Genebank Management at the Institute of Crop Science and Plant Breeding of the FAL

by

Dr. L. Seidewitz

INTRODUCTION

Plant breeders had expected that documentation would facilitate access to basic plant material held in genebanks in other parts of the world. When FAL [Institute of Crop Science and Plant Breeding of the Federal Research Centre of Agriculture Braunschweig-Völkenrode] started its genebank activities in 1970, it was decided that the institute would be responsible for both seed storage and information handling, although more importance was attached to the latter. By June 1984, the collection of plant genetic material had grown to a total of 43,682 samples and there was a corresponding increase in the amount of data on the accessions .

The computer in the Federal Research Centre of Agriculture is a SIEMENS machine, model 7541 with 4 mega bytes CPU which is at the centre of a network having different smaller computers and more than 100 terminals.

CHARACTERISTICS OF DATA DOCUMENTATION

Handling of data is an important part of plant genetic resources work. Any activity and all decision-taking depend on information for which the existence of corresponding data is required. For the purpose of computer aided information handling, all information relevant for genebank work is reduced to the essential fraction of factual data.

The data are presented as follows:

- individual comments have been omitted;
- output from a documentation system can be included in so-called "data banks" or "data bases" for factual data;
- factual data are immediately available;
- any single factual datum is accessible;
- factual data can be carried on paper (listings), on magnetic equipment (floppy discs, magnetic tapes), or transmitted via telephone lines; and
- factual data are easily exchangeable - as long as they are compatible with other documentation systems.

CLASSES OF FACTUAL DATA OF INTERNAL AND EXTERNAL INTEREST

Figure 19 shows the important activities of a genebank. These activities generate the data upon which any decision taking and successive activities depend. These data can be subdivided into two classes as shown on Figure 20:

- non descriptive (functional) data;
- descriptive (characterization and evaluation) data

As indicated in Figure 20, certain data of cooperating institutions are of mutual interest; both functional and descriptive data, therefore, should be recognized as being of possible interest to institutions. Regarding functional data from external sources, these data may be useful in reference to activities such as exploration, collection and accessioning. Descriptive data usually are of external interest with regard to taxonomic, botanic, agronomic and/or utilization orientated traits.

This type of external data will be used in any decision taking, thereby aiming to avoid duplication of effort.

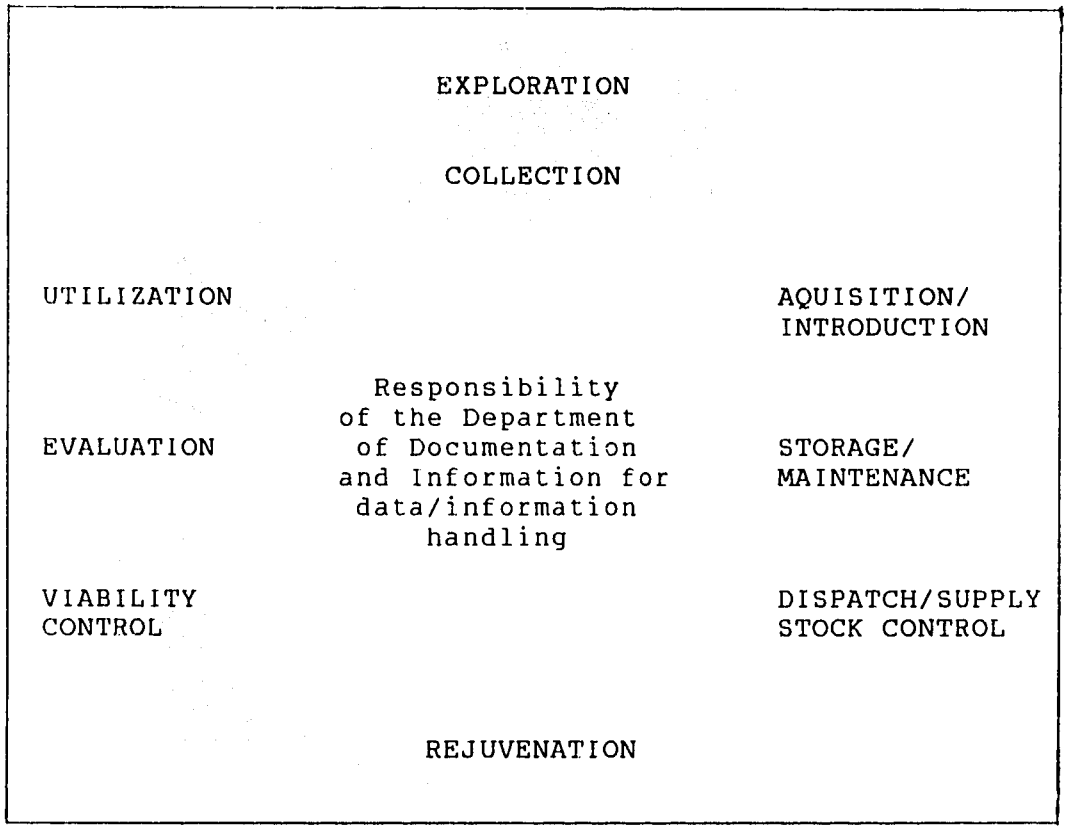

Figure 19. Responsibility in information handling (amended from April 1979) (FAL)

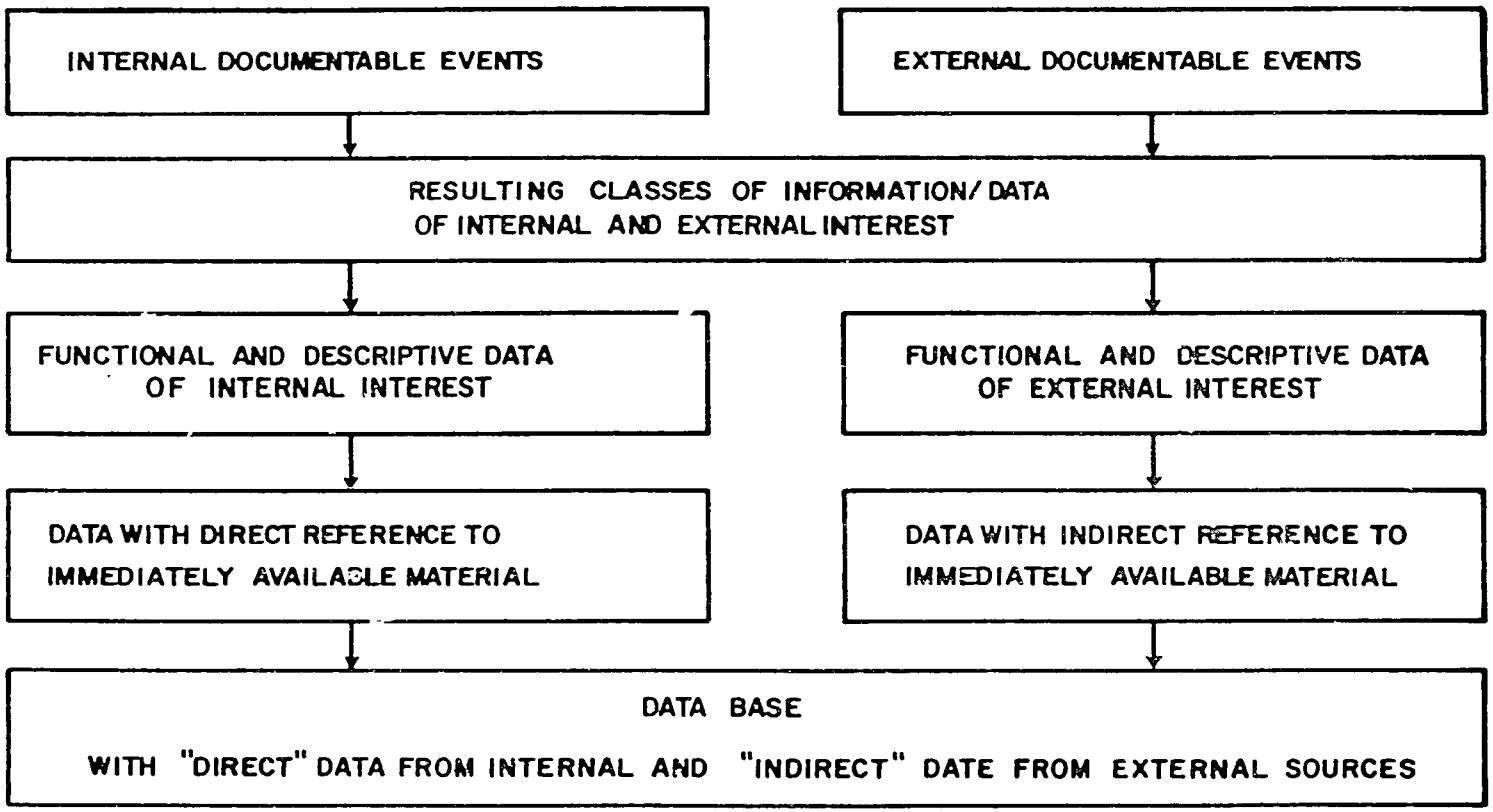

Figure 20. Internal and external interest in data on plant genetic material (FAL)

