EUROPEAN COOPERATIVE PROGRAMME FOR CROP GENETIC RESOURCES NETWORKS (ECP/GR)

Report of a Working Group on Forages

Sixth meeting
6-8 March 1997
Beitostølen, Norway

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IPGRI is an institute of the Consultative Group on International Agricultural Research (CGIAR)

The International Plant Genetic Resources Institute (IPGRI) is an autonomous international scientific organization, supported by the Consultative Group on International Agricultural Research (CGIAR). IPGRI's mandate is to advance the conservation and use of plant genetic resources for the benefit of present and future generations. IPGRI's headquarters is based in Rome, Italy, with offices in another 14 countries worldwide. It operates through three programmes: (1) the Plant Genetic Resources Programme, (2) the CGIAR Genetic Resources Support Programme, and (3) the International Network for the Improvement of Banana and Plantain (INIBAP). The international status of IPGRI is conferred under an Establishment Agreement which, by January 1998, had been signed and ratified by the Governments of Algeria, Australia, Belgium, Benin, Bolivia, Brazil, Burkina Faso, Cameroon, Chile, China, Congo, Costa Rica, Côte d'Ivoire, Cyprus, Czech Republic, Denmark, Ecuador, Egypt, Greece, Guinea, Hungary, India, Indonesia, Iran, Israel, Italy, Jordan, Kenya, Malaysia, Mauritania, Morocco, Pakistan, Panama, Peru, Poland, Portugal, Romania, Russia, Senegal, Slovakia, Sudan, Switzerland, Syria, Tunisia, Turkey, Uganda and Ukraine.

The European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) is a collaborative programme among most European countries aimed at ensuring the long-term conservation and facilitating the increased utilization of plant genetic resources in Europe. The Programme, which is entirely financed by the participating countries and is coordinated by IPGRI, is overseen by a Steering Committee (previously Technical Consultative Committee, TCC) composed of National Coordinators nominated by the participating countries and a number of relevant international bodies. The Programme operates through ten broadly focused networks in which activities are carried out through a number of permanent working groups or through ad hoc actions. The ECP/GR networks deal with either groups of crops (cereals, forages, vegetables, grain legumes, fruit, minor crops, industrial crops and potato) or general themes related to plant genetic resources (documentation and information, *in situ* and on-farm conservation, technical cooperation). Members of the working groups and other scientists from participating countries carry out an agreed workplan with their own resources as inputs in kind to the Programme.

Cover: Bee visiting alfalfa flowers. Courtesy Dr L. Mazza, CONASE (Consorzio Nazionale Sementi), Ravenna, Italy.

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Contents

Part I. Discussion and Recommendations

Introduction

Welcoming Address

Eva Thörn, director of the Nordic Gene Bank (NGB), welcomed the participants to the beautiful country of Norway. She said that it was a pleasure for the Nordic Gene Bank to be associated with the organization of the meeting. NGB as a regional genebank strongly supports the regional work of IPGRI and is willing to do what it can to strengthen and widen the network. NGB, a common institute for Denmark, Finland, Iceland, Norway and Sweden, has almost 20 years of experience in regional activities. The aim of the genebank is to conserve material of Nordic origin and of importance to agriculture and horticulture and to promote the utilization of the conserved material. The concept is based on close collaboration with Nordic plant breeders and researchers organized in crop-related working groups. These people are supporting the staff with expertise and practical work with the conserved material. Eva Thörn stressed the importance of the people in their own working groups as well as the participants in the ECP/GR network. She said that although the participants are spread all over Europe in different environments and different organizations, all have a common task and a common goal: to conserve plant genetic resources for food and agriculture for future needs and to see that the conserved material will be used in a sustainable manner for future generations. She encouraged the participants to bring back all the commitments and recommendations which will be made during the meeting to their colleagues as well as to policy-makers, and to encourage plant breeders to actively take part in the important work of conservation and utilization of plant genetic resources (PGR) in a sustainable way. She underlined the importance of a good system for information and documentation designed according to the needs of the users of PGR. She also said that it must be kept in mind that PGR as such have no value until they are used by someone for a specific reason. She expressed her sincere hope that the world community will be able to make such agreements that plant genetic resources will be freely available and preferably also free of charge in the future and stressed that all participants could contribute to that process. Finally she wished the participants interesting and fruitful discussions during their stay in Norway.

Presentation of participants

Petter Marum welcomed the members attending and those corresponding to the Forages Working Group meeting for the first time. He asked all the participants to briefly introduce themselves. The apologies of Vincent Connolly from Ireland, who was not able to attend, were transmitted to the Group. It was noted that many contributions were received from other members unable to attend.

Information on ECP/GR

Lorenzo Maggioni introduced himself as the new ECP/GR Coordinator. He welcomed the participants on behalf of IPGRI and thanked P. Marum for the excellent organization of the meeting. He also thanked E. Thörn for her encouraging and appropriate opening words, and then informed the participants, a number of whom were present for the first time at an ECP/GR meeting, of the changes in the structure and mode of operation of the Programme, as decided in the meeting of the Technical Consultative Committee (TCC) in Nitra, Slovakia, in September 1995. He described the new structure of the Programme which is composed of crop-specific networks and thematic networks and illustrated the type of activities carried out within each of these. He summarized the most recent ECP/GR events, such as the Documentation meeting in Budapest (October 1996) and the participation of non-EU

countries in EU-funded projects (EC 1467/94), such as the project on Potato genetic resources. The existence of a Web site for ECP/GR was mentioned, as well as the ongoing preparation of a prototype for the Internet Information Platform under the ECP/GR umbrella.[1] This will be the framework to interconnect and provide on-line access to the European Central Crop Databases. The imminence of the end of Phase V of ECP/GR (at the end of 1998), was mentioned, emphasizing the need to formulate recommendations for the future of the Forages Working Group to the Steering Committee.

Demetrios Droushiotis and Loek van Soest suggested that the Forages Working Group might benefit from being split into two or more Forages Working Groups, for example on temperate forages and Mediterranean forages. There was a discussion on the relative merits of splitting or remaining as one Group. The majority conclusion was that the Working Group would overall gain more benefit from remaining as one Group.

Chairperson's Report

Petter Marum
The Norwegian Crop Research Institute, Heggenes, Norway

Since the fifth meeting of the Working Group, held in Hissar, Bulgaria, in March-April 1995, the following activities have been carried out:

European forage databases

Changes in responsibility

In the last 2 years there have been several changes in responsibility for the different databases. The *Trifolium pratense* database was transferred from RAC, Changins, Switzerland to the Institute for Agrobotany in Tápiószele, Hungary. The database for annual *Lolium* was transferred from CNR, Bari, Italy to IGER, Aberystwyth, UK. The *Phalaris* database was transferred from CNR, Bari, Italy to the Nordic Gene Bank, Sweden. The *Poa* database was transferred from FAL, Braunschweig, Germany to the IPK branch Station at Malchow, Germany, and the *Dactylis* and *Festuca* databases were transferred from IHAR Radzików, Poland to the Botanical Garden of IHAR at Bydgoszcz, Poland.

New databases

New databases have been developed or are under development for *Agrostis* at NGB, Sweden, for *Agropyron* at IPGR, Bulgaria, and one for 'other perennial forage legumes' (*Anthyllis, Melilotus, Lotus* and *Onobrychis*) at the Institute for Agrobotany in Hungary.

Updating

During the last 2 years most of the databases have been updated. Reports about the updating will be given later during this meeting.

Searching for unduplicated material

During the last meeting in Bulgaria it was recommended to develop a computer programme to search for unduplicated material. It turned out to be more difficult than anticipated to develop such a programme that would do a good job for the European forage databases.

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[1] The European Information Platform on Crop Genetic Resources is now available at http://www.cgiar.org/ecpgr/platform

EGDS-ECP/GR Workshop on Central Crop Databases

Many of the European forage database managers attended the joint EGDS-ECP/GR workshop on Central Crop Databases held in Budapest in October 1996. Among the topics discussed were the role of Central Crop Databases (CCDBs), the inclusion of evaluation data in CCDBs, the standardization of CCDBs, the role of the database managers, and the facilitation of access to CCDBs.

The workshop adopted a slightly revised version of a multicrop passport descriptors list proposed by FAO and IPGRI.

To make the CCDBs widely accessible it was decided to establish an Internet-based information platform.

The question was raised why the forages are split into so many databases, even within some genera. It should be recommended that in the future, any change would go in the direction of merging rather than splitting databases.

European Phleum *Database*

After the recommendations of the EGDS-ECP/GR Workshop, the *Phleum* database was put on the Internet in a searchable form in November 1996 at the NGB. This was the first ECP/GR database to be put on-line in a searchable form. *Agrostis, Phalaris* and *Poa* databases will follow soon.

Lolium perenne *Core Collection*

The *Lolium perenne* core collection was established at 16 locations in the spring of 1995, and at two locations in 1996, in a total of 17 countries. Ruaraidh Sackville Hamilton and Ian D. Thomas elaborated the protocol for scoring the plants based on the discussions in our previous meeting in Bulgaria. Dirk Reheul made the protocol for the quality analysis. Five countries will do the quality analysis. Thirty-eight accessions were analyzed for isozymes by François Balfourier.

EU projects on genetic resources (EC 1467/94)

Three project proposals were submitted to the EU, one on *Medicago*, one on *Lolium* and *Festuca*, and one on Vicieae. The proposal on *Lolium* and *Festuca* was coordinated by Ruaraidh Sackville Hamilton, the proposal on *Medicago* was coordinated by Vincent Gensollen and the proposal on Vicieae by Frank Bisby. None of the proposals was successful or resubmitted in the following second call for proposals in 1996. A new call for proposals is expected to be announced in 1998.[2]

Mid-term progress report

A mid-term report was distributed to all members of the Working Group in July 1996, providing summaries of activities implemented since the previous meeting of the Working Group.

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[2] The Third call for proposals for the Community programme on the conservation, characterization, collection and utilization of genetic resources in agriculture was published on 9 April 1998 (closing date for proposal submission 9 July 1998).

The European Central Forages Databases (updating and opportunities for standardization)

Representatives from the countries hosting the ECP/GR Forages Databases presented an update of the status of these databases. Since the last meeting of the Working Group, updating has proceeded for several of these.

Status reports from the database managers

(for more detailed information, see also Part II)

IPGR, Sadovo, Bulgaria* - Agropyron *spp.

Siyka Angelova reported on the *Agropyron* database, maintained at IPGR, Plovdiv, Bulgaria. The database, on dBaseIII software, currently contains data received from the IPK-Genebank, Gatersleben, Germany (78 wild, semi-natural) and IPGR, Sadovo, Bulgaria (27 advanced cultivars and 29 wild, semi-natural). The database manager is currently collecting information to further update the database.

She recommended that her colleagues send her the data available, especially from countries with big collections, such as the Russian Federation, Poland and Greece.

***OSEVA PRO Ltd., Czech Republic* - Arrhenatherum elatius *and* Trisetum flavescens**

Magdalena Sevcíková reported on the *Arrhenatherum elatius* and *Trisetum flavescens* databases, maintained at OSEVA PRO Ltd., Grassland Research Station, Zubrí, Czech Republic. Updating started in 1996, with requests for data sent to 15 institutes. Replies were received from eight institutes, and their data were entered in the database, which now includes passport data of 148 accessions. The software used is FoxPro 2.5.

IBEAS, Pau, France* - Lathyrus *spp.

François Balfourier presented a report received from Daniel Combes on the European Database for *Lathyrus* maintained at IBEAS, Pau, France, containing about 4000 accessions. It includes four wild or semi-wild perennial species: *Lathyrus latifolius* L., *L. tuberosus* L., *L. heterophyllus* L. and *L. sylvestris* L., and two annual species: *L. sativus* L. (cultivated grass pea) and *L. cicera* L., probable wild ancestor of *L. sativus*. The database was established in 1985 and is updated approximately every year. Passport descriptors used are those indicated by IPGRI, and were modified according to IPGRI/FAO Multicrop Passport Descriptors. The database is accessible through the Internet, on the site of Pau University (http://www.univ-pau.fr).

Mr Combes was thanked for sending a comprehensive report and for his proactive interaction with the Working Group.

INRA-GEVES, Surgères, France* - Medicago *(perennial species)

François Balfourier reported on the perennial *Medicago* databases, maintained at INRA/GEVES, France. A catalogue was published in 1995 by France, with the support of ECP/GR. It contains about 2900 accessions from 13 countries.

The data file is currently being transformed into a database with a normal structure, which will also include accessions from other species of fodder crops from the French national collection. This work is supported by the French Agriculture Ministry. The software used is Access. The database will allow a better search for duplicated accessions. Owners of accessions can then be contacted to decide whether it is necessary to withdraw certain accessions. Regarding the completeness of descriptors, institutes which collaborate with the perennial *Medicago* database could send any available informations. If possible, this should be done in accordance with the mechanism for updating the European central forages databases.