DESCRIPTORS AND DESCRIPTOR STATES

The presentation of factual data is identical to that of "structured information" for which matrices (tables) are used. Matrices are formed of so-called "fields". Each field has a "field name" and a "field content". A field name is identical to the name of a variable or characteristic of plant genetic material. The field itself carries an index to the respective variable or a degree of expression of a characteristic. It is a widespread custom to use the terms "descriptor" instead of "field name", "variable" or "characteristic", and "descriptor state" instead of "field content", "index" or "degree of expression". It should be recognized that "descriptor" and "descriptor state" are terms which represent the most important elements of an information system.

Descriptors simultaneously serve as the names used for characteristics and terminology in the recuperation of data (information) from any documentation system. About 1400 descriptors are in use at Braunschweig.

STRUCTURING OF INFORMATION FOR COMPUTER INPUT

Tables are required for data input into the computer. For this purpose a standard printed form is used. Computer printed listings are also employed. Verbal information is written on these listings before typing them into the computer. In this phase, coding of descriptor states takes place and descriptors are verified in the thesaurus.

Records are allowed to comprise up to 250 fields, with 965 bytes each.

Information structuring is followed by data input into the computer. For this procedure, 2 terminals are available. Data input requires a table in the computer which corresponds to the printed one; in this way, files are created.

THE FILE CONCEPT

No single file will be capable of holding all the data of a genebank. There are several reasons for which different files should be used. A large amount of space is required on either discs or tapes when a comprehensive file is moved from a tape onto a disc or vice versa. In addition files with a huge number of records need too much computing for any retrieval run. Finally, large files are difficult to sort. For these reasons, it was decided that smaller files with well-defined content should be created and maintained.

Basically, a distinction is made whether data refer to plant

genetic material or to its maintenance, supply, etc. (Figure 21). In other words, two groups of files with "descriptive" (crop plant related) and "non-descriptive" data (not crop plant related), are distinguished.

The group of files with "non descriptive" or "functional" data comprises:

-- files with data in relation to material maintenance;
-- files with data in relation to material supply;
-- files with regard to data base administration; and
-- control of terminology (employed descriptors, thesaurus).

Files with 'descriptive' data are further subdivided into the groups:

- files that refer to the genebank's own material; and
- files that refer to other genebanks' material.

In both cases, a distinction is made between data that refer to plant genetic material that is "directly" or "indirectly" available. So-called "direct" data are subdivided into two groups, according to when it is available. Data that arrive together with plant genetic material are treated as "primary" data while additionally available evaluation data are treated as "secondary" data.

For special reasons, a group of files with inventory data has been assigned, on the basis of one file per crop plant. In a few exceptional cases, when dealing with many accessions, one single file was found to be too long and the data are kept in two files (Figure 21).

HANDLING OF DATA/INFORMATION IN CONNECTION WITH ACCESSION, MAINTENANCE AND SUPPLY OF GENE BANK MATERIAL

This category comprises all but characterization and evaluation data and performs a key function in material administration, cataloguing of accessions, production of directories and stock and viability control. This portion of the data is handled and computerized as "non-descriptive" data.

IDENTIFICATION OF GENEBANK MATERIAL

Computerization of information in connection with the identification of accessions gave rise to a series of descriptors which also reflect the type and kind of traceable data from the data base:

The following are taxonomy orientated descriptors:

-- FAMILY, GENUS, SPECIES, SUBSPECIES, VARIETAS, SUBVARIETAS, FORMA, FORMA SPECIALIS.

1. Files with "Descriptive" Data

1.1. files with direct data (on the genebank's own material)

1.1.1. primary data (that arrived together with the material when it was accessed)

HORDEUM.BGRC.[illegible]
HORDEUM.BGRC.SO.TUM

1.1.2. secondary data (evaluation data)

HORDEUM.BGRC.EVAL

1.2. files with inventory data

HORDEUM.INDEX.SO (spring barley)

1.3. files with indirect data

SOLANUM.FIDAS.CPC (Commonwealth Potato Collection)

2. Files with "Non-Descriptive" Data

2.1. file with data in relation to material maintenance

MAINTENANCE

2.2. files with data in relation to material supply

SUPPLY.BGRC.1983
SUPPLY.BGRC.1984

2.3. files with data in relation to data base administration

BGRC.DESCRIPTORS
BGRC.DESCRIPTORS.HORD
THESAURUS.NEW.01
THESAURUS.NEW.DESCRIPTOR STATES
THESAURUS.NEW.BROADER TERMS

Figure 21. The File Concept (FAL)

Each taxonomic unit also includes its authority. Descriptors in this case read:

-- AUTHOR SPECIES, AUTHOR SUBSPECIES etc.

If important, synonymous taxonomic information is kept with its respective set of descriptors:

-- SPECIES SYNONYM, SUBSPECIES SYNONYM etc.

It was found useful to define crop plants with their respective common name in a field called:

-- CROP.

In a few cases, the genotype has been specified in a single field:

-- GENOTYPE.

Sample names and figures used for the identification of cultivars, landraces, lines, clones etc. are entered in the field:

-- DESIGNATION.

The number of chromosomes and level of ploidy are placed in the following fields:

-- CHROMOSOME NUMBER n
-- CHROMOSOME NUMBER 2n
-- PLOIDY LEVEL X.

ACCESSION OF GENEBANK MATERIAL

All accessions are assigned an accession number upon receipt by the genebank. Accessions are numbered sequentially in this field:

-- BGRC ("Braunschweig Genetic Resources Collection").

Any donor's accession or collection number is also kept in the system. Accessions can, therefore, be traced by the genebank's own or by any donor's accession or collection number. The donor and donor country identifying data are stored in the fields:

-- DONOR and DONOR COUNTRY.

The nature of samples is specified as "cultivar", "landrace", "line" etc. in the field:

-- SELECTION LEVEL.

Origin related information provides data for special fields such as:

-- ORIGIN COUNTRY, ORIGIN REGION, ORIGIN, LOCALITY etc.

Knowledge of the countries of origin provides an important source of information in order to determine the degree of completeness of a collection of plant genetic material with regard to the geographic distribution of diversity.

Origin and accession information would be incomplete if not incorporated together with the respective dates of origin and accession. For a computerized storage of these data the following fields are used:

-- ORIGIN YEAR, ORIGIN MONTH, ORIGIN DAY, ACCESSION YEAR, ACCESSION MONTH, ACCESSION DAY.

The age of the accession is specified by the following descriptors:

-- HARVEST YEAR AT DONOR'S, BGRC HARVEST YEAR.

The quantity of seeds in stock is reported as either number of grains or quantity in grams. Respective descriptors are:

-- QUANTITY ACCESSED IN G, GRAIN NUMBER IN STOCK.

MAINTENANCE OF GENEBANK MATERIAL

A series of descriptors has been assigned to provide the corresponding number of fields for consultation of threshold values in viability, number of seeds per accession, maximum moisture content, number of years between two viability tests, etc. In addition, the number of regenerations is recorded. The number of seeds per viability test, number of seeds per accession for long-term storage and seed number to be distributed per sample are recorded and relate to maintenance of the collection.