IPK, Malchow, Germany* - Poa *spp.

Evelin Willner reported on the *Poa* database maintained since 1995 at the IPK-Genebank, Malchow station, Germany, where it was transferred from FAL Braunschweig, in connection with the retirement of Dr Seidewitz, and according to a decision of the ECP/GR Forages Working Group in 1995. Letters requesting *Poa* passport data updates were sent to 26 institutions in 19 countries holding relevant germplasm. The accessions in the database are reported to originate from 42 different countries, with more than 50% from Poland. Data received from contributors were transformed into a unique format, based on earlier recommendations of the ECP/GR Forages Working Group (*'Guide to ECP/GR Forages Databases,'* 1991) and on the FAO/IPGRI *'Multicrop Passport Descriptors'* (draft version, January 1997).

The authors of the database are highly interested in receiving Poa *data from other institutions who, for different reasons, could not send their updates in time. Data should be sent to E. Willner or H. Knüpffer by Email or on diskettes, preferably in the form of .dbf files (dBase or FoxPro) or .xls (Excel) files. ASCII files are also welcome. There is not, as yet, any possibility to import databases created in the format of Microsoft Access. Information about available evaluation data is also welcome. The database will be made accessible via Internet in 1997, thanks to a collaboration between IPK and ZADI.*[3]

Institute for Agrobotany, Tápiószele, Hungary* - Bromus, Trifolium pratense *and other perennial legume forage species

Lajos Horváth reported on the *Bromus*, *Trifolium pratense* and other perennial legume forage species databases, maintained at the Institute of Agrobotany (RCA), Tápiószele, Hungary. According to the decision of the fifth meeting of the Working Group, the *Trifolium pratense* database was transferred from Switzerland to the RCA, after it had been updated by the Swiss coordinator in 1995. The database contains passport data of 1901 accessions, belonging to 19 collaborating institutes. The duplicates within this database are marked with the same ECP number. The European *Bromus* Database has been updated during this period, and its structure is also renewed. The new database contains the passport data of 583 *Bromus* accessions, but duplicates are not included in it.[4] The fifth meeting also decided on the establishment of the 'Other Perennial Forage Legumes Database', which would compile the passport data of the European *Anthyllis, Onobrychis, Lotus* and *Melilotus* collections. IPGRI supplied the addresses of 45 possible collaborators. Until the reporting time 10 institutions had answered the request, and the new database contains 88 *Anthyllis*, 323 *Melilotus*, 677 *Lotus* and 348 *Onobrychis* accessions. Their total number is 1316. The three databases are available in dBaseIV format.

***ARO, Bet Dagan, Israel* - Trifolium alexandrinum *and* T. resupinatum**

Information on the database, maintained at ARO, Bet Dagan, Israel was not received before this meeting.

CNR, Bari, Italy* - Vicia *spp.

(Information extracted from a report prepared by the database manager, Pietro Perrino, in October 1996). The Central Database for *Vicia* contains 5520 accessions. A little more than 40% of the accessions are stored in the Bari genebank. The other 60% are stored in nine other genebanks. The number of known species in the database is nearly 80.

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[3] The database was uploaded in June 1997 at http://www.dainet.de/genres/eccdb/poa/poa.htm

[4] The *Bromus* database is now available on the Internet at http://www.ngb.se/Databases/ECP/Bromus

***IHAR, Bydgoszcz, Poland* - Dactylis *and* Festuca**

Petter Marum presented a report received from Wlodzimierz Majtkowski on the *Dactylis* and *Festuca* databases, maintained at IHAR, Bydgoszcz, Poland. The databases were updated in 1997. Information was received from 23 institutes. The *Dactylis* database contains 8700 accessions in 10 taxa from 14 institutes. Most of the accessions belong to the species *Dactylis glomerata* L. (98.5%). Of all accessions, 89.5% were classified as ecotypes and 6.7% as advanced cultivars and breeders' lines. Among the advanced cultivars and breeding lines, 44% were duplicated in one or more genebanks. The *Festuca* database contains 7366 accessions in 27 taxa from 17 institutes. Most of the accessions belong to the species *Festuca pratensis* Huds. (71%), *Festuca arundinacea* Schreb. (18%) and *Festuca rubra* L. (5%). A total of 82.8% of the accessions were classified as ecotypes and 14% as advanced cultivars and breeders' lines. Among the advanced cultivars and breeding lines, 55% were duplicated in one or more genebanks.[5]

The compiler of the database, Grzegor Żurek, recommends to update the database once every year, to add identification of duplicates to future activities, to collect information about other European species, and to standardize the taxonomy of the genus Festuca.

Mr Majtkowski was thanked for sending his accurate report and for his good example of effective interaction as a corresponding Working Group member.

***INIA, Badajoz, Spain* - Trifolium subterraneum *and annual* Medicago**

Francisco Gonzalez Lopez reported on the *Trifolium subterraneum* and annual *Medicago* databases, maintained at the Servicio de Investigación y Desarrollo Tecnológico (SIA), Spain. Updates were received from IPGR, Sadovo, Bulgaria, BAL, Braunschweig, Germany and the Royal Botanic Gardens Kew, UK. These were included in the databases. Data are recorded in dBaseIII and Access v. 2.0. The *T. subterraneum* database contains 3077 records, while the *Medicago* database contains 1776 records. All data are freely available.

***IGER, Aberystwyth, UK* - Lolium *and* Trifolium repens**

Ian Thomas reported on the *Lolium* and *Trifolium repens* databases maintained at IGER, Aberystwyth, UK using Microsoft Access v. 7.0. A common record description is used for both databases based on the IBPGR Descriptor List for Forages (1985) with modifications to accommodate all contributed data. At the end of 1995 all institutes identified by IPGRI as holding genetic resources of *Lolium* and *T. repens* were contacted and during 1996 the databases underwent a significant update. New or revised data sets were received from 15 Institutes and the new (1997) databases contain 8417 records for 25 species or subspecies of *Lolium* and 1285 records for five species or subspecies of *T. repens*. Also received was the database on annual *Lolium* from Bari, Italy, although this has yet to be incorporated into the main *Lolium* database.

Some institutes which supplied data for the old databases (pre-1995) did not reply to the request for new information. Rather than erroneously transfer obsolete records their data has not been included in the new databases. These institutes will be contacted during 1997 to ascertain the status of their data.

IGER would welcome any further information to help make the databases as complete as possible. Data may be sent by Email or on diskette, preferably in Access, dBase or Excel format. It should be clearly indicated whether they are **N**ew records, **M**odifications to existing records or records to be **D**eleted from the database.

An attempt was made to identify duplicated/unduplicated accessions. However, the outcome was not very satisfactory and it was decided to postpone the exercise pending further discussions.

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[5] The databases are now available on the Internet at http://www.ngb.se/Databases/ECP/Dactylis; http://www.ngb.se/Databases/ECP/Festuca

The new databases will be available during 1997 for downloading from the IGER World Wide Web site.[6] They can also be made available on CD-ROM. Smaller subsets of the data in response to specific *ad hoc* requests may be available on floppy disk or by Email.

***University of Southampton, UK - other* Vicieae**

Ruaraidh Sackville Hamilton indicated that the database has not been updated and remains in the same state as reported at the previous meeting in Bulgaria. This situation is due to lack of funds for personnel to work on the database.

***Nordic Gene Bank, Alnarp, Sweden* - Phleum, Agrostis *and* Phalaris**

Merja Veteläinen reported on the *Phleum*, *Agrostis* and *Phalaris* databases, maintained at the Nordic Gene Bank, Alnarp, Sweden. The updating of *Phleum*, *Phalaris* and *Agrostis* databases started in 1995 and is still ongoing. Information of some of the largest collections is not yet included in the central databases. The database management system is dBase for Windows. The *Phleum* database is already available on Internet and the *Phalaris* and *Agrostis* databases will also be published on the Internet during 1997.[7] Databases can be delivered on diskettes upon request. The *Phleum* database contains information from 19 institutes and for about 4200 accessions. In the *Phalaris* database information from eight institutions and 231 accessions is included. In both databases duplications and other gaps will be screened in the database and this information will be delivered to the respective institutions. The *Agrostis* database includes passport data from eight institutions and 271 accessions. The database will be managed as the other central forage databases at the Nordic Gene Bank.

Since several mistakes were found among the data received from contributors, these will be sent to the original database managers to make appropriate corrections. This exercise of correction is considered to require 1 year before being completed.

Mechanisms for updating

Ian Thomas presented an overview of updating mechanisms in Central Crop Databases. Institutes presenting data for inclusion in a Central Crop Database are not always aware of the difficulties encountered by the CCDB manager in incorporating the new data set into the main database. Using the *Lolium* CCDB as an example, this presentation discusses problems encountered in obtaining, reconciling and interpreting new data. It also covers the use of coded data fields and the automatic validation of data. Finally the question of unique accession names is addressed and a suggestion made to help avoid future problems.

Opportunities for standardization

Petter Marum introduced a discussion on the possibility for further standardization of the forages databases. In a former meeting of the Working Group on Forages in 1985, a standardized format for the forages databases was adopted. In 1997 most of the databases had a different structure. These differences make updating of the databases difficult. A standardized format would make the updating of the databases easier. Petter Marum presented a suggested descriptor list based on the FAO/IPGRI Multicrop Passport Descriptors and the main descriptors used today in the different forages databases. He suggested standardizing the data to the agreed structure before it is sent to the database managers. He also noted the large variability in the environmental descriptors used in IPGRI's descriptor lists, even within the forages, and suggested that a definitive IPGRI Multicrop Environmental Descriptor list would be of great advantage.

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[6] At time of printing of the report the *Lolium* database is now loaded on the NGB server at http://www/ngb.se/Databases/ECP/Lolium

[7] At time of printing of the report these databases are available respectively at
http://www.ngb.se/Databases/ECP/Phleum
http://www.ngb.se/Databases/ECP/Phalaris
http://www.ngb.se/Databases/ECP/Agrostis

Recommendations

- *To facilitate the centralization of data from genebanks into the Central Forages Databases, the Working Group members should actively contact the genebanks in their own country from which data are missing or incomplete, unless the reason for the delay is due to acknowledged lack of resources or temporary unavailability of the data.*
- *The Working Group members have an important role to play, as representatives of the Forages genetic resources community of their country, to raise the awareness of relevant national authorities, to the importance of the national commitment to inputs in kind to European Cooperation, such as the management of Central Crop Databases, the improvement of data about collections and the supply of these data to the CCDBs.*
- *The usefulness of data is not necessarily linked to the availability of seeds. Environmental and geographical data can help in the definition of gaps in the collection. Therefore the Working Group recommends that data be sent to the Central Forages Database Manager even in the case of unavailability of the respective seeds.*
- *The Working Group agreed on the adoption of the FAO/IPGRI Multicrop Descriptors List recommended during the EGDS-ECP/GR Workshop in Budapest, October 1996.*[8] *It also agreed on the addition of a few other descriptors as suggested by P. Marum. These will be listed with letters (A to M), to distinguish them from the Multicrop Descriptors. Apart from descriptors A (Collector's name), B (Breeding institute) and C (Breeding method), they are mainly environmental descriptors (D to I). Also a character on seed availability (J) and two characters related to the European Forage Collection (K and L) were added. Character M (Date of safety-duplication) was included in the FAO WIEWS Descriptors list. In addition, the ECP/GR Working Group on Forages allows for a subdivision of the descriptor 14 of the Multicrop Descriptors list: Status of sample, code 1 (wild): 1A for "natural ecotype" and 1B for "semi-natural ecotype". The complete 'Forages Passport Descriptors List', as agreed by the Working Group on Forages, is reported in Appendix I.*
- *The Working Group agreed that the supplier of the data to the central database manager should standardize the data in conformity with the adopted format and ensure the complete accuracy of the data, including procedures for formal validation before they are sent.*
- *The Working Group agreed that the adopted 'Forages Passport Descriptors List' will be the standard format for minimum data exchange; other types of data, such as further passport data, and characterization and evaluation data are welcome. The Working Group recognizes that complete coverage of descriptors for old data will not be requested.*
- *The Working Group considered that the FAO/IPGRI Multicrop Descriptors List was a good basis for harmonization, but a similar standardization should be carried out by IPGRI for a Multicrop Environmental Descriptors List*
- *The Working Group welcomes FAO's offer to revise the list of Institute codes.*

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[8] Lipman, E., M.W.M. Jongen, Th.J.L. van Hintum, T. Gass and L. Maggioni, compilers. 1997. Central Crop Databases: Tools for Plant Genetic Resources Management. International Plant Genetic Resources Institute, Rome, Italy / CGN, Wageningen, The Netherlands.