Other descriptors provide for the recording of the dates when the long-term storage began, seed moisture content and viability at start of storage and dates of first viability test.

Descriptors in this connection read as follows:

STORAGE STARTED MONTH
STORAGE STARTED YEAR
STORAGE TEMPERATURE
WATER CONTENT IN % AT STORAGE START
VIABILITY IN % AT FIRST TEST
SECOND TEST etc.
DATE OF FIRST VIABILITY TEST
DELIVERABLE SEED NUMBER PER SAMPLE
SEED NUMBER PER VIABILITY TEST
MINIMUM SEED NUMBER FOR LONG-TERM STORAGE
MINIMUM VIABILITY IN %
UPPER LIMIT OF WATER CONTENT IN % AT START OF LONG-TERM STORAGE
NUMBER OF YEARS BETWEEN 2 VIABILITY TESTS
TIMES REGENERATED.

SUPPLY OF GENEBANK MATERIAL

It has been found useful to trace where and when material has been supplied in order that the number of samples supplied per crop plant and year can be reported, and so that the quantity submitted and details of mailing and phytosanitary certificates can be included when keeping data related to the supply of genebank material. The following descriptors serve this purpose:

ADDRESSEE
SAMPLE DELIVERS MONTH
SAMPLE DELIVERY YEAR
KIND OF MATERIAL DISPATCHED
QUANTITY SUBMITTED
PHYTOSANITARY CERTIFICATE NUMBER
EXPORT PERMIT NUMBER
MAIL REGISTRATION NUMBER.

Appendix IV (cont'd.)

Management of Internal Information at the Polish Genebank

by

J. Serwinski

The genebank information system is a tool in a genebank manager's hands to facilitate the capture, maintenance and processing of the data relevant to the diverse activities of the genebank, which include introduction, conservation, characterization, evaluation, distribution etc. of plant material. Most of the data which enter the information system are of direct interest to the genebank users. The external value of information, such as the origin and characteristics of accessions, is self-evident and a strong emphasis has always been placed on the management and dissemination of these data to breeders, scientists and cooperating genebanks. There is however, a considerable amount of data in a genebank which is virtually of no external value but nonetheless is essential so that management procedures are organized and performed in an efficient way. Monitoring of the quality and quantity of seeds in store, preparing and handling of regeneration, identification of samples to be evaluated and distribution of seeds are examples of procedures which require careful screening of many files before the actual work with the seed or plant material begins. This kind of information does not have to be standardized on the international level, such as is necessary with passport, morphological or evaluation data.

The management information is arranged in a similar way to the data for external use, i.e. using descriptors. Both types of information must be combined to form a complete documentation system.

In the genebank in Radzikow the documentation system is implemented on a minicomputer PDP-11/34a (Digital Equipment Cooperation). The software used is an interactive data management system DATATRIEVE-11. The data management facilities include data definition, data entry, selective data retrieval, sorting, update and printing reports. The system supports simple, easy to learn language for communication with users. The experience over the last three years of using this system has proved that it is of value for genetic resources documentation. The system is versatile enough to handle the data for different crops without any large scale modifications.

The information stored in the documentation system is separated into functional files for each crop. Figure 22 shows the information flow between the different activities of the genebank. The data flow is controlled by the computer programs, which are in the form of procedures in the DATATRIEVE-system or are independent programs written in such languages as FORTRAN or PASCAL.

ARRANGEMENT OF DATA FILES

Each accession in the genebank has a unique number which is assigned when the sample is first introduced into the genebank. The accession number is very important also from the data processing point of view as it is a linkage descriptor between the files. Cross-referencing of records by the accession number (and also by any other descriptor) in order to retrieve the data stored in different files is one of the most important features of DATATRIEVE.

The data relating to the various aspects of the work of the genebank are kept in five files. Figure 23 shows the record structure of particular files as well as linkages between them.

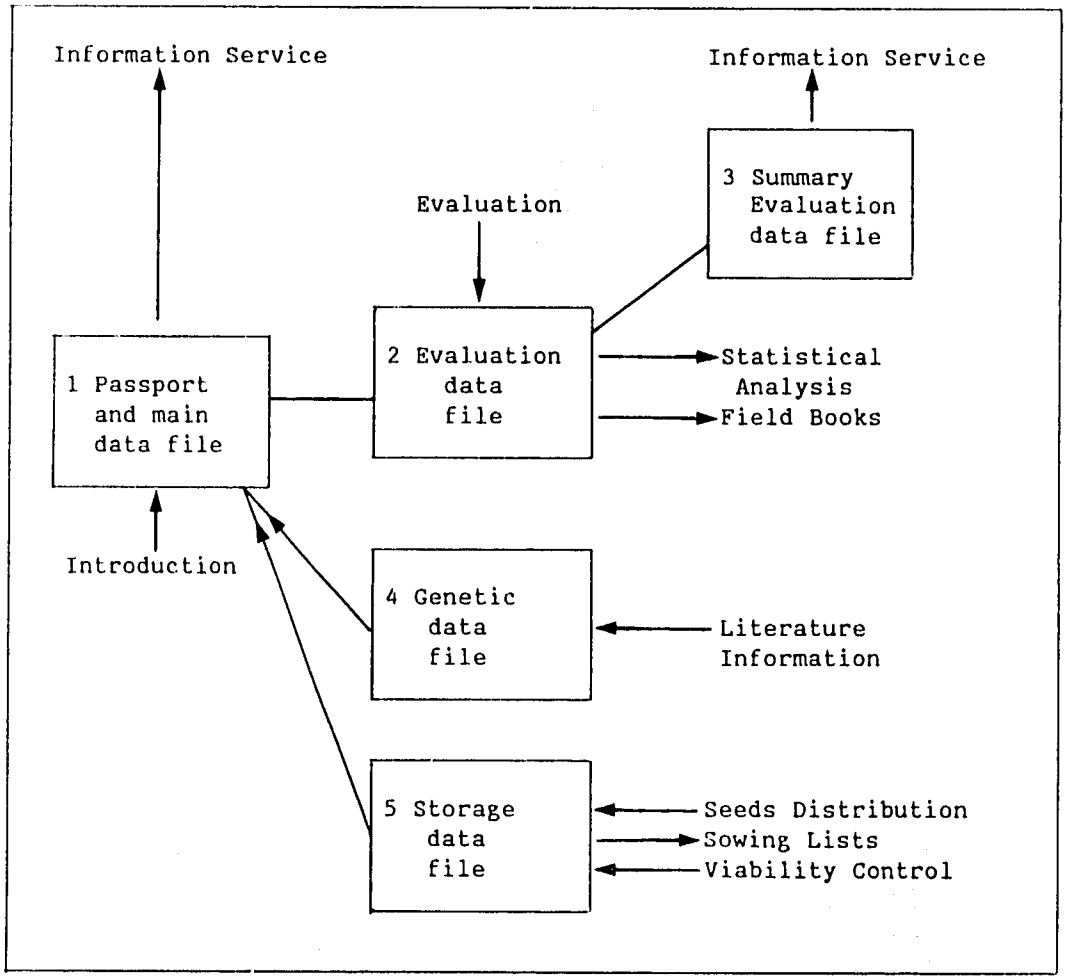

Figure 22. Inter-relation of data files (Polish Genebank)

1. Passport and main data file

This includes information relating to the identification of each accession in the genebank e.g. accession number, accession designation (name), botanical characteristics, origin etc. Apart from this, the field plot numbers used for evaluation in respective years are stored. The genebank adopted the approach to evaluate each accession for at least three years and it was found useful to record the fact of evaluation in one record. In the case when the accession is sown in many plots only the plot number of the first repetition is stored in the passport data file and all following evaluation plot numbers will be stored in the "Evaluation data file". As shown on Figure 23, "plot numbers" are also used as linkage descriptors between the passport file and the files with evaluation data.

2. Evaluation data files

The files store the results of field and laboratory evaluation in a particular year. A code is used to indicate the type of evaluation (for example "00" means one repetition evaluation, "01" is a random block method, "02" is a latin square method, "03" is a split plot method). The structure of each file allows storage of information in the same form as in the experimental book.