Status of national collections

Petter Marum reported on the results of a questionnaire to the Working Group members regarding the number of accessions, storage conditions, the number of accessions in urgent need of regeneration, number of accessions regenerated every year, and availability. He presented in a summarized form the information received. In total there were 97 872 accessions. On average 45% of the accessions are stored under long-term conditions and 42% under medium-term conditions. Twenty-seven percent of the accessions with available information were in urgent need of regeneration

The Working Group recommended establishment of a small subgroup consisting of Petter Marum, Merja Veteläinen and Ian D. Thomas, to update the summaries with data that were not available before the meeting. The update will be sent to all participants for validation before it is entered into the final report (Appendix IV of present report).

Reports from countries not included in the previous Working Group report

Information regarding National Collections not included in the previous report was made available during this meeting for the following countries (see also Part II).

Lithuania

Nijole Lemeziene reported on the status of the national collection of perennial grasses and legumes in Lithuania. The collection, held at the Lithuanian Agricultural Institute, Dotnuva, consists of semi-natural and wild ecotypes, old varieties, registered varieties and valuable breeding material. The greatest attention is given to the most important species for Lithuanian agriculture, that is *Medicago sativa* L., *Onobrychis sativa* Scop., *Trifolium pratense* L., *Trifolium repens* L., *Dactylis glomerata* L., *Festuca pratensis* Huds., *Festuca rubra* L., *Lolium perenne* L., *Phleum pratense* L. and *Poa pratensis* L.

The Netherlands

Loek J. M. van Soest presented the status of the forages collections maintained at CGN, Wageningen, consisting of 465 accessions of eight different species: *Lolium perenne* L., *L. multiflorum* Lam., *L.* × *hybridum* Hausskn., *Phleum pratense* L., *P. bertolonii* DC., *Dactylis glomerata* L., *Trifolium pratense* L. and *T. repens* L. The accessions of the different forage species are documented for passport data in GENIS, the CGN information system, based on the database management system ORACLE. So far no characterization/evaluation data of the forage collections are included in GENIS. Activities planned for the next 5 years include broadening the collection, particularly with original Dutch material; collecting activities (CIS countries, e.g. Uzbekistan), regeneration of about 300 accessions, updating of passport data and inclusion of evaluation data.

Slovakia

Jarmila Drobná presented the status of the forages collections of Slovakia. Institutions dealing with forage genetic resources and/or related activities include the Research Institute of Plant Production (RIPP) in Piešt'any, national coordination centre (674 forage accessions); the Plant Breeding Station Levočské Lúky (1666 accessions) and the Plant Breeding Station Horná Streda (337 accessions); the Grassland and Mountain Agriculture Research Institute Banská Bystrica; LEGUMEN, a production and commercial company, Piešt'any (*Lathyrus* spp. 106 accessions); the Slovak University of Agriculture, Nitra (*Lotus* spp.)

F.R. Yugoslavia

Zorica Tomić presented the status of the forages collections of F.R. Yugoslavia. The collection of genetic resources of forage crops of legumes and perennial grasses is part of breeding and prebreeding research conducted at the Agricultural Research Institute, Novi Sad, on *Medicago sativa* L., and at the Center for Forage Crops, Kruševac, on *Trifolium repens* L., *T. hybridum* L., *T. pratense* L. and perennial grasses. Because of high reduction in viability of some accessions, a part of the active collection of the Genebank was multiplied last year in the Forage Crops Center in Kruševac and the regenerated seed will be forwarded to the Genebank of Yugoslavia.

Duplication in forages collections

(see also full papers in Part II)

On the identification of duplicate accessions

At the Fifth meeting of the ECP/GR Working Group on Forages in Bulgaria (1995), a subgroup was formed to develop a protocol for identifying duplicates. The subgroup presented a protocol covering only the first step in the expensive, painstaking procedure of identifying duplicates with sufficient precision to permit their elimination.

The report defines historical duplicates (originated from the same original collected or bred material without undergoing deliberate selection by breeders) and biological duplicates (accessions which have been demonstrated to have the same genetic composition). Distinction is also made between Possible Historical Duplicates (PHDs) (with identical or 'matching' passport data) and Confirmed Historical Duplicates (CHDs).

Owing to time and costs constraints in the confirmation of historical duplicates and identification of biological duplicates, emphasis is set on preliminary identification of PHDs, and on the identification of accessions that are demonstrably unique, particularly those that are no longer stored in their country of origin.

The report introduces a simple protocol for partial identification of PHDs using only limited fields from the passport data, which achieves the same objective of assigning accessions to primary holders but with relative little investment of time and resources. A suggested protocol is presented in Appendix II.

Safety-duplication of genebank accessions in Europe

L. Maggioni introduced a discussion about the concept of safety-duplication – that is, the duplication of an accession for safety reasons. He mentioned how safety-duplication is essential for ensuring a sound conservation, with a minimized risk of losses and that this is also beneficial for the rationalization of collections, since accessions that are safely duplicated once do not need to be conserved as multiple duplicates in many places. As important criteria for safety, he quoted the adoption of international standards for long-term conservation as well as the need to establish formal agreements for safety-duplication. Such agreements, preferably undertaken between different countries, would strengthen the mutual trust and the sharing of responsibilities. The formality of the agreements would ensure official recognition to the safety-duplication and also that any emergency situation could be dealt with according to procedures planned in advance. L. Maggioni mentioned the example of the recommendation of the External Review of the CGIAR genebank operations to establish international agreements for safety-duplication. He showed the information available on the safety-duplication status within the Forages Working Group and asked the Group to forward information in order to fill the gaps. The Memorandum of Understanding between the Nordic Gene Bank and the Institute of Biology, Latvia, was presented as an example of a safety-duplication agreement with a 'black box' type of arrangement. He also mentioned the recent decisions of the *Brassica* Working Group, which acknowledged the cost-effectiveness of the 'black box' arrangement and recommended that genebank managers inform the Bras-EDB and the ECP/GR Coordinator about safety-duplication. The decisions of the *Secale* Group, where a more elaborate commitment was taken to safety-duplicate all the accessions defined as belonging to a *Secale* European Collection, were illustrated as a possible reference for a similar choice to be considered by the Forages Working Group.

Sharing of responsibilities

Sharing of responsibilities for the conservation and use of French forage genetic resources

François Balfourier presented the French decentralized system of genetic resources management. The approach taken in France was to have a network of voluntary partners to collectively manage a set of resources. A national structure, the BRG (Bureau des Ressources Génétiques = Genetic Resources Board) is in charge of the coordination of activities relating to animal, plant and microbial genetic resources.

For forage crops species, the genetic resources network is constituted of different research stations of public institutes (INRA, GEVES) and private companies (ACVF). Information concerning the status of the different collections are given in IPGRI's 'Directory of European Institutions Holding Crop Genetic Resources Collections', 4th edition (1995).

A National Charter has been written, with BRG, to define the objectives of the partners in the network, the obligations of each and the method of operation of the network. In particular the Charter defines:

- what accessions could be introduced in the French collection in accordance with international recommendations on genetic resources
- how to manage accessions (conservation, multiplication, distribution, etc.).

Work is underway to establish the national collection and a specific database for all fodder crop species. The quality status of the national French collection can be considered as that of the collection held by the GEVES station at Le Magneraud (Surgères) as described in the above IPGRI publication.

The European Forage Collection

The following text results from a discussion of the Working Group of an initial draft prepared by Petter Marum on the basis of the recommendations of the ad hoc *Group on* Secale.[9] *The text was then modified by a task force including P. Marum, F. Balfourier, L. van Soest, R. Sackville Hamilton and T. Gass, and resubmitted to the Working Group for approval.*

Introduction and recommendation

The objectives of the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) include ensuring the safe long-term conservation and promoting the exchange and utilization. At the establishment of the ECP/GR in 1980, it was recommended that forage genetic resources be given high priority by the Programme. This led to the creation of the Working Group on Forages. This Group has proven to be a valuable forum for the discussion of specific constraints facing the collection holder of forage species, the exchange of germplasm, the planning of collaborative collecting activities, the development of joint research projects, the sharing of research results and other relevant information, and the organization of scientific exchange and training activities. Regularly status reports of conservation activities in the respective ECP/GR member countries are being presented to the Group and workplans established to address identified problems. A number of Central Crop Databases (CCDBs), maintained by participating institutions as inputs in kind, provide a regional overview of the resources maintained in the different genebanks. Besides the reports of the Working Group meetings, these databases constitute the principal interface of the Group with potential users of the germplasm. They allow the rapid location of germplasm which can be selected on the basis of passport data and in a few cases characterization data. The CCDBs also form a useful basis for the Group to address issues

[9] Gass, T., W. Podyma, J. Puchalski and S.A. Eberhart. 1998. Challenges in rye germplasm conservation. Proceedings of an International Conference 'Crops Germplasm Conservation with Special Emphasis on Rye' and an ECP/GR Workshop 2-6 July 1996, Warsaw/Konstancin-Jeziorna, Poland. International Plant Genetic Resources Institute, Rome, Italy.

such as the need for further collecting, prioritizing for safety-duplication of germplasm, the development of core collections, etc.

Today, genebanks in the 30 ECP/GR countries conserve a total of about 97 000 accessions of forage species, of which approximately 65% have already been recorded in European Central Crop Databases (see relevant sections of the present report; Report of the Budapest documentation meeting, Oct. 1996).[10] These countries are heavily interdependent with regard to forages genetic resources. Europe has a long history and tradition of collaboration and free germplasm exchange. This has allowed significant progress to be made, in particular in rapidly raising the frequency of quantitative traits in breeding collections. The increasing privatization of breeding activities in the region is seen as potentially driving breeders to address short-term rather than long-term goals, resulting, *inter alia*, in neglecting the conservation of genetic resources. Furthermore, the exchange of germplasm and collaboration among breeders could be strongly reduced, bringing about a narrowing of the genetic basis of commercial varieties and ultimately an increased vulnerability of crops.

Recognizing

- that the long-term conservation of genetic resources and making these available to users is predominantly a public sector responsibility,
- that a restriction of access to genetic resources among European countries would seriously impede the efforts of breeders,
- that economic constraints call for a clear prioritization of genebank activities,
- that no single country in Europe can, on its own, conserve all the forage genetic resources, and
- that the Preparatory Meeting for Europe (Nitra, Slovakia, September 1995) and the Global Plan of Action (GPA) adopted in Leipzig, Germany (June 1996) call on ECP/GR to play a key role in facilitating the implementation of the GPA for the European region,

the Working Group recommends the establishment of a decentralized European Forage Collection comprising the forage accessions that European genebanks would agree to maintain on behalf of all member countries of ECP/GR.

Objectives

The objectives of establishing this collection would be:

- to formalize the sharing of responsibilities for the conservation of European forage genetic resources
- to ensure the safe conservation of these accessions
- to ensure the continued access to these accessions to all ECP/GR countries
- to make information about the forage genetic resources available to the users through adequate forms of documentation (e.g. Central Crop Databases, European Internet Information Platform on Crop Genetic Resources, published reports of Working Group meetings, etc.)
- to promote an intensive exchange of germplasm
- to enhance the use of forage genetic resources
- to reduce the workload for each country and allow a more effective conservation

[10] Lipman, E., M.W.M. Jongen, Th.J.L. van Hintum, T. Gass and L. Maggioni, compilers. 1997. Central Crop Databases: Tools for Plant Genetic Resources Management. International Plant Genetic Resources Institute, Rome, Italy/CGN, Wageningen, The Netherlands.

- to contribute towards the development of a multilateral system of benefit-sharing mechanism (since benefits such as the sharing of germplasm, the collaboration in research projects and collecting missions, and the sharing of opportunities for training and scientific exchange are available to any *bona fide* user in member countries through the participation of either a corresponding or an attending member in the Working Group)
- to contribute towards countries' efforts to implement the CBD.

Scope of the European Forages Collection

The European Forages Collection would include wild and cultivated species:

- of the following genera:

Agrostis	*Lotus*
Agropyron	*Medicago*
Arrhenatherum	*Phalaris*
Bromus	*Phleum*
Dactylis	*Poa*
Festuca	*Trifolium*
Lathyrus	*Trisetum*
Lolium	*Vicia*

- of the following types:
  - cultivated varieties in current use and newly developed varieties
  - obsolete varieties
  - primitive varieties or landraces
  - wild populations
  - breeding material (if well documented and at the discretion of the breeder).

- of the following status:
  - material for which distribution is not restricted
  - material of indigenous origin (bred or collected)
  - material collected or obtained from other countries if the safe conservation of or access to this material is unsure.

The inclusion in the collection of registered varieties is useful as these provide valuable traits for breeding. In many countries, however, access to this material requires prior informed consent from breeders.

Workplan for the establishment of the European Forage Collection

1. The database managers for the different species would suggest a genebank as the 'primary collection' for each original accession. This would be the first step of a close interaction between database manager, genebank and the respective national programme for PGR to determine the 'home' of the accession, frequently this would be the country in which the accession was collected or bred (a discussion paper on this subject is included in Appendix II).
2. National commitment would be sought for long-time conservation and to provide access to the accessions. **It is understood that this responsibility would imply a custodianship, and would not be meant to have any implication of 'ownership'**.
3. National programmes would be requested to provide to the respective database manager a list of accessions for which the country would accept to take long-term conservation responsibility on behalf of the ECP/GR countries. A copy of this list would be deposited with the ECP/GR Coordinator.
4. Database managers would record the institute that holds the 'primary collection' in the European database for that accession under the descriptor 'Holder of primary collection'.

Responsibilities

The primary collection would:

- Ensure that the material is maintained under long-term conditions in compliance with international standards (references: FAO/IPGRI Genebank Standards 1994, Guidelines for the regeneration of accessions in seed collections of the main perennial forage grasses and legumes of temperate grasslands, this report, Appendix III).
- Ensure that an appropriate safety-duplicate is deposited in a genebank preferably within another ECP/GR country and that relevant information about this safety-duplication is provided to the respective European Forage Database Manager (ref. Forages Passport Descriptors list, Appendix I).
- Respond in reasonable time to germplasm requests. In the case of a shortage of seeds the requesting party may exceptionally be asked to participate in its multiplication. Requests which are clearly counter to the spirit of the present initiative (e.g. requests for most accessions in a collection) can be referred to the Working Group on Forages for arbitration.
- Provide unrestricted access to the declared accessions to *bona fide* users from ECP/GR Member Countries (exemption is made for registered varieties, see above) and ensure through the use of Material Transfer Agreements that receiving parties do the same.
- Endeavour to give high priority to the adequate characterization, evaluation and documentation of accessions which are part of the European Forages Collection.
- In the case of an impossibility to honour the commitment for long-term conservation, inform the respective European Forage Database Manager and actively seek a new 'primary collection', willing to maintain the material.
- If a new host genebank cannot be found, maintain the material under long-term condition for at least another 2 years.

The European Forage Database Manager would:

- Facilitate the repatriation of material by distributing relevant information about accessions conserved in foreign countries.
- Update the database every 1-2 years and make it available to the collection holders.
- Effect changes to the database when informed by the collection holders.
- Rapidly forward to the 'primary collection' any requests for seed.
- Provide the collection holders and the Working Group with information about the degree of safety-duplication of the collections.
- Analyze the database and advise the Working Group with regard to duplication or gaps in the collections, establishment of core collections, planning of collecting missions, etc.

The genebank hosting safety-duplicates would:

- Maintain a sufficient quantity of the safety-duplicated material in long-term storage conditions in compliance with international standards and under 'black-box arrangement' (see Appendix II).
- Not distribute the material.
- Clearly designate as safety-duplicate the accessions provided for this purpose and not include them on *index seminae*/distribution lists.
- Immediately notify the 'primary collection' in case of any problem with the safety-duplicate.
- Not carry out viability tests.
- Not regenerate the safety-duplicated material.

The ECP/GR Forages Working Group

- This Group is composed of representatives of each country who are nominated by the respective National Coordinators and participate in the Group either as Attending or Corresponding Members. Institutions which participate as observers to ECP/GR are also invited to nominate representatives to the Working Group (e.g. ASSINSEL, FAO, etc.).
- The Working Group would have the technical oversight over the European Forages Collection. It would address issues such as quality standards and if necessary control their implementation.
- It would endeavour to establish the necessary links with potential users of the genetic resources through mechanisms such as core collections, evaluation networks, etc.
- In collaboration with the ECP/GR Coordinator, the Chair of the Working Group would report on an annual basis to the ECP/GR Steering Committee on the status of the European Forages Collection, the central databases and the progress in implementing the Working Group's Workplan.

Standards for regeneration

The following background information was presented by R. Sackville Hamilton together with draft standards for the regeneration of perennial forage species. It was agreed that a subgroup composed of R. Sackville Hamilton, P. Marum and L. Maggioni would revise this draft further and circulate it to the Group before publication in the present report.

Guidelines for the regeneration of accessions in seed collections of the main perennial forage grasses and legumes of temperate grasslands

The main protocol is presented as Appendix III. This section is a summary of the paper presenting further background details (full text, page 103).

Decisions for regeneration protocols represent a compromise between maximizing the number of accessions that can be regenerated each year within available resources, and maximizing the genetic integrity of accessions. An important element of the regeneration protocol is based on the interaction between base and active collections as recommended in the Genebank Standards (FAO/IPGRI 1994). The impact of loss of genetic integrity on the distinctness of accessions was a second major consideration in developing the protocol. There are three primary causes of loss of genetic integrity: drift, selection (natural and artificial, conscious and unconscious), and contamination with alien genes (through alien pollen, alien seed, alien plants, or even through incorrectly identifying and labelling accessions). Most perennial forage grasses and legumes are obligate outbreeders, and so display high genetic variance within populations, high potential for genetic changes by drift and selection during regeneration, and present a high risk for cross-pollination between regeneration plots if they are not adequately isolated. There is also a high risk for contamination with alien plants, seed and pollen, and exceptionally high variation in fecundity between plants in a single population, with a corresponding potential for rapid genetic changes in response to selection pressures. The recommended conditions for prevention of contamination with alien pollen are more stringent than currently used by some genebanks. This reflects not only the adverse impact of contamination on genetic integrity, but also a more cautious interpretation of the literature on pollen flow. Examples of studies of contamination rates found in *Lolium perenne* and *Melilotus* show that insect pollinators fly as far as they need to find a flower but no further. They express preferences for the type of flower they visit, so the most effective barrier crop will have flowers identical to the plot being regenerated.

The *Lolium* Core Collection

Current status of the Core Collection

The current status of evaluating the core collection was presented by P. Marum in relation to objectives remaining to be achieved.

Objectives

Objectives for the coming year are to assemble all available data, analyze it statistically and publish in refereed papers. Emphasis of the analysis will be on interpreting G×E interactions for evaluation data in terms of adaptive variation among populations. This will require comprehensive data on the environments of (a) the original collecting sites and (b) the evaluation sites, in addition to the evaluation data.

Collecting site data

Passport data on 232 accessions (of these 162 had sufficient seed available for inclusion in the Core Collection Trial), considered by the participating institutes to represent the variation available in their countries, were collated in an Access database. The database contains information in the following groups: Expedition Details, Location Details, Sampling Details, Site Description, Management Details, Soil Details and General/Donation Details. The record description of the database was presented with a summary of the database contents showing the percentage of each descriptor containing data.

Most of the descriptors are well under 100% populated. This can be expected in many cases, e.g. site and management descriptors. However other descriptors such as Accession Status, Latitude, Longitude and Altitude should be available for all collecting sites and participants are requested to ensure that all available data have been presented for inclusion in the passport database.

The database is available from IGER, Aberystwyth in Access or Excel format.

Evaluation site data

Some sites have already presented data for inclusion. To make the database as complete as possible, Institutes are requested to provide the following information:

- **Site**
  Latitude, longitude, altitude
- **Weather**
  Rainfall (mm); temperature (°C) - soil (10 cm), minimum air, maximum air, grass minimum; humidity - dry bulb, wet bulb (°C), or relative humidity (%); wind speed - maximum gust speed (m/s), total wind run (km); net radiation (MJ/m).
  If possible, daily observations over the time period of the trial should be supplied, particularly for temperature, to enable analysis of heading date in terms of cumulative degree-days.
- **Soil**
  Soil analyses performed to date show considerable variation between evaluation sites. To standardize the data, participants are requested to send soil samples (about 500 g) to IGER, Aberystwyth where they will be analyzed for NA, K, P, Mg, Ca and pH.

Evaluation data

Evaluation data have been supplied by 11 institutes on disk or by Email. Formats which have been used are Access, Excel, dBase and Lotus 1-2-3. Any institute which has data available should send it to IGER, Aberystwyth.

Isozyme studies

In France, isozyme studies were performed on a sample of the European *Lolium* core collection. So far, 38 populations (3 from Belgium, 3 from Switzerland, 3 from Ireland, 2 from The Netherlands, 1 from Norway, 1 from Czech Republic and 25 from France) have been analyzed with two starch gels and two different buffer systems. This permitted us to observe 12 readable loci. Another study on 120 other European populations gives an idea of the genetic structuration of the diversity and the interest of carrying on such a study on the European *Lolium* core collection.

Depending on funds available, France proposes to perform analyses on a subsample of the European *Lolium* core collection, in order to draw maps of allelic distribution by means of geostatistical analyses using both agronomic and isozyme results.

As most of the diversity is found within a population, it will be necessary to analyze about 75 plants / population to observe allelic frequencies with good accuracy. For example, the analysis of a subset of 80 populations requests about 12 man-months of labour (two populations per week).

Project applications to the European Commisssion

Council Regulation (EC) 1467/94 on the conservation, characterization, collection and utilization of genetic resources in agriculture

Thomas Gass introduced the subject by providing a brief overview of the EU genetic resources programme, its background, underlying principles and the activities carried out to date. He summarized the outcomes of the first two calls for proposals following which a total of 12 projects on plant genetic resources have been selected for funding by the European Commission. Shortly after its initiation this programme has already suffered serious financial constraints, leading to the postponing of a third call for proposals to possibly 1998.[11] T. Gass noted that some of the requirements for project proposals were implicit rather than explicit and that uncertainty prevails on a number of issues such as the optimal number of partners and the involvement of private sector and NGOs. The participation of institutions from non-EU countries is currently being facilitated for six of the 12 above-mentioned projects. In the case of two projects, institutions from non-EU countries were included as official partners in the project, albeit not requesting any funding from the European Commission. Participation of NGOs and a strong orientation toward direct utilization and private sector interests seem to be favourable traits in project proposals. Furthermore, it is expected that the projects should address as directly as possible the objectives of the current Common Agricultural Policy (e.g. extensification of agriculture, providing alternatives in crops, contributing towards solving environmental problems, etc.).

T. Gass concluded by saying that although the amount of funding provided through this programme is highly insufficient to allow any sustainable conservation activities at the EU level, Groups that have been succesful in proposing projects have so far benefited from these. The additional money and the commitment to report to the European Commission on the achieved progress have provided additional motivation to accomplish agreed workplans. He encouraged the Group to revise and resubmit the proposals which had been unsuccessful in previous calls (i.e. the *Lolium* and *Festuca* project coordinated by IGER, the *Medicago* project coordinated by GEVES-INRA and the Vicieae project coordinated by the University of Southampton).

A discussion followed regarding the scope, the number of participants and the possible re-orientation of the above-mentioned projects.

Recommendations

The Working Group agreed that the previous project on Lolium *and* Festuca *would be revised to focus only on* **Lolium**, *and to provide more outputs which are of direct relevance to germplasm users such as breeders. Opportunities for associating private breeders with the project (either directly or through letters of recommendation) will be investigated. The offer of D. Reheul (Belgium) to coordinate this new proposal was welcomed by the Group. The following participants expressed an interest in participating in the project as designated partners: F. Lassacher (Austria), F. Balfourier (France), P. Marum (NGB), B. Boller (Switzerland), R. Sackville Hamilton (UK), E. Willner (Germany). The following wished to be involved as complementary partners: M. Sevcíková, Grassland Research Station Zubrí (Czech Republic), V. Negri (Italy), T. Vaitsis (Greece), L. Horváth (Hungary), Z. Tomić (F.R. Yugoslavia) and possibly M. Tavares de Sousa (Portugal). The participation of CGN, The Netherlands as designated partner will be confirmed.*

F. Balfourier agreed to enquire whether GEVES/INRA would be interested in coordinating a resubmission of the **Medicago** *project. The following participants expressed interest in participating as designated partners: V. Negri (Italy), T. Vaitsis (Greece), D. Droushiotis (Cyprus), and possibly*

[11] The Third call for proposals for the Community programme on the conservation, characterization, collection and utilization of genetic resources in agriculture was published on 9 April 1998 (closing date for proposal submission 9 July 1998).

M. Tavares de Sousa (Portugal), the Research Institute of Plant Production (Czech Republic), Piešt'any (Slovakia) and AARI, Izmir (Turkey). The Research Institute for Fodder Crops Troubsko, Czech Republic (J. Nedelnik) wished to be involved as complementary partner.

R. Sackville Hamilton will contact Frank Bisby, University of Southampton[12] *with regard to the possible resubmission of the* ***Vicieae*** *project and provide this information to the Chair for distribution to interested members of the Group (Bulgaria, Cyprus and Turkey are interested in participation).*

BAL, Irdning (Austria) will consider the planning of a project for the **in situ** ***conservation of forages in marginal and mountainous areas****, to be submitted to the EU. The Working Group gave its strong support to the implementation of this idea in collaboration with NGB, Italy and Bulgaria.*

[12] Now University of Reading, see p. 69.