3. Evaluation data summary file

This stores summary evaluation data for all accessions of a particular crop from evaluations carried out up to the current year. As indicated above, the evaluation is usually carried out for three years, although not necessarily consecutive years. This file is used to store the results of statistical analysis of raw data maintained in the file mentioned in (2). For some descriptors, these are averages of results from all experiments, for others minimum or maximum values, etc. The algorithm selected to calculate the summary data is defined by the crop curators. As the raw data are always available the data summary file can always be recalculated.

4. Genetic data file

This stores information concerning the pedigree and valid gene symbols for a particular accession. The main source of this information is the literature. All gene symbols are stored in one field (descriptor 'Genotype') and are separated by one character (usually by comma). This arrangement saves a lot of space but the selective retrieval of information is slower than for other data because the field has to search for a particular symbol or symbols. The search function (CONTAINING) is supported by DATATRIEVE.

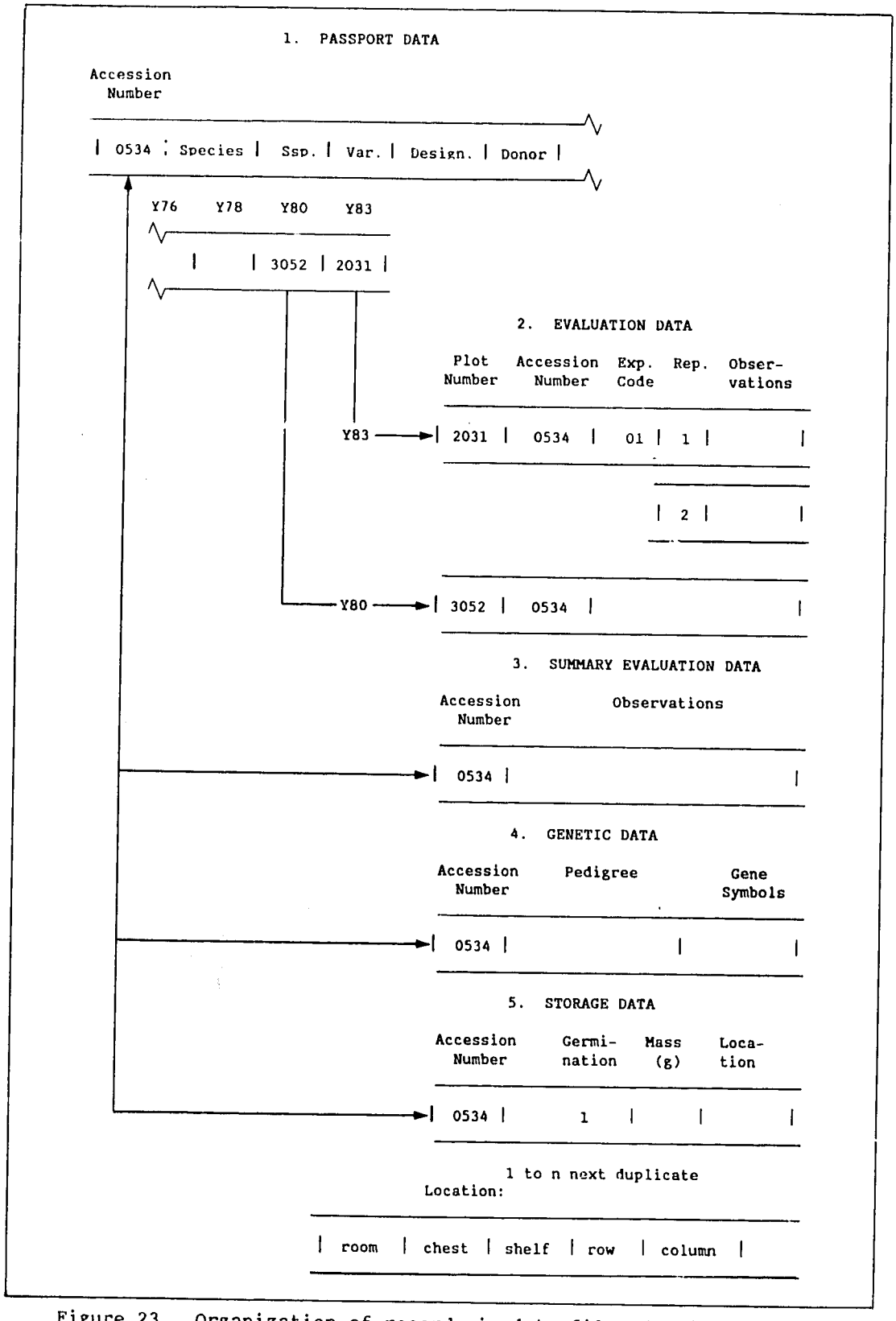

Figure 23. Organization of records in data files (Polish Genebank)

5. Storage data file

This contains all information about the location and storage characteristics of the accessions in the genebank, e.g. weight of seeds in store, germination ability. If there are sub-samples of the same accession, due to large seed quantity, a list of all locations of samples are cross-referenced to this record. The location of the container in the store is given by the following parameters (Figure 23):

1 room number
2 chest number
3 shelf number
4 row number on the shelf
5 column number on the shelf

The organization of the files containing genetic resources information as presented above allows the use of the documentation system for preparation of several lists for genebank management, for example:

- Sowing lists for multiplication. These are prepared on the basis of quantity of seeds (less than a defined minimum) and the viability (less than a defined minimum for a particular crop). The system prints a list of accessions and their location in the store.

- Seed distribution lists. Receipt or distribution of accessions is noted in the documentation system with automatic correction of the quantity of seeds in the storage file.

- Field books. Once accessions have been selected for field experiments, the system prints a field book, including the list of accession names and numbers, their order in experimental plots for each replication and headings for recording the data which will be observed.

Appendix IV (cont'd.)

Management of a User-Orientated Genetic Resources Collection

by

I.D. Thomas and B.F. Tyler

INTRODUCTION

The Welsh Plant Breeding Station (WPBS) is primarily a forage grass and legume breeding institute with a remit to study breeding techniques and to demonstrate their validity by producing cultivars. The genetic resources unit of this institute has as a primary objective to assemble and characterize forage grass and clover genetic resources for breeding and related research activities. This programme has been in operation since 1964 and the unit's initial priority was to demonstrate the importance of a characterized genetic resources collection as a prerequisite for successful breeding.

Serious computerized documentation at the WPBS is a relatively recent event, although a first attempt was made in 1969 using an Elliot Mainframe Computer at the University of Wales, Aberystwyth. Our progress has been influenced by the accelerating improvements in hardware and the need to be conversant with the appropriate software; we have moved from the Commodore PET micro to the Apple II micro and at the moment use the Digital Vax mini-computer.

DATA ENTRY FORMS

The continual revision of our data records is to some extent a reflection of changes in hardware/software, but has also been necessitated by our involvement in the ECP/GR Programme [European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources] and from alterations suggested by user experience. Consequently, the data entry forms used at present have been constructed in such a way that alterations can be relatively easily effected. For instance, in descriptors where a limited number of states are valid, e.g. accession status or site description, lists of valid descriptor-states have been itemized in notes to be used in conjunction with the form, rather than being presented on the form itself.

Four data entry forms are in use, one of which, the Seed Storage Data and Registration Form (Figure 24) is completed for all seed samples entering the genebank. This form was constructed so that rapid entry of existing accessions could be effected and the collection could still be managed. The form thus contained some characterization data

WELSH PLANT BREEDING STATION - GENETIC RESOURCES UNIT

SEED STORAGE DATA

9. STORAGE DATA

1	-	Species code	: ___
1.1		Accession name	
2	-	|prefix	: ____ ___
3	-	|number	: _____ .| ___
4	-	Comment	: _____
			cont. _____
5	-	Bag number	: _____
6	-	Medium tray number	: _____
7	-	Long tray nunmber	: _____
8	-	Date of storage	: __/__/__
9	-	Date of last transaction	: __/__/__
10	-	Percentage germination	: ____
11	-	Mean germ. time (days)	: ___.__
12	-	Amount (grams)	: ____.___
13	-	Chromosome number	: ___
14	-	B-Chromosomes	: ___
15	-	Replcate sample at Kew	: __
16	-	Available for distribution	: __

9. STORAGE DATA

1	-	Species code	: ___
1.1		Accession name	
2	-	|prefix	: ____ ___
3	-	|number	: _____
4	-	Comment	: _____
			cont. _____
5	-	Bag number	: _____
6	-	Medium tray number	: _____
7	-	Long tray number	: _____
8	-	Date of storage	: __/__/__
9	-	Date of last transaction	: __/__/__
10	-	Percentage germination	: ____
11	-	Mean germ. time (days)	: ___.__
12	-	Amount (grams)	: ____.___
13	-	Chromosome number	: ___
14	-	B-Chromosomes	: ___
15	-	Replcate sample at Kew	: __
16	-	Available for distribution	: __

Figure 24. Seed storage data form (WPBS)

which was required immediately but which will eventually be transferred to the correct form.

One of the other three is completed depending on the status of the sample, as follows:

(i) Collection data form (Figure 25) - this is used for our own collections and relevant information generally is completed on site; other information such as latitude and longitude, etc. may be completed on return. Transfer is then directly to the computer;

(ii) Donation collection data form (Figure 26) - completed when seed from other collections is donated to the genebank and where minimum passport data is available;

(iii) Donation data form - this is used when cultivars or botanical garden collections are donated and no passport data is available.

DESCRIPTORS

In order to describe our management system it is necessary to consider some of the descriptors necessary for effective management. IBPGR recommended descriptors have been used when possible. Where they coincide, the IBPGR number from their Descriptor List has been included.

The following descriptors refer to the seed storage data and registration form:

1. Species Code - Each species is arbitrarily allocated a code number.

2. Accession Name is equivalent to IBPGR Accession number 1.1 in the descriptor list. Accession Name is a composite descriptor containing a prefix - the genebank identifier, a genus code and a six digit number (the accession root) followed by a period (full stop) and the year of regeneration, if relevant. Original seed is designated "00".

3. Comment - This field was used to enter certain passport data before data was available on the database. This may eventually become redundant.

4. Bag No. - On receipt each seed accession is dried, a sample is taken for germination, and the remainder is weighed. Depending on amount of seeds, the sample is divided into three lots: 5 g for long-term storage, a 5 g duplicate for Royal Botanic Gardens (RBG), Kew and the remainder bagged and stored in medium-term storage for evaluation, distribution, etc. A sequential non-reusable number which is common to each sub-sample is then allocated.

5. Date of last transaction - This field is a peculiarity of the Beta database program used with the Apple II micro-computer and needed to be present when transactions were entered.

WELSH PLANT BREEDING STATION - GENETIC RESOURCES UNIT
COLLECTION DATA

3. COLLECTION DATA - ACCESSION DETAILS

1	-	Species code	:
2	1. 5.1	Genus	:
3	1. 5.2	Species	:
4	1. 5.3	Sub-taxa	:
5	-	Taxonomic authority	:
	1. 1	Accession name	
6		|prefix	:
7		|number	:
8	2.11	Accession status	:
		- EXPEDITION DETAILS	
	2. 1	Collection name	
9		|expedition title	:
10		|site number	:
11		|collection number	:
12	2. 2	Collector's code & Inst.	: -
13	-	Collector's initials	:
14	2. 3.1	Collection date	: / /
		- LOCATION DETAILS	
15	2. 4.3	Geographical region	:
16	-	Geographical sub-region	:
17	2. 4.1	Country	:
18	2. 5	Administrative region	:
19	2. 6.1	Location	:
		cont.	
		cont.	
20	-	O.S. Map reference (U.K.)	:
21	2. 6.2	Atlas	:
22	-	Atlas location	:
23	-	Atlas coordinates	:
24	2. 7	Latitude	: .
25	2. 8	Longitude	: .
26	2. 9.1	Altitude (m.a.s.l.)	:
27	2. 9.2	Aspect (degrees)	:
28	2. 9.3	Slope (degrees)	:
29	2.14.2	Photograph numbers	:
		- SAMPLING DETAILS	
30	2.15	Collection sample type	:
31	2.13.1	Number plants collected	:
32	2.13.4	Weight seed collected	: .
33	2.13.3	Size of site	:
34	2.13.2	Size of area sampled	:
35	2.16.1	Abundance	:
36	2.16.2	Distribution	:

Figure 25. Collection data form (WPBS)

- SWARD COMPOSITION

37 2.17.1 Dominant species :
38 2.17.2 Dominant grass species :
39 2.17.4 Characteristic species :

- SITE DESCRIPTION

40 - Coastal :
41 - Regional physiography :
42 2.18 Site physiography :
43 - note :
44 - Site habitat general :
45 - note :
46 - Site habitat marine :
47 - Site habitat freshwater :
48 - Site habitat disturbed :
49 - Site habitat rock feature :
50 - Site habitat man made :
51 - note :

- SITE MANAGEMENT

52 2.19.3 Grassland management :
53 - note :
54 2.20 Age of grassland :
55 - Cutting :
56 - Grazing :
57 2.21 Irrigation :
58 2.22 Flooding :
59 - Poaching :
60 - Treading :
61 2.23.1 Organic fertiliser :
62 2.23.2 Inorganic fertiliser :
63 - note :
cont.
cont.
cont.

- SOIL TYPE

64 2.24 Soil type :
65 - Bedrock :
66 2.25 Drainage :
67 2.26.1 pH :
68 2.26.2 P.ppm :
69 2.26.3 K.ppm :
70 2.26.4 Ca.ppm :
71 - Na.ppm :
72 - Mg.ppm :
73 - Comment :
cont.
74 - Associated collections :

Figure 25. Collection data form (WPBS) (cont'd.)

WELSH PLANT BREEDING STATION - GENETIC RESOURCES UNIT

DONATION COLLECTION DATA

2. DONATION DATA - ACCESSION DETAILS

1	-	Species Code	: |||
2	1. 5.1	Genus	: ||||||||||||||||
3	1. 5.2	Species	: ||||||||||||||||
4	1. 5.3	Sub-taxa	: ||||||||||||||||
5		Taxonomic authority	: ||||||||||
	1. 1	Accession name	
6		|prefix	: |||| |||
7		|number	: ||||||| || |||
8	2.11	Accession status	: ||||||||||||||||

- DONATION DETAILS

9	1. 2	Donor's code & Inst.	: |||||-||||||||||||||||
10	1. 3	Donor's number(s)	: |||||||||||||||||||||||||||
11	1. 7	Donation date	: || |/| ||
12	-	Donation sample type	: |||||
13	1. 9.1	Weight seed donated	: ||| ||.| || (g)
14	1. 9.2	Number plants donated	: ||||
15	-	Country of origin	: ||||

- VARIETAL INFORMATION

16	1. 6.1	Cultivar/Breeding line name	: ||||||||||||||||
17	1. 6.2	Breeder's code & Inst.	: |||||-||||||||||||||||
18	1. 6.3	Breeding method	: ||||||||||||||||||
19	1. 6.4	Male parent	: |||||||||||
20	1. 6.5	Female parent	: |||||||||||
21	1. 6.6	Country of approval	: ||||
22	1. 6.7	Year of approval	: |||

- REGENERATION DETAILS

23	1. 8.1	Year of last regeneration	: |||
24	1. 8.3	Country last regeneration	: ||||
25	1.10	Number of regenerations	: |||

Figure 26. Donation collection data form (WPBS)

2. COLLECTION DATA - DONATION ONLY

- EXPEDITION DETAILS

26	-	Expedition title	:
27	2. 2	Collector's code & Inst.	: -
28	-	Collector's initials	:
29	2. 3.1	Collection date	: / /

- LOCATION DETAILS

30	2. 4.3	Geographical region	:
31	2. 4.1	Country	:
32	2. 5	Administrative region	:
33	2. 6.1	Location	:
		cont.	
		cont.	
34	2. 6.2	Atlas	:
35	-	Atlas location	:
36	-	Atlas coordinates	:
37	2. 7	Latitude	: .
38	2. 8	Longitude	: .
39	2. 9.1	Altitude (m.a.s.l.)	:
40	2. 9.2	Aspect (degrees)	:
41	2. 9.3	Slope (degrees)	:
42	2.15	Collection sample type	:
43	-	Further information	:

Figure 26. Donation collection data form (WPBS) (cont'd.)