Collecting activities

The following countries reported on their collecting activities: Bulgaria, Cyprus, Czech Republic, Germany, Hungary, Lithuania, Poland, Portugal, Russian Federation, Slovakia, Spain, Turkey, United Kingdom and F.R. Yugoslavia. The full reports are given in Part II, Presented papers, section Collecting activities.

Research activities

Reports of ongoing or concluded research activities
(see also Part II)

Austria - Recultivation of alpine areas with seed of alpine plants

Summer and winter tourism and the associated interventions, together with natural erosion, cause severe damages in the Alps every year. The recultivation of such areas is very difficult. The use of seed of lowland species, not really adapted to the climatic conditions, is expensive and not satisfying. To obtain a permanent green cover, a well-adapted vegetation of alpine plants is required. At BAL Gumpenstein the suitability of 12 alpine species of well-chosen grasses and Leguminosae (*Festuca nigrescens (*Lam.) Asch. et Ev., *F. pseudodura* Steud., *F. supina* Schur, *F. violacea* Gand. s.stv., *Phleum alpinum* L.emend. Gaudin, *P. hirsutum* Honck., *Poa alpina* L., *Trifolium badium* Schreb., *T. pratense* L. subsp. *nivale* Arc.) were tested for commercial seed production in low altitudes. Seed properties and the 1000-seed weight are described. The germinative capacity increased after cultivation and was equal to related lowland species. The seed productivity for most of the alpine grasses was surprisingly high. Some provenances of *Poa alpina* and *Festuca nigrescens* showed an annual yield of more than 1000 kg/ha. Contrary to a widespread view the research results clearly showed that seed multiplication of those 12 species in lowland regions is possible. In the last 5 years, many recultivation trials in alpine areas have been undertaken with this material. The results emphasize the value and the possibilities of the use of alpine seed mixtures for permanent recultivation in alpine areas.

Czech Republic

- The following joint research projects are coordinated by the Research Institute for Plant Production, Prague:
  - National programme for the conservation and utilization of the plant genepool.
  - Mapping, gathering and conservation of landraces and wild species related to cultivated crops in the Czech Republic and bordering European regions.

Other research projects are coordinated as follows:

- Research Institute for Fodder Crops in Troubsko
  - Use of forage crops and other species in farming and landscaping.
  - New crops for cultivation in marginal areas and their energetic and industrial use.
  - Collecting of and research on clovers genetic resources.
- Grassland Research Station in Zubrí
  - Selection and evaluation of wild grass species suitable for the enhancing of biodiversity of perennial grass swards.
  - Creation of regional collections of wild grasses and herbaceous plant populations for the restoration of flower grassland.

Germany - A knowledge base for disease resistance of selected cultivated plant species

A **knowledge base** reviewing the current knowledge on disease resistance of plant species investigated in the genebank branch station North (Malchow) of IPK-Gatersleben was set up. More than 350 publications on disease resistance of the last 25 years were considered, concerning 116 host-pathogen combinations of *Brassica napus* L. var. *oleifera*, *Dactylis glomerata* L., *Festuca arundinacea* Schreb., *F. pratensis* Huds., *F. rubra* L., *Lolium perenne* L., *Medicago sativa* L., *Phleum pratense* L., *Poa pratensis* L., *Trifolium pratense* L. and *T. repens* L. Sixteen priorities are taken into consideration such as resistant genotypes, methods of checking resistance, genetics of resistance and breeding for resistance. The **knowledge base** can be made topical and complete continuously and can be searched and used throughout the IPK genebank branch station Malchow. Seed samples can be requested from the genebank in Malchow. In the near future this information will be recorded on the Internet with the support of ZADI / IGR, Bonn.

Greece - Breeding for drought resistance, persistence and forage productivity

- Breeding of *Medicago sativa* L. (alfalfa) was in the first priorities of the research conducted during the last 15 years. Samples collected in different regions were evaluated in the field and great variability was found. The best plants were selected to create new populations, clones and synthetic varieties. Traditional alfalfa varieties and modern bred varieties, indigenous or introduced, were screened and the best were tested in contrasting environments under or without irrigation. The semidormant Greek varieties Dolichi, Hyliki, Hypati and Florina proved to be the most persistent and the most productive varieties under or without irrigation. Cheronia, a nondormant Greek variety, was also a good producer, but only under irrigation.
- *Medicago arborea* L. is a drought-resistant shrub, suitable for marginal rocky soil reclamation in Mediterranean dry-hot conditions. The collection of indigenous germplasm was completed, including a total of 38 accessions. A mass selection variety named Naxos has been registered on the national list of varieties and a large number of clones and lines have been produced by selection for drought and cold resistance, leafiness and forage production.
- *Dactylis glomerata* L., *Festuca arundinacea* Schreb., *Lolium perenne* L. (cocksfoot, tall fescue and perennial ryegrass): wild and bred populations were given a preliminary evaluation under irrigation or rain-fed conditions in individual plants or in dense sowing for heading time, drought resistance, persistence and forage production. Large variability was found for all characteristics within and between populations and was used in further breeding work of the wild indigenous germplasm, aimed at creating more productive and more persistent varieties, better adapted to dry-hot conditions. The productivity of Greek varieties, tested in Central Greece, was similar to that of foreign varieties under irrigation, while it was much higher under rain-fed conditions. Metsovo tall fescue and Olympion ryegrass are both suitable for use all over Greece under irrigation or under rain-fed conditions in cool regions. Perrevia cocksfoot could be grown well under rain-fed conditions even in the dry-hot southeastern Greece.

Italy - RAPD fingerprints as a tool for characterizing the genetic background of* Medicago sativa *L. germplasm

Lucerne is the most important forage legume crop in Italy. This study was conducted to assess the suitability of RAPD markers in detecting the genetic variability among and within lucerne landraces from central Italy. In a first experiment genetic variability estimations based on bulked plant DNA samples were assessed in 16 landraces from the Marche region; in a second experiment genetic variability estimations based on single-plant DNA samples were assessed in six landraces from the Tuscany, Umbria, Abruzzi and Lazio regions. Most landraces from Marche were found to share a common genetic background and to have a limited genetic variation within population, whereas landraces from the other regions

showed greater between- and within-population genetic variation. RAPD markers appeared to be a useful tool in describing the genetic background of landraces, although plant DNA bulking procedures underestimated the level of genomic diversity, especially within lucerne accessions. Single-plant analysis has to be considered essential in detecting the level of genetic variability within lucerne landraces. Bulked DNA analysis could be used as a first approach in screening large germplasm collections (1) with the purpose of identifying a core collection, (2) when there is urgency for regeneration and not enough resources and (3) when suitable populations need to be selected for breeding programmes.

Slovakia - Research activities relevant to forage genetic resources (RIPP)

- Cytogenetic characterization of genetic resources
  Computer construction of caryotypes and ideotypes (Š. Masár).
- Cytogenetics of *Medicago* and *Trifolium*
  Production and identification of distant hybrids in alfalfa.
  Production and identification of autotetraploids in red clover (A. Mištinová).
- Characterization of selected species of *Agropyron, Aegilops*, and *Elymus* genera
  Characterization and utilization for interspecific hybridization (V. Šudyová).
- Phytopathological tests
  Testing GR of alfalfa for resistance to *Ditylenchus dipsaci, Clavibacter michiganensis* subsp. *insitiosum*, *Verticillium alboatrum* Reinle et Berth., *Fusarium* Lk. spp. (V. Gubiš).
  Testing GR of red clover for resistance to *Fusarium* subsp. (B. Vanco).
- Looking for genotypes resistant to abiotic factors
  Testing alfalfa genotypes resistant to salinity, low pH, and increased aluminium content (P. Hauptvogel).
  Collecting *Rhizobium* strains mostly from red and white clovers and alfalfa (T. Krupová).
- Dynamic model of alfalfa variety maintenance
  Selection of initial populations and detection of initial level of genetic variability (M. Uzík).
- Recurrent selection for somatic embryogenesis response in alfalfa commercial cultivars, preparing highly-regenerative germplasm and genetic transformation of plants via *Agrobacterium tumefaciens* (E.F. Smith *et* Townsend) Conn -mediated gene delivery (J. Farago).

Turkey - Evaluation of common vetch collections

Common vetch (*Vicia sativa* L.) (119 accessions) collected from different regions of Turkey were analyzed for 13 characters. There were significant differences among populations for all characters studied. Four principal components were found to express 62.7% of the total variation. Pod dimensions and seed weight per plant came out as the major sources of diversity. Main stem length, 1000-seed weight and hay yield per plant had the largest variances.

United Kingdom - Research at IGER on* in situ *conservation of botanical diversity in agricultural grasslands

The influence of a range of managements (fertilizing, grazing, cutting) on botanical diversity in different types of grassland is compared and their effects are measured on productivity, species diversity and soil status. The selected management regimes correspond to traditional local farming practices, intensive management, and alternative low-input systems.

Different types of grassland differ in their potential to increase species diversity following the implementation of more environmentally sensitive management regimes. When grasslands cannot respond quickly to improved management, consideration is given to artificially reintroducing species that have been lost. Projects in progress at IGER are determining optimal procedures for introducing seed and the importance of using locally provenanced seed is assessed.

Re-establishment of hedges in field margins is being promoted as a valuable component of *in situ* conservation of biodiversity within agricultural landscapes, mainly with commercially available hawthorn (*Crataegus monogyna* Jacq.) of eastern European origin. However, studies show that local races are superior in terms of adaptation to UK winters, development of a high-quality dense hedge structure, and thorniness, and therefore superior both in terms of habitat quality for wildlife, and in their effectiveness as a barrier to sheep and cattle. Discussions are in progress with seed companies to promote awareness of the benefits of using local races.

Finally, there is particular concern over the genetic integrity of species that have evolved as dominant or subdominant components of grasslands but have now become rare, existing only as small isolated populations, with the risk that the remnant populations will become too inbred. IGER addresses this problem through a project assessing geneflow between model populations of *Lotus* monomorphic for different isozyme marker alleles and sown in various spatial arrangements.

Future research activities

The following plans for collecting and research activities to be carried out in the near future were announced:

Bulgaria

Activities at IPGR, Sadovo, will be put forward in three directions: (1) definition of measures for the conservation of forage species, (2) plans for *in situ* conservation, and (3) plans for linkage between agricultural needs and plant genetic resources conservation.

Cyprus

The Agriculture Research Institute, Nicosia, collected *Medicago*, *Avena* and *Hordeum* species within the country and started the evaluation.

Greece

A new national research project started in 1997 on the breeding of perennial legumes and grasses under rain-fed conditions. Another research project is planned to start next season in cooperation with Cyprus to supplement the previous collections and to continue the preliminary evaluation of some annual and perennial forage species.

Germany

A 2-year programme for the primary evaluation of 800 *Lolium perenne* accessions collected in Malchow and Braunschweig will be carried out at IPK, Malchow / Poel starting in Spring 1997, in collaboration with German breeders and institutes. Subsequently selected material will go through a second evaluation step and data will be entered in the database. Results will be reported during the next meeting of the Working Group on Forages.

Nordic Countries

NGB is planning to elaborate projects for the *in situ* conservation of forages.

Turkey

An expedition to collect forage legumes will be made to northern Turkey. A research project for the evaluation of cold tolerance in *Vicia villosa* has recently started at AARI, Menemen.

Recent international developments in PGR-related issues

Thomas Gass presented international negotiations and conferences held since the begining of 1995 which are of particular relevance to ECP/GR. These include:

- The Regional Preparatory Meeting for Europe (Nitra, Slovakia, September 1995) held in conjunction with a meeting of the ECP/GR Steering Committee. The former recommended, *inter alia*, the establishment of a multilateral agreement including all PGR for food and agriculture and ensuring unrestricted access to the resources to all members to the agreement. The Regional Meeting also welcomed the broadening of the structure of ECP/GR and recommended that the programme be considered as the platform for implementation of the Global Plan of Action (see below) for Europe.
- The Revision of the International Undertaking (IU) by the FAO Commission for Genetic Resources for Food and Agriculture (Rome, Italy, in June 1995, November 1995, April 1996, December 1996). These negotiations are advancing very slowly with main issues of disagreement including the sharing of benefits, farmers' rights, and financial commitments. A relative progress is being made in defining the scope of a possible multilateral system. More practical outputs of the FAO Global System on PGRFA include the International codes of conduct for plant germplasm collecting and transfer and the preparation of guidelines on regeneration.
- The Conference of the Parties to the Convention on Biological Diversity (CBD/COPIII) (Buenos Aires, November 1996) paid particular attention to agricultural biodiversity and welcomed the Global Plan of Action adopted in Leipzig (see below). It encouraged the FAO Commission on Genetic Resources for Food and Agriculture to rapidly conclude its revision of the International Undertaking which could eventually become a protocol under the Convention on Biological Diversity.
- The International Technical Conference on PGR for Food and Agriculture (Leipzig, June 1996) was probably the single most important international event for the plant genetic resources community. Its principal output, the Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture contains 20 Priority Activities providing a useful basis for the development of national strategies for conservation, funding, etc. Most relevant Priority Activities (PA) for the ECP/GR Forages Working Group include:
    - Surveying and inventorying PGRFA (PA 1)
    - Supporting on-farm management and improvement of PGRFA (PA 2)
    - Promoting *in situ* conservation of wild crop relatives and wild plants for food production (PA 4)
    - Sustaining existing *ex situ* collections (PA 5)
    - Regenerating threatened *ex situ* accessions (PA 6)
    - Supporting planned and targeted collecting (PA 7)
    - Expanding the characterization, evaluation and number of core collections to facilitate use (PA 9)
    - Increasing genetic enhancement and base-broadening efforts (PA 10).