Page 3

ACC. NUMBER	COMMENT	BAG NOS	MED TRAY NOS	LONG TRAY NOS	PERCENT GERM	AMOUNT (GRAMS)	DIST.
8515.67	CV:VALINGE	19	1	-	6	1.25	N
8528.81	COLAHC 67	1411	68	16	92	46.28	Y
8576.00	D:MADRID	19	1	-	5	1.02	N
8580.00	D:MADRID	19	1	-	65	0.87	N
8581.00	D:MADRID	19	1	-	60	0.71	N
8582.00	D:MADRID	19	1	-	96	1.08	N
8583.00	D:MADRID	19	1	-	72	0.96	N
8584.00	D:MADRID	19	1	-	65	0.52	N
8587.00	ITA 67	20	1	-	38	2.07	N
8590.00	ITA 67	21	1	-	60	11.66	Y
8590.73	ITA 67	22	1	-	12	5.30	N
8591.00	ITA 67	23	1	-	62	26.81	Y
8593.00	ITA 67	24	1	-	26	12.47	N
8595.00	ITA 67	25	1	-	52	3.93	N
8595.82	ITA 67	1580	76	17	96	14.55	S
8596.00	ITA 67	26	1	-	70	2.20	N
8596.73	ITA 67	27	1	-	96	3.50	N
8596.79	ITA 67	1275	59	13	96	45.48	S
8596.81	ITA 67	1412	68	16	97	67.53	Y
8596.82	ITA 67, EEC 6	1581	76	17	98	51.00	Y
8597.00	ITA 67	28	1	-	46	18.66	Y
8598.00	ITA 67	29	1	-	24	18.50	N
8599.73	ITA 67	30	1	1	44	17.83	Y
8599.00	ITA 67	31	1	-	40	19.03	Y
8600.00	ITA 67	32	1		62	16.89	Y
8602.00	ITA 67	33	1	-	99	46.06	S
8603.00	ITA 67	34	1	-	80	22.98	Y
8604.00	ITA 67	35	1	-	96	71.50	S
8605.00	ITA 67	36	1	-	92	18.47	S
8606.00	ITA 67	37	1	-	58	37.74	Y
8608.00	ITA 67	38	2	-	52	39.46	Y
8611.00	ITA 67	39	2	-	4	19.27	N
8612.00	ITA 67	40	2	-	68	50.30	Y
8614.00	ITA 67	41	2	-	92	13.96	S
8616.00	ITA 67	42	2	-	74	32.94	S
8617.00	ITA 67	43	2	-	96	76.95	Y
8618.00	ITA 67	44	2	-	28	8.80	N
8620.00	ITA 67	45	2	-	100	39.28	Y
8621.00	ITA 67	46	2	-	60	3.35	N
8621.01	ITA 67	1583	77	17	97	35.80	Y
8621.79	ITA 67	1276	59	13	96	9.68	Y
8621.82	ITA 67	1582	76	17	96	55.40	S
8622.00	ITA 67	47	2	-	12	25.65	N
8622.73	ITA 67	48	2	1	40	15.60	Y
8624.00	ITA 67	49	2	-	24	47.20	Y
8624.73	ITA 67	50	2	1	82	15.32	Y
8625.00	ITA 67	51	2	-	48	7.20	N
8630.00	ITA 67	19	1	-	2	0.07	N
8637.00	CV:SCEEMPTER PASTURE	603	25	7	60	8.66	Y
8638.00	CV:PERMA	604	25	7	41	20.59	Y
8643.00	D:FUNDULEA	53	2	-	44	25.90	Y
8645.00	CV:DOUBLET HAY	605	25	-	72	3.16	N
8646.00	CV:ODENWALDER	605	25	-	37	2.43	N
8647.00	CV:LATE VIKTORIA TRI	606	25	7	52	47.83	Y
8648.00	CV:ODSTEIN	607	25	7	19	86.72	Y
8649.00	CV:DRIEL	608	25	7	7	55.71	N
8650.00	CV:MISO	609	25	7	1	36.39	N

Figure 27. Sample of an inventory (WPBS)

6. Percent germ. - An estimate of germination percent (after 14 days) is made prior to storage. Four replications of 100 seeds are aimed at but smaller numbers are used depending on accession size. Further samples of large accessions are identified for monitoring at 5 year intervals.

7. Mean germ. time - An estimate of mean time to germination is obtained from the daily germination counts and may give an indication of seed lots likely to have a lower storage life. With the resources available from regeneration, it is not possible to multiply all accessions which are identified as having low germination and mean germination time can be used to identify poor-vigour seed lots. However, certain accessions which are considered rare, valuable or in great demand are given priority.

8. Chromosome number and presence of B-chromosomes - This information was necessary because the construction of the database occurred when information on these characters was being requested. They will be removed from this form and transferred to the relevant section in due course.

9. Kew - Indication of distribution of duplicate sample to RBG, Kew.

10. Availability for distribution - This is determined from seed amount and germination percentage and seed is available for distribution when (germ. % x amount in g)/100 >5.

PRODUCTION OF CATALOGUES

Inventory (Figure 27)

This can be ordered by species, usually in accession number order with any required information listed.

An updated inventory in accession number order is always available for simple manual search for specific accessions when the number is known. In this connection it has been found that the use of a suffix (.83) to indicate regeneration gives a rapid indication of the seed state of an accession because all accessions with the same root will follow in sequence.

Seed exchange list (Figure 28)

Since the information required to produce the list is now computerized, the publication of annual lists can be easily and quickly done.

The present policy is to include only those accessions collected by the unit and where the quantity of germinable seed available is greater than 5 g.

SEED EXCHANGE - 1985 - Page 1

ACCESSION NAME	COUNTRY	ATLAS LOCATION	ATLAS COORD.	LOCATION
LOLIUM PERENNE - L.				
ABY-BA 9968.00	ROM	BRASOV	82K5	BOD
ABY-BA 9969.00	ROM	ROMAN	82K4	DULCESTI
ABY-BA 9970.00	ROM	HALAUCESTI	82K3	TUPILATI
ABY-BA 9971.00	ROM	FALTICENI	82K3	VADU MOLDEVEI
ABY-BA 9972.00	ROM	CODAESTI	82L4	CODAESTI
ABY-BA 9973.00	ROM	CODAESTI	82L4	CODAESTI
ABY-BA 9974.00	ROM	CODAESTI	82L4	REDIN
ABY-BA 9975.00	ROM	TIRGU FRUMOS	82L3	TIRGU FRUMOS
ABY-BA 9976.00	ROM	TIRGU FRUMOS	82L3	TIRGU FRUMOS
ABY-BA 9977.00	ROM	IASI	82L3	LETCANI
ABY-BA 9978.00	ROM	IASI	82L3	LETCANI
ABY-BA 9979.00	ROM	IASI	82L3	LETCANI
ABY-BA 9980.00	ROM	GURU HUMORULUI	82K3	ILISESTI
ABY-BA 9981.00	ROM	BORSA	82J3	RODNEI MNT.
ABY-BA 9982.00	ROM	SIGHET	82H3	SIGHET
ABY-BA 9983.00	ROM	CAREI	82G3	PETRESTI
ABY-BA 9984.00	ROM	LES	82G4	LES
ABY-BA 9986.00	ROM	TINCA	82G4	GURBEDIU
ABY-BA 9987.00	ROM	LUDUS	82J4	CUCI
ABY-BA 9988.00	ROM	LUDUS	82J4	CUCI
ABY-BA 9989.00	ROM	CRISTURU-SECUIESC	82J4	CRISTURU-SECUIESC
ABY-BA 9990.00	ROM	SFINTU GHEORGHE	82K5	SUGAS BAI BARAOLTULUI MNT.
ABY-BA 10410.00	GBW	LLANRWST	57F6	MOEL-YR-IWCH UCHAF, NEBO,LLANRWST
ABY-BA 10411.00	GBW	BETWS-Y-COED	57F6	CAE'R FELIN SSSI, YSBYTY IFAN, BETWS-Y-COED
ABY-BA 10412.00	GBW	DRUID	57G7	TY'N Y RHOS, MAERDY, CORWEN
ABY-BA 10413.00	GBW	DRUID	57G7	PENTRE LLAWEN, MAERDY
ABY-BA 10414.00	GBW	DOLGELLAU	56D2	PLAS DE BRITHDIR, WENALLT
ABY-BA 10415.00	GBW	DOLGELLAU	56D2	GRAIG, DOLGELLAU
ABY-BA 10416.00	GBW	PENNAL	56D2	NEXT TO LLYN BWTRI, PENNAL
ABY-BA 10417.00	GBW	PENNAL	56D2	LLYN BWTRI-R.DYFI, PENNAL

Figure 28. Sample of a seed exchange list (WPBS)

DATABASE MANAGEMENT SYSTEM

Data is structured using DATATRIEVE. The following are favourable features in its use in the management of genetic resources:

1. Interactivity

A batch system, the alternative to an interactive system, is of optimum value in the routine processing of large amounts of data as in stock control procedures. The use of an interactive data query language such as DATATRIEVE allows interrogation of the records such that the answer to one query can be followed by subsequent questions, which are dependent on the answer given by the original query. This

interactive system has been found to be of considerable value in genetic resources work.

2. Query-language

The syntax of DATATRIEVE is very similar to spoken English and is thus relatively easy to learn and use.

3. Software

Software for use on the VAX DIGITAL computer is written by Digital and their policy is to produce compatible packages which can be obtained separately but used in conjunction. For instance records created on DATATRIEVE can be handled by FMS (Forms Management System.)

4. Restructuring

Data is held as ASCII files in fixed format. The record definition (Figure 29), however, is held independently and may be restructured if necessary, to include new descriptors or to remove those which become redundant.

5. Simple database structure

The DATATRIEVE concept of sets of associated data, or 'domains' is used in the present database such that the different species have separate 'domains' as do the seed storage, collection, donation and evaluation data. The use of domains in discrete manageable units saves space and time in operation. Access across 'domains' is a straightforward procedure and the creation of new 'domains' for future characters gives the database ample scope for expansion.

An example of an interactive search both within and across 'domains' is given in Figure 30. The query was for a contrasting range of Lolium perenne accessions from western Europe with sufficient germinable seed for experimentation. This is typical of requests received both for seeds for experimental work and for breeding material. Both seed storage data and collection data need to be examined. The relevant domains are first specified (1) in this case Lolium perenne collection data (BACOL1) and Lolium perenne seed storage data (BASEED1). Within the collection data the GEOGRAPHICAL REGION is searched for western Europe (2). It will be noted that some accessions do not contain GEOGRAPHICAL SUB-REGION data. These are eliminated in the next search and also sorted in GEOGRAPHICAL SUB-REGION order (3). At this stage the seed storage 'domain' is included and the seed amount searched for (4). The accessions in the seed storage domain contain both original and regenerated seed, hence there was an increase from 112 to 143 in the number of records found. For example BA 9966 has been regenerated twice, once in 1981 and again in 1982. Both of these records are found in the print-out.

```
DELETE SEED2_DATA;
DEFINE RECORD SEED2_DATA USING
01 STORAGE_DATA.

   03 SPECIES_CODE                          PIC X(2)
                                            QUERY_NAME IS SPEC_CDE
                                            QUERY_HEADER IS "SPEC."/"CODE"
                                            DEFAULT VALUE IS "1".

   03 ACCESSION_DETAILS                     QUERY_NAME IS ACC_DET.

      05 ACC_INST                            PIC X(3)
                                            QUERY_HEADER IS "ACC."/"INST."
                                            DEFAULT VALUE IS "-".

      05 ACC_PRE                             PIC X(2)
                                            QUERY_HEADER IS "ACC."/"PREFIX".

      05 ACC_INDEX                           QUERY_NAME IS ACC_IND
         07 ACC_ROOT                        PIC X(6).
         07 ACC_SIGN                        PIC X.
         07 ACC_YEAR                        PIC X(2).

      05 ACC_NOS REDEFINES ACC_INDEX         PIC X(9)
                                            QUERY_HEADER IS "ACC."/"NUMBER".

   03 ACC_NME                                PIC X(14)
                                            QUERY_HEADER IS "ACCESSION"/"NAME"
                                            COMPUTED BY ACC_INST|
                                                        ACC_PRE||
                                                        ACC_INDEX
                                            EDIT_STRING IS XXX-X(11).

   03 COMMENT                               PIC X(30)
                                            DEFAULT VALUE IS "-".

   03 STORAGE_DETAILS                       QUERY_NAME IS STR_DET.

      05 BAG_NOS                             PIC 9(5)
                                            MISSING VALUE IS 0
                                            EDIT_STRING IS ZZZZZ?"    -".

      05 MED_TRAY_NOS                        PIC 9(4)
                                            QUERY_NAME IS MED_TRAY
                                            MISSING VALUE IS 0
                                            EDIT_STRING IS ZZZZ?"   -".

      05 LONG_TRAY_NOS                       PIC 9(4)
                                            QUERY_NAME IS LONG_TRAY
                                            MISSING VALUE IS 0
                                            EDIT_STRING IS ZZZZ?"   -".

   03 STORE_DATE                            USAGE IS DATE
                                            EDIT_STRING IS DD-NN-YY.

   03 TRANS_DATE                            USAGE IS DATE
                                            EDIT_STRING IS DD-NN-YY.
```

Figure 29. Record definition (WPBS)

```
03 GERMINATION_DETAILS          QUERY_NAME IS GERM_DET.

   05 GERM                      PIC 9(3)
                                QUERY_HEADER IS "PERCENT"/"GERM"
                                MISSING VALUE IS 0
                                EDIT_STRING IS ZZZ?"  -".

   05 MEAN_GERM                 PIC 99V9
                                QUERY_HEADER IS "MEAN GERM."/
                                                "TIME (DAYS)"
                                MISSING VALUE IS 0
                                EDIT_STRING IS Z9.99?" -   ".

03 AMOUNT                       PIC 9(4)V99
                                QUERY_HEADER IS "AMOUNT"/"(GRAMS)"
                                EDIT_STRING IS ZZZ9.99?"   -".

03 CHROMOSOME_DETAILS           QUERY_NAME IS CHROM_DET.

   05 CHROM_NOS                 PIC 99
                                QUERY_HEADER IS "CHR."/"NOS."
                                MISSING VALUE IS 0
                                EDIT_STRING IS 99?" -".

   05 CHROM_B                   PIC XX
                                QUERY_HEADER IS "CHR."/"B".

03 KEW_SAMP                     PIC X
                                QUERY_HEADER IS "KEW"
                                VALID IF KEW_SAMP EQ "Y", " ","-"
                                DEFAULT IS "-".

03 DISTRIBUTION                 QUERY_NAME IS DIST.

   05 DIST_IN                   PIC X
                                DEFAULT IS "-"
                                VALID IF DIST_IN EQ "-","S","Y","N".

   05 DIST_IND                  QUERY_HEADER IS "DIST."/"INDEX"
                                COMPUTED BY (AMOUNT * GERM)/100.

   05 DIST_OUT                  PIC X
                                QUERY_HEADER IS "DIST."
                                        COMPUTED BY CHOICE
                                        (DIST_IN NE "-") THEN DIST_IN
                                        (DIST_IND EQ 0) THEN "*"
                                        (DIST_IND LT 5) THEN "N"
                                        (DIST_IND GE 5) THEN "Y"
                                        ELSE "*"
                                        END_CHOICE.
```

Figure 29. Record definition (WPBS) (cont'd.)

The final query specifies the seed amount and eliminates low germinating accessions (5). It is now possible to manually select a range of ecotypes within western Europe from contrasting geographical sub-regions with sufficient seed and high germination.