The consequences of the GPA for ECP/GR will be given much attention in the formulation of a draft strategy, workplans and budgets for the forthcoming Phase VI of ECP/GR.

Conclusion

During the morning of 8 March the participants had the opportunity to visit the facilities of the Løken Research Station.

The Section 'Discussion and Recommendations' of the report was presented to the participants and adopted after some corrections. A task force consisting of Petter Marum, Ruaraidh Sackville Hamilton and Lorenzo Maggioni will finalize the ***Guidelines for the regeneration of accessions in seed collections of the main perennial forage grasses and legumes of temperate grasslands*** (Appendix III) while a second task force consisting of Petter Marum, Merja Veteläinen and Ian Thomas will finalize the ***Summary of germplasm holdings*** (Appendix IV). The participants agreed to supply missing information about ***Safety-duplication capacities*** to L. Maggioni for inclusion in the report (Appendix V).

NGB and Sackville Hamilton will revise and finalize the ***Protocol for designating primary holders of accessions*** (Appendix II) by the end of June 1997. Both Appendixes II and III will be circulated to the Group before printing of the report.[13]

The participants strongly recommend to the Steering Committee that Phase VI of ECP/GR be implemented and that this include the contribution of the Forages Working Group. The Group also strongly recommends that the system with a full-time Coordinator be continued or even strengthened.

The Group welcomes the rapid progress made during Phase V, which was achieved thanks to the appointment of a full-time Coordinator.

Petter Marum was elected Chairperson of the Group until the end of next meeting.

The next meeting was programmed tentatively for the first semester of 1999. However, this date may be affected by the initiation of Phase VI of ECP/GR.

[13] Appendix II and Appendix III were not circulated to the entire Group before printing, to avoid further delay of the publication of the present report. These documents remain the responsibility of the authors. However, relevant comments raised by the Group during the meeting, and subsequently by the specific task forces, were taken in due consideration by the authors.

Part II. Presented papers

European Central Forages Databases

The following reports are from the ECP/GR Central Crop Database managers. Note that the databases are ordered by country of the host institute; when full contact details are not given, please refer to Appendix VII.

European Central Forages Databases

The European *Agropyron* database
The European *Arrhenatherum* and *Trisetum* Databases
The European Central *Lathyrus* spp. Database
The European Central Perennial *Medicago* Database
The European *Poa* Database
The European *Bromus, Trifolium pratense* and other perennial forages databases
The European *Trifolium alexandrinum* and *T. resupinatum* databases
The European *Vicia* database
The European *Dactylis* and *Festuca* databases
The European databases of *Medicago* spp. (annual species) and *Trifolium subterraneum*
The European *Phleum, Phalaris* and *Agrostis* databases
The European *Lolium* and *Trifolium repens* databases
The European database on 'other Vicieae'

The European *Agropyron* database

Manager: Siyka Angelova
Institute for Introduction and Plant Genetic Resources, Sadovo, **Bulgaria**

Institute	Advanced cultivars	Landraces	Wild, semi-natural
BGRIPGR	27	–	29
DEUIPK	–	–	78

Updating

Collecting of information about *Agropyron* spp. is in progress. Since October 1996 (meeting of the Forages Working Group at the EGDS-ECP/GR workshop on Central Crop Databases), documentation has been received from the IPK-Genebank, Gatersleben, Germany and from IPGR, Sadovo, Bulgaria.

The European *Arrhenatherum* and *Trisetum* Databases

Manager: Magdalena Sevcíková
Oseva PRO Ltd., Grassland Research Station, Zubrí, **Czech Republic**

Establishment of the database: 1991
Only data from two institutes in Hungary and former Czechoslovakia were recorded manually.

Updating: 1996
Requests for data were sent to 15 European institutes holding genetic resources of *Arrhenatherum* and *Trisetum.* Up to now eight institutes have responded. Data have been computerized.

Software: FoxPro 2.5.

Database content: passport data for 148 accessions.

Table 1. The European *Arrhenatherum* and *Trisetum* accessions classified by contributing institute[†]

	Number of accessions			Advanced cultivars		Ecotypes (wild, semi-natural)		Status unrecorded	
Institute	*Arrh.*	*Trisetum*	Total	*Arrh.*	*Triset.*	*Arrh.*	*Triset.*	*Arrh.*	*Triset.*
CZE082	18	9	27	12	4	6	5	–	–
DEU001	1	6	7	–	6	1	–	–	–
DEU146	15	3	18	3	1	–	–	12	2
GBR004	5	1	6	–	–	3	1	2	–
GBR016	1	1	2	1	1	–	–	–	–
HUN003	42	0	42	3	–	39	–	–	–
SVN019	1	0	1	1	–	–	–	–	–
SVK012	25	20	45	14	2	11	18	–	–
Total	108	40	148	34	14	60	24	14	2

[†] FAO's institution codes are available from the European Information Platform for Crop Genetic Resources at http://www.cgiar.org/ecpgr/platform

Table 2. Completeness of descriptors

	Field	% of accessions with data
Accession details	ECP number	0
	Institute	100
	Accession number	99.3
	Accession status	90.5
	Genus	100
	Species	100
	Subtaxa	0.7
	Country of origin	87.2
Donation details	Donor's code	32.4
	Donor's number	9.5
	Donation year	35.8
Collection details	Collection number	16.7
	Collector's code	10.7
	Collection date (day, month, year)	47.6 - 50.0 - 50.0
	Geographical subregion	41.7
	Administrative region	1.2
	Collection site	50.0
	Latitude (deg, min, sec, suffix)	4.8, 4.8, 2.4, 4.8
	Longitude (deg, min, sec, suffix)	4.8, 4.8, 2.4, 4.8
	Altitude	25.0
	Aspect	9.5
	Slope	0
	Regional relief	0
	General habit	13.1
	Grassland management	11.9
	Collection comment	16.7
Breeder's details	Breeder's code	31.2
	Cultivar name	100
	Pedigree	20.8
	Breeder's comment	6.2
Seed availability		37.8
Update year		100

The European Central *Lathyrus* spp. Database

Manager: Daniel Combes
IBEAS, University of Pau, **France**

URL: http://www.univ-pau.fr

As mentioned in the last joint ECP/GR workshop in Budapest, the *Lathyrus* database in Pau contains about 4000 accessions. It includes four wild or semi-wild perennial species – *L. heterophyllus, L. latifolius, L. sylvestris* and *L. tuberosus* – and two annual species – *L. sativus* (grass pea), which is cultivated, and *L. cicera*, which is assumed to be one of the wild ancestors of *L. sativus*.

The database was established in 1985 after a meeting on *Lathyrus* held in Pau. It is updated regularly (every year approximately). Countries of origin of the accessions are mostly European, but include North Africa, Middle East, Ethiopia and India. About 40 countries are represented.

Descriptors are the passport descriptors indicated by IPGRI. They have been modified as suggested in Budapest to provide information on genus (in Pau, until then, it did not seem useful, as only *Lathyrus* is concerned) and on species (until then we did not mention it, as the database is subdivided species by species). But as the objective is now a multicrop passport database, we completely agreed with this modification.

The database has been recently enriched with data on Spanish accessions, kindly provided by Dr Isaura Martin (Madrid) after the Budapest meeting. The sofwares used in Pau are both FoxPro and Access. The database is freely available upon request, on floppy disk or paper.

It is also freely accessible through Internet, on the Web site of the University of Pau (see above) pointing on 'Recherche' then on 'Biologie'. It is not yet really user-friendly, but in a few weeks it will be set under Oracle and so this drawback should be abolished. It is also accessible through Dirk Enneking's CLIMA site (Australia) with whom we are cooperating.

One important point has not really been dealt with: looking for duplicates. In fact, as we are mostly working with wild species, real duplicates should be rare. A few populations from the Pau region (Pyrénées mountains) have been collected more than once (mostly twice) in different years. But, as they are natural cross-pollinated populations, the different samples are almost certainly genetically different, especially since population sizes are generally big (100 or more) and we have generally not paid attention to which individuals have been sampled. So the fact that different accessions have the same descriptors data does not mean that they are real duplicates and we may have difficulties in asserting it.

The European Central Perennial *Medicago* Database

Manager: Vincent Gensollen
GEVES La Valette, Montpellier, **France**

A catalogue was published in 1995 by France, with the support of ECP/GR. It contains about 2900 accessions from 13 countries. At present, the data file is being transformed into a database with a normal structure.

This database will also include accessions from other species of fodder crops from the French national collection. This work is done with the support of the French Ministry of Agriculture. The software used is Access.

The database will allow better searching for duplicated accessions. The owner of the accessions can then be contacted to decide whether it is necessary to withdraw certain accessions.

Regarding the completeness of descriptors, institutes which collaborate for the perennial *Medicago* database could send us any available information. If possible, this should be done in accordance with the mechanism for updating the European central forages databases.

The European *Poa* Database[14]

Manager: Evelin Willner
IPK-Genebank, Aussenstelle Malchow, Malchow/Poel, **Germany**

URL: http://www.dainet.de/genres/eccdb/poa/poa.htm

In the European Catalogue of *Poa*, 12 institutes from nine countries with a total of 2636 accessions are listed (Table 1), as a result of the recent updating of the European *Poa* Database. Letters requesting *Poa* passport data were sent to 26 institutions in 19 countries holding relevant germplasm.

Until 1995, the European *Poa* database was maintained by Dr L. Seidewitz at BGRC Braunschweig. In connection with his retirement, and according to a decision of the ECP/GR Forages Working Group in 1995, the responsibility for maintaining and updating the *Poa* database was transferred to the Genebank for Oil and Forage Crops in Malchow/Poel, which is part of IPK's genebank. Dr Seidewitz sent a copy of the database and some updates which he had received but not yet incorporated, to Malchow in 1995. The former *Poa* Database arrived in a text format, where fields were delimited by '$'.

Data from institutions which had sent updates later were excluded from the 1995 database. The remaining data (belonging to institutions from which no updates were received) were retained and transformed into the new structure.

Other data received from contributing institutions (updates and/or new contributors) arrived in different formats, mainly .dbf (dBase or FoxPro), .xls (Excel) or ASCII files of various structures. They were transformed into a unique format, which was developed based on earlier recommendations of the ECP/GR Forages Working Group (Guide to ECP/GR Forages Databases; 1991) and the IPGRI Multicrop Passport Descriptors (Draft of January 1997). The actual descriptors included in the new *Poa* database were chosen according to the descriptors present in the data files of contributors. Some of the original fields were put together into one resulting field, for example, different fields describing different aspects of the habitat of the collecting site. Information which could not easily be assigned to any field from the proposed structure was put into a 'Remarks' field.

No attempt was made to standardize names of institutions which appear mainly in the fields 'Donor', 'Breeding Institute' or 'Collecting Institute'. The variety of formats and the level of detail of this kind of information in the original data files was so big that it seemed impossible to standardize such acronyms in the time available. A new version of the FAO list of institute acronyms (author: J. Serwinski) was not yet available. In addition, often the information about such institutions is incomplete (e.g. only the name of a person, or the town, without further details), and such incomplete data cannot be linked to any existing list of addresses. Often even the institute providing such data will not be able to give more complete information.

Neither was it possible to standardize the scientific names. Only the spelling of scientific names was standardized, and authors were added in cases where the same name appeared with and without author in the database. In cases where the name appeared only without author, no attempt was made to identify the author. This could be done later. The accessions included in the database belong to 27 different species, the most frequent being *Poa pratensis* with 2376 accessions, followed by *P. bulbosa* (68) and *P. nemoralis* (35).

[14] Report by H. Knüpffer (IPK-Genebank, Gatersleben), S. Harrer (ZADI/IGR, Bonn), and E. Willner.

Table 1. Overview of the European *Poa* Database (H. Knüpffer and E. Willner)

Country	Institute acronym	ECP/GR Database Numbers, range	Data received (formats, structures, etc.) Remarks	Number of accessions 1995	1997
BEL	CLOGRVP	1-29	29 records from the 1995 *Poa* DB (no update received)	29	29
CHE	RAC	95-154	60 recs. received via E-mail	17	60
CZE	ZUBRI	2173-2391	219 recs. received in 1995; update received very recently, not yet included in the database	97	219
DEU	BGRC	2392-2526	135 recs. received end of 1996	115	135
	GAT	2094-2137	44 recs.	42	44
DEU	IPKM	1607-2093	487 recs.	–	487
GBR	RBGK	2138-2172	103 recs. received as Excel file	–	103
GBR	IGER	2527-2629	35 recs. received as text file	19	35
HUN	RCA	30-81	52 recs. from the 1995 *Poa* DB (no update received)	52	52
POL	IHAR	155-1606	1452 recs. received in 1995 (no recent update)	792	1452
ROM	SUCEAVA	2630-2636	7 recs. received as printout	–	7
TUR	ARARI	82-94	13 recs. received as printout	7	13
Total				**1170**	**2636**

Table 2. Number of accessions per species

Poa species	No. of accessions	*Poa* species	No. of accessions
alpina L.	9	*fibrifera*	1
altaica Trin.	1	*iberica*	1
ampla Merr.	2	*lanuginosa*	1
angustifolia L.	9	*ligularis*	6
annua L.	4	*nemoralis* L.	35
arctica R. Br.	1	*palustris* L.	22
asperiflora	1	*pamirica*	1
badensis Haenke	3	*pannonica*	1
binata Nees.	6	*pratensis* L.	2376
bulbosa L.	68	*remota* Forselles	5
caesia Smith	2	*Poa* sp.	26
caespitosa Spreng.	2	*subcaerulea*	1
chaixii Vill.	6	*supina* Schrad.	1
compressa L.	22	*trivialis* L.	23

Table 3. *Poa* Database: overview of accessions by status of sample (H. Knüpffer and E. Willner)

Genebank	Advanced cultivars, bree-der's lines (5, 4)	Primitive cultivars, landraces (3)	Semi-natural (ecotypes) or wild material (1, 2)	Unknown, other (empty, 6, 7)
BELCLOGRVP	2	27		
CHERAC				60
CZEZUBRI	155		61	3
DEUBGRC	59	1	11	64
DEUGAT	8			36
DEUIPKM	220		9	258
GBRIGER	57	1	33	12
GBRRBGK				35
HUNRCA			30	22
POLIHAR	61	1297	94	
ROMSUCEAVA				7
TURARARI			7	6
Total	562	1326	245	503
Total for all accessions: 2636				

Ten species are represented by only one accession each. Twenty-six accessions that came without a species designation are designed as '*Poa* sp.' For an overview of the species and their frequencies in the database, see Table 2.

The accessions in the database are reported to originate from 42 different countries. More than 50% of the accessions (1409 accessions) originate from Poland, followed by 210 from former GDR, 115 from the Netherlands and 104 from Germany. Eleven countries are represented by one accession each. Only 172 accessions came without information about country of origin.

Table 3 gives a survey about the status of the samples (according to FAO/IPGRI Multicrop Passport Descriptors).

The 'Guide' of 1991 distinguishes three parts in forage crop databases: (1) Advanced cultivars and breeders' lines, (2) Primitive cultivars and landraces, and (3) Semi-natural (ecotypes) or wild material. The numbers given in Table 3 are the descriptor numbers according to the 'Guide'. The descriptors for these parts of the databases are mainly overlapping. Therefore, it was decided to compile only one single *Poa* database, from which the sub-databases can be created if necessary. Since not all contributors provided information about the status of samples, there would have been a certain part of the database which could not be classified in any of these three parts.

A first investigation of the compiled database shows that there are 658 named accessions with a total of 400 different accession names (if upper and lower case letters considered identical). Table 4 shows the most frequent accession names (four or more accessions). It can be seen that the most frequent 'duplicates' are not real accession names, such as '*P. pratensis*' and 'Dikorastuschaja' which means 'wild growing' in Russian. A total of 274 named accessions seem to be 'unique' accessions (without matching accessions by accession name). A draft printout of all accessions with accession names was circulated during the Working Group meeting.

The database is available as a computer printout or as .dbf files on diskettes. In a few weeks (by end of March 1997), the database will be accessible on the Internet. This will be done in cooperation between IPK (Gatersleben and Malchow) and ZADI/IGR, Bonn.[15]

The authors of the database are highly interested in receiving *Poa* data from other institutions who could, for different reasons, not yet send their updates in time. Data should be sent to E. Willner or H. Knüpffer by Email or on diskettes, preferably in the form of .dbf (dBase or FoxPro) or .xls (Excel) files. ASCII files are also welcome. We do not have (yet) the possibility to import databases created in the format of Microsoft Access.

Information about available evaluation data is also welcome.

Table 4. Most frequent accession names in the *Poa* database

Accession name	No. of accessions
P. pratensis L.	45
Dikorastuschaja	12
Skrzeszowicka	9
Primo	6
Merion	5
Roznovska	5
Alicja	4
Baron	4
Barzan	4
Bristol	4
Campus	4
Cello	4
Fylking	4
Golf	4
Kimono	4
Monopoly	4
Mosa	4

[15] The database is now available on-line at http://www.dainet.de/genres/eccdb/poa/poa.htm

The European *Bromus*, *Trifolium pratense* and other perennial forages databases

Manager: Lajos Horváth
Institute for Agrobotany, Tápiószele, **Hungary**

The Institute for Agrobotany (RCA) has reported about the current status of three databases. According to the decision of the fifth meeting of the Working Group, the *Trifolium pratense* database was transferred from Switzerland to the RCA, after it had been updated by the Swiss coordinator in 1995. The database contains the passport data of 1901 accessions belonging to 19 collaborating institutes. The duplicates within this database are marked with the same ECP number.

The European *Bromus* Database has been updated during this period, and its structure is also renewed. The new database contains the passport data of 583 *Bromus* accessions, but duplicates are not included in it.

The fifth meeting also decided on the establishment of the Other Perennial Forage Legumes Database, which would compile the passport data of the European *Anthyllis, Onobrychis, Lotus* and *Melilotus* collections. IPGRI supplied the addresses of 45 possible collaborators. Up to the reporting time 10 institutions had answered the RCA call letter, and the new database contains 88 *Anthyllis*, 323 *Melilotus*, 677 *Lotus* and 348 *Onobrychis* accessions. Their total number is 1316.

The three databases are available in dBaseIV format.

The European Bromus *Database*

URL http://www.ngb.se/Databases/ECP/Bromus

Last updating: 1996-97

Twelve requesting letters were sent to the possible partners in August 1996 and we had received five responses by February 1997.

When	From where	Form
16 Sept 1996	Institute of Crop Science, Federal Research Centre for Agriculture,.Braunschweig, Germany	Email (DBF)
5 Sept 1996	Polish Gene Bank, Poland	Email (DBF)
4 Oct 1996	Aegean Research Institute, Menemen, Turkey	Letter
Nov 1996	Royal Botanic Garden, Kew	Diskette
4 Feb 1997	IPK, Gatersleben, Germany	Diskette

Acronyms of the 10 participating institutes in the *Bromus* database:

DEUBGRC	DEUGAT
FRAINRAMAG	FRAINRALUS
GBRRBG	GRCFCPI
HUNRCA	ITAIDG
POLBYDG	TURARARI

Table 1. The completeness of the European *Bromus* Database

Field name	Number of records	% complete
ECP_NUMBER	583	100.00
COORD_GBAN	583	100.00
SPECIES	583	100.00
GB_DESIGN	583	100.00
ACC_NUMBER	565	96.91
ASSOC_NUMB	228	39.11
DONOR_INST	393	67.41
COLLECTOR	183	31.39
DONOR_NUMB	82	14.07
ACC_NAME	52	8.92
AVAILABIL	253	43.40
DON_COUNTR	249	42.71
ORIG_COUNT	291	49.91
ACQUI_YEAR	354	60.72
GEO_SITUAT	74	12.69
LOCALITY	125	21.44
NAT_HABITA	235	40.31
COLL_SITE	122	20.93
LATITUDE	176	30.19
LONGITUDE	171	29.33

The European Trifolium pratense *Database*

Last updating: 1995

Acronyms of the 19 participating institutes:

BELCLOGRVP	BGRIIRG	BGRIIPR
CHEFAP	CHERAC	CSKPIEST
CSKTROUBSK	DDRGAT	DEUBGRC
FRAINRAGEVES	GBRRBG	GRCFCPI
HUNRCA	ITAIDG	ITAIMGV
NGB	NLDCGN	POLIHAR
TURARARI		

Table 2. Completeness of the European *Trifolium pratense* Database

Field name	Number of records	% complete
ECP_NUMBER	1901	100.00
ACCESSION	1895	99.68
NAME_OF_AC	1347	70.86
ORIGIN_COU	1784	93.85
DONOR_COUN	1397	73.49
GENEBANK_D	1901	100.00
DONOR_NUMB	169	8.89
DONOR_INST	707	37.19
ACCESSION_	1901	100.00
BREEDING_M	237	12.47
COLLECTING	520	27.35
COLLECTING	576	30.30
BREEDER_MA	370	19.46
PLOIDY_LEV	637	33.51
SEED_AVAIL	1222	64.28
SUBTAXA	89	4.68
PROVINCE_S	463	24.36
LOCATION	629	33.09
LONGI_TUDE	694	36.51
LATI_TUDE	694	36.51
ALTI_TUDE	400	21.04
COLLECT-_T	669	35.19

Compiling of the Other Perennial Forages Legumes Database

We sent 45 requesting letters to the probable collaborators in May 1996. The responses received are listed below:

When	From where	Form	*Athyllis*	*Melilotus*	*Lotus*	*Onobrychis*	Total
1996							
13 June	Braunschweig, Germany	diskettes, (DBF)	0	1	1	19	**21**
3 July	Royal Botanic Garden Kew, West Sussex, UK	diskettes, (ASCII)	40	29	88	26	**183**
4 July	RICP, Praha, Czech Republic	diskettes (DBF)	4	46	34	4	**88**
11 July	SAVE (Safeguard for Agricultural Varieties in Europe)	letter, 2 new addresses	0	0	0	0	**0**
15 July	Centro de Recursos Fitogenéticos, Madrid, Spain	diskettes (DBF), 1 new address	0	0	12	4	**16**
17 July	The Hebrew University of Jerusalem, Israel	letter	0	0	0	0	**0**
9 Aug	Pro Specie Rara, St. Gallen, Switzerland	letter, 4 new addresses	0	0	0	0	**0**
12 Aug	Agricultural Research Organization, Bet Dagan, Israel	diskettes, (TXT)	0	208	75	26	**309**
1 Oct	Istituto di Miglioramento Genetico Vegetale, Perugia, Italy	letter	27	0	201	120	**348**
17 Dec	IPK-Gatersleben, Germany	diskettes, (DBF)	13	33	55	54	**155**
1997							
3 March	RCA, Hungary		4	6	346	148	**504**
3 March	**Total**		**88**	**323**	**677**	**348**	**1316**

The European *Trifolium alexandrinum* and *T. resupinatum* databases

Manager: Noa Diwan
The Israeli Gene Bank for Agricultural Crops, Volcani Center
50250 Bet Dagan
Israel
Tel: (972-3)9683490
Fax: (972-3)9669642
Email: diwan@netvision.net.il

Table 1. List of descriptors used and % of accessions documented for *Vicia* spp. (*V. faba* not included)

Descriptors List Part I			Descriptors List Part II					
		%			%			%
Genus	Genus	100	Genus	Genus		Genus	Genus	
Species	Species	85	Accnum	Accession number		Accnum	Accession Number	
Accnum	Accession Number	100	Othnum	Other numbers	13	Designat	Designation	2
Subspe	Subspecies	10	Collnum	Collection number	12	Othdesig	Other Designation	1.8
Cultivar	Cultivar	22	Georeg	Geographic Region	18	Seqgb	Seqgb	3.5
Convar	Convarietas	4	Locsit	Local Situation	16	Cridref	Cridref	1.4
Varietas	Varietas	7	Prov	Province	18	Farmname	Farmer's name	1.4
Locname	Local name	9	Ordistr	Origin District	17	Brdcomp	Breeding company	1.3
Selev	Selection level	3	Orlocal	Origin Locality	10	Brdmeth	Breeding method	1.1
Seedav	Seed Available	4	Countcoll	Country Collected	3	Pedigree	Pedigree	5.0
Genebank	Genebank	100	Collexp	Collector Expedition	2	Growhab	Grow habitat	1.1
Sigla	Sigla	100	Collinst	Collecting Institute	18	Nathab	Nature of habitat	1.4
Orcount	Country of Origin	54	Datacoll	Data Collected	2	Status	Status of sample	14
Donor	Donor	86	Othobs	Other Observation	6	Enduranc	Endurance	5
Sigdon	Sigla Donor	86	Genebank	Genebank		Locmod	Local modern	13
Doid	Donor Identification	47	Sigla	Sigla		Origin	Origin	34
Doco	Donor Country	78				Genebank	Genebank	
Breinst	Breeding Institute	6				Sigla	Sigla	

Table 2. Contents of the *Vicia* Database (excluding *V. faba*)

			Contents (%)				
Country	**Institution**	**Total no of accessions**	**Wild species**	**Landraces/ local varieties**	**Breeding/ inbred lines**	**Unknown**	**Accessions of local origin**
Italy	ITAIDG	2643	54.0	48.5	0	51.5	36.1
Israel	ISRIGB	123	23.6	4.6	0	95.4	0
Poland	POLIHAR	66	0	3.9	0	96.1	0
Turkey	TURARARI	739	48.3	0	0	0	0
Great Britain	GBRRBG	79	60.8	0	0	0	2.6
Cyprus	CYPARI	81	18.5	100.0	0	0	0
Germany	DEUBGRC	170	40.6	7.2	0	92.8	14.8
Czechoslovakia	CSKRUZYNE	277	24.9	89.9	0	10.1	18.1
Greece	GRCFCPI	629	100.0	17.9	0	82.1	0
Bulgaria	BGRIIPR	713	48.2	27.6	0	72.4	52.9
Total		5520					

The European *Vicia* database[16]

Manager: Pietro Perrino
Istituto del Germoplasma (IDG)
Consiglio Nazionale delle Ricerche
Via G. Amendola 165/A
70126 Bari
Italy
Tel: +39-80 558 36 08
Fax: +39-80 558 75 66
Email: germpp04@area.ba.cnr.it

General information

Date of establishment of the database: 1992
Last update: 1994
Frequency of updating: annual
Software: SAS
Number of participating countries: 10
Number of participating institutions: 10
Total number of accessions recorded: 5520

List of descriptors used and completeness of data (Table 1)

The total number of descriptors is 44. Because of the heterogeneity of the documentation provided from the different genebanks, in previous meetings it was suggested and agreed to divide descriptors in three Parts. In Part I it was decided to group descriptors of the passport data, those for which the percentage of accessions documented was relatively high and some of those for which it was thought that there would not have been lack of information. In Part II and Part III, besides some descriptors, like genus, accession number, genebank, etc., which had to be reconfirmed for identification needs, it was decided to list the rest of the descriptors which were documented with less and less frequency.

All accessions have genus, accession number and name of institution (genebank). The descriptors species and donor are documented only for 85 and 86% of the accessions, respectively. About 78, 54 and 47% of the accessions are documented respectively for the following descriptors: donor country, country of origin and donor identification. For most of the other important descriptors (19) the percentage of documented accessions is very low: from nearly 1 to 22%. The origin (site of collecting) is known only for 34% of the accessions.

Contents of the database (Table 2)

A little more than 40% of the accessions are stored in the Bari genebank. The other 60% is stored in the other nine genebanks. It was not possible to provide information about the number of inbred lines and about the number of accessions mantained in other collections. In the first case it may be because there are no inbred lines or alternatively the Manager has no information and this may explain why the percentage of accessions about which there is no information (unknown) is high. In the second case lack of information is clearly due to the fact that corresponding numbers of the same accessions were never provided to the central database. The percentage of landraces/local varieties includes also local names, cultivars, etc. Since in some countries even wild species have a local name,

[16] Compiled from information received at the Joint EGDS-ECP/GR Workshop on Central Crop Databases, Budapest, Hungary, 13-19 October 1996.

the sum of the percentages of wild species and that of the next column (% landraces/local varieties) is not 100%. In compiling the table for percentage of unknown accessions, the percentage of accessions without any name or indication about landrace, local variety, local name, etc. must be understood. In fact the sum of the percentages refering to landraces, etc. and that of unkown is equal to 100%. It is surprising to note that in the collections of Israel, Poland, Turkey, Cyprus and Greece there are no local accessions. About this information one can make two hypotheses. The first and the most probable is that the information (descriptor) was not provided and the second, but unlikely, is that there are no accessions of local origin. This second hypothesis may be accepted for some countries, but not at all for Israel, Turkey, etc.

Other relevant information

The database has been created using the SAS system (Statistical Analysis System) and is stored at the Main Frame c/o High Studies and Advanced Technology (CSATA-TECHNOPOLIS) of Valenzano, Bari, Italy.

At the moment access to the database is possible only by mail and Email requests. Information may be provided by normal mail, Email, on hard copy and floppy disk. There is not yet computerized registration of users of the database. The most frequent users of the database are research centres and seed companies. The most frequent questions asked by the users concern yield, resistance to certain diseases and adaptability to certain environments.

***List of species and/or subspecies of* Vicia**

The number of known species in the database is nearly 80. Since it seems that 15% of the accessions of the database lack this descriptor and since it is probable that the missing information may be related to the difficulty of classification and/or identification of some species, one may argue that the number of species present in the genebanks and hence in the database may be higher than 80.

Going through the list of species (Table 3) of *Vicia* present in the database and comparing it with that of the European flora one can note that there are several species not represented in the database and therefore not collected and stored in the listed genebanks.

Acronyms used:

ITAIDG	Germplasm Institute, Via G. Amendola 165/A, 70126 Bari, Italy
ISRIGB	Israel Gene Bank for Agricultural Crops, Volcani Center, PO Box 6, 50-250 Bet Dagan, Israel
POLIHAR	Plant Breeding and Acclimatization Institute, Radzików, 05 870 Blonie, Poland
TURARARI	Aegean Regional Agricultural Research Institute, PO Box 9, Menemen Izmir, Turkey
GBRRBG	Royal Botanic Garden Kew, Wakehurst Place, Ardingly, Haywards Heath West Sussex RH17 6TN, United Kingdom
CYPARI	Agricultural Research Institute, PO Box 2016, Nicosia, Cyprus
DEUBGRC	Institute für Pflanzenbau und Pflanzenzuchtung (FAL), Bundesallee 50, 3000 Braunschweig, Germany
CSKRUZYNE	Research Institute of Plant Production, 161 06, Prague 6-Ruzyn, Czechoslovakia
GRCFCPI	Fodder Crops and Pastures Institute, Larissa, Greece
BGRIIPR	Institute for Plant Genetic Resources, 4122 Sadovo, Plovdiv district, Bulgaria

Table 3. *Vicia* species and number of accessions

Species	No. of access.	Species	No. of access.
amoena	2	*michauxii* Sprengel	2
amorensis	1	*microphylla* d'Urv.	1
amphicarpa Dorthes	4	*monantha* Retz	8
anatolica Turril	1	*narbonensis* L.	94
angustifolia L.	27	*neglecta*	2
articulata Hornem.	12	*noeana* Reuter ex. Boiss.	3
atropurpurea Desf.	42	*obovata*	1
benghalensis L.	16	*ochroleuca* Teu.	1
biennis L.	3	*onobrychioides* L.	2
bithynica (L.) L.	32	*orobus* DC.	2
caesarea	3	*pannonica* Crautz	89
calcarata Desf.	8	*pannonica C*ran.	16
cassubica L.	3	*peregrina* L.	59
cordata Wulfen ex Hoppe	64	*pilosa*	1
cracca L.	41	*pisiformis* L.	3
cretica Boiss. & Heldr.	3	*platisperma*	1
dalmatica A. Kerner	3	*pseudorobus*	2
dasycarpa Ten.	82	*pubescens* (DC.) Link	2
disperma DC.	6	*pyrenaica*	1
dumetorum L.	2	*sativa* L.	2626
eriocarpa Hausskn.	4	*sativa + benghalensis*	1
ervilia (L.) Willd.	249	*sativa + cordata*	5
gigantea	1	*sativa + grandiflora*	1
grandiflora Scop.	10	*sativa + macrocarpa*	1
hayastana	68	*sativa + nigra*	6
hirsuta (L.) S.F. Gray	6	*semiglabra*	2
hyaeniscyamus Mout.	1	*sepium* L.	22
hybrida L.	46	*sicula* (Rafin.)Guss.	3
hirsuta (L.) Gray	18	spp.	15
incana Gouan	3	*sylvatica* L.	3
incisa M. Bieb.	2	*tenuifolia* Roth.	6
incisaeformis	3	*tenuissima* (Bieb.) Schinz & Thell.	7
johannis (Popov) H. Schäfer	12	*tetrasperma* (L.) Schreb.	9
lathyroides L.	6	*unijuga*	2
lutea L.	74	*vicioides*	1
macrocarpa (Moris) Arcangeli	6	*villosa*	128
megalotropis	1	*villosa* Roth.	53
melanops Sibth. & Smith	10	*villosa + eriocarpa*	1
meyeri	1	*villosa + microphylla*	1

The European *Dactylis* and *Festuca* databases

Manager: Grzegorz Žurek
Botanical Garden, Plant Breeding and Acclimatization Institute (IHAR)
Bydgoszcz, **Poland**

URL: http://www.ngb.se/Databases/ECP/Dactylis
URL: http://www.ngb.se/Databases/ECP/Festuca

Introduction

Central Crop Databases combine the data available for one crop from local documentation systems into one central database and make the combined data sets available to the contributors and to others (van Hintum 1994). Central Databases are the key tool for the management of collections by the crop-specific working groups as well as for individual curators (Lipman *et al.* 1996). They are also helpful in promoting the utilization of genetic resources and the regional coordination of conservation activities (IPGRI 1995).

The databases of the forage grasses *Dactylis* spp. and *Festuca* spp. were updated for the last time in 1987. Since then no further work has been done on the databases. During the fifth meeting of the Working Group on Forages (Hissar, Bulgaria, 1995) it was decided that a new update of these databases would be prepared by the staff of the Botanical Garden of the Plant Breeding and Acclimatization Institute in Bydgoszcz, Poland (Gass *et al.* 1995). According to an agreement between IPGRI and the Botanical Garden of IHAR, US$3790 were assigned for hardware improvement in the Botanical Garden.

Materials and methods

The structure of the database was prepared according to recommendations of IBPGR (Tyler *et al.* 1985) and is similar to the structures of the European Catalogue of *Phleum* sp. and the European Catalogue of *Medicago* perennial species (INRA/GEVES 1995). See formats used in Annex 1.

From the 'Directory of Institutions Holding Crop Genetic Resources Collections' (Frison and Serwiński 1995) 48 foreign institutions were recognized as potential owners of data on *Dactylis* and *Festuca* collections (Table 1). The proposed structure of the database was then distributed to all institutions mentioned in Table 1.

Database management softwares used were dBaseIII, FoxPro and Excel. Accepted sources for taxonomic descriptions were 'Flora Europaea' vol. 5 (Tutin *et al.* 1980) for European species and 'Poaceae URSS' (Tzvelev 1976) for non-European species.

Results

A total of 23 positive responses was received (including Polish institutions). Five were unable to transfer their data and 22 did not respond. Data were prepared both on disks in the proposed structure, and on hard copies. After compilation of the databases for both genera a total of 16 066 accessions was identified (7366 for *Festuca* and 8700 for *Dactylis*).

Table 1. European institutions holding collections of *Dactylis* and *Festuca* and their replies

No.	Inst. code	Acronym	ECPAcronym	Person and Institution	Resp.[†]
1	BEL087			Dr L.A. Dutilleux Conservatoire Botanique de Ressources Genetiques de Wallonie 1 rue Fievez B-1470, Genappe Tel: (32-2)6332025	Yes
2	BGR001	IPGR	BGRIIPR	Dr Ivan Lozanov Institute of Plant Introduction and Genetic Resources 'K. Malkov' 4122, Sadovo, District Plovdiv Tel: (359-32)393118/2221 Telex: 44444 IPGR BG Fax: (359-32)270270(post)	Yes
3	CHE001	RAC	CHERAC	Station Federale de Recherches Agronomiques de Changins Route de Duillier - BP 254 CH-1260, Nyon Tel: (41-22)3634722 Telex: 419975 Fax: (41-22)3621325	Yes
4	CZE079	PRUHON	CSKPRUHON	Ing. J. Dostal Research Institute of Ornamental Gardening Pruhonice 252 43, Pruhonice Tel: (42-2)67750027 Telex: 123 320 VUOZ C Fax: (42-2)67750023 Email: adm@vuoz.cz	Yes
5	CZE082	ZUBRI	CSKZUBRI