In future, characterization and evaluation data in separate 'domains' will be included in the database. Similar interactive searches to the above will then be possible using performance and biological characters as the criteria for selection.

```
(1)DTR> READY BACOL1, BASEED1

(2)DTR> FIND BACOL1 WITH LOC-REG EQ "W.EUROPE"
   [262 records found]

   DTR> FOR FIRST 10 CURRENT PRINT ACC-NME, LOC-REG, LOC-CNTRY, LOC-SUB-REG

      ACCESSION          GEOGRAPHICAL                    GEOGRAPHICAL
        NAME               REGION          COUNTRY       SUB-REGION

   ABY-BA   8414.00 W.EUROPE                GBE    -
   ABY-BA   8416.00 W.EUROPE                GBE    -
   ABY-BA   8456.00 W.EUROPE                FRA    BRITTANY
   ABY-BA   8528.81 W.EUROPE                GBE    VALE OF YORK
   ABY-BA   8630.00 W.EUROPE                FRA    FRENCH ALPS
   ABY-BA   8992.73 W.EUROPE                GBW    -
   ABY-BA   8993.73 W.EUROPE                GBW    -
   ABY-BA   8994.73 W.EUROPE                GBW    -
   ABY-BA   8995.73 W.EUROPE                GBW    -
   ABY-BA   9064.72 W.EUROPE                BEL    ARDENNE PLATEAU

(3) DTR> FIND CURRENT WITH LOC-SUB-REG NE "-" SORTED BY LOC-SUB-REG, ACC-NOS
   [112 records found]

   DTR> FOR FIRST 10 CURRENT PRINT ACC-NME, LOC-REG, LOC-CNTRY, LOC-SUB-REG

      ACCESSION          GEOGRAPHICAL                    GEOGRAPHICAL
        NAME               REGION          COUNTRY       SUB-REGION

   ABY-BA   9966.81 W.EUROPE                GBE    (THAMES VALLEY)
   ABY-BA  10299.83 W.EUROPE                GBE    (WEALD)
   ABY-BA   9097.72 W.EUROPE                CHE    ALPS-BERNER
   ABY-BA   9098.00 W.EUROPE                CHE    ALPS-BERNER
   ABY-BA   9093.72 W.EUROPE                CHE    ALPS-PRE
   ABY-BA  10278.83 W.EUROPE                CHE    APPENZELL
   ABY-BA  10279.83 W.EUROPE                CHE    APPENZELL
   ABY-BA   9064.72 W.EUROPE                BEL    ARDENNE PLATEAU
   ABY-BA   9066.72 W.EUROPE                BEL    ARDENNE PLATEAU
   ABY-BA   9067.72 W.EUROPE                BEL    ARDENNE PLATEAU

(4) DTR> FIND CURRENT CROSS BASEED1 OVER ACC-ROOT
   [143 records found]

   DTR> FOR FIRST 10 CURRENT
   [Looking for statement]

   CON> PRINT BASEED1.ACC-NME, LOC-REG, LOC-CNTRY, LOC-SUB-REG, AMOUNT

      ACCESSION          GEOGRAPHICAL                    GEOGRAPHICAL      AMOUNT
        NAME               REGION          COUNTRY       SUB-REGION       (GRAMS)

   ABY-BA   9966.81 W.EUROPE                GBE    (THAMES VALLEY)          2.66
   ABY-BA   9966.82 W.EUROPE                GBE    (THAMES VALLEY)         16.40
   ABY-BA  10299.83 W.EUROPE                GBE    (WEALD)                 67.10
   ABY-BA   9097.72 W.EUROPE                CHE    ALPS-BERNER              8.40
   ABY-BA   9098.00 W.EUROPE                CHE    ALPS-BERNER              0.65
   ABY-BA   9093.01 W.EUROPE                CHE    ALPS-PRE                 5.82
   ABY-BA   9093.72 W.EUROPE                CHE    ALPS-PRE                 1.00
   ABY-BA  10278.83 W.EUROPE                CHE    APPENZELL               28.10
   ABY-BA  10279.83 W.EUROPE                CHE    APPENZELL               41.40
   ABY-BA   9064.72 W.EUROPE                BEL    ARDENNE PLATEAU         12.20
```

Figure 30. Example of an interactive search (WPBS)

```
(5) DTR> FIND CURRENT WHERE AMOUNT GREATER-THAN 15.00 AND -

    CON> GERM GREATER-THAN 90
    [33 records found]

    DTR> FOR CURRENT
    [Looking for statement]

    CON> PRINT BASEED1.ACC-NME, LOC-CNTRY, LOC-SUB-REG, AMOUNT, GERM, STR-DET
```

ACCESSION NAME	COUNTRY	GEOGRAPHICAL SUB-REGION	AMOUNT (GRAMS)	PERCENT GERM	BAG NOS	MED TRAY NOS	LONG TRAY NOS
ABY-BA 9966.82	GBE	(THAMES VALLEY)	16.40	100	1603	78	-
ABY-BA 10299.83	GBE	(WEALD)	67.10	95	1961	102	22
ABY-BA 9076.81	FRA	AUXOIS	46.66	92	1416	69	16
ABY-BA 9078.82	FRA	AUXOIS	130.10	98	1584	77	17
ABY-BA 9079.01	FRA	AUXOIS	16.54	92	1284	59	-
ABY-BA 10288.83	CHE	BERNER-ALP	34.30	94	1950	101	22
ABY-BA 9118.72	FRA	CHAMPAGNE-HUMIDE	114.35	98	146	4	-
ABY-BA 9118.82	FRA	CHAMPAGNE-HUMIDE	134.40	99	1588	77	17
ABY-BA 10280.83	CHE	JURA	59.40	93	1942	101	21
ABY-BA 9108.79	CHE	JURA MNTS.	33.16	99	1279	59	13
ABY-BA 9106.72	CHE	LEVENTINA VALLEY	56.20	100	135	4	2
ABY-BA 9111.82	FRA	LORRAINE PLAIN	145.80	96	1587	77	17
ABY-BA 9113.72	FRA	LORRAINE PLAIN	20.05	96	141	4	2
ABY-BA 10285.83	CHE	OBERLAND	64.00	91	1947	101	21
ABY-BA 10286.83	CHE	OBERLAND	21.40	94	1948	101	21
ABY-BA 9070.72	BEL	PAYS DE HERVE	35.80	91	102	3	1
ABY-BA 9094.72	CHE	RHONE VALLEY	28.35	100	124	3	2
ABY-BA 9100.72	CHE	RHONE VALLEY	23.20	98	130	3	2
ABY-BA 9101.72	CHE	RHONE VALLEY	27.25	100	131	3	2
ABY-BA 10013.82	GBE	ROMNEY MARSH	120.20	99	1606	78	18
ABY-BA 9082.81	FRA	SOANE VALLEY	57.25	91	1418	69	16
ABY-BA 9083.72	FRA	SOANE VALLEY	56.15	92	113	3	1
ABY-BA 9083.82	FRA	SOANE VALLEY	112.80	97	1585	77	17
ABY-BA 9960.82	GBE	SOMERSET LEVELS	80.70	97	1598	78	18
ABY-BA 10294.83	GBE	SOUTH DOWNS	134.70	91	1956	102	22
ABY-BA 9088.82	CHE	SWISS PLATEAU	151.40	93	1586	77	17
ABY-BA 9089.81	CHE	SWISS PLATEAU	18.47	98	1419	69	16
ABY-BA 9090.72	CHE	SWISS PLATEAU	29.55	96	120	3	1
ABY-BA 9091.72	CHE	SWISS PLATEAU	21.93	98	121	3	1
ABY-BA 10284.83	CHE	TOSSTAL	24.60	98	1946	101	21
ABY-BA 8528.81	GBE	VALE OF YORK	46.28	92	1411	68	16
ABY-BA 10017.80	GBW	W. WALES	15.44	100	1272	59	-
ABY-BA 9105.72	CHE	ZURICH UPLANDS	16.35	98	134	4	2

```
    DTR> CLOSE LOG
```

Figure 30. Example of an interactive search (WPBS) (cont'd.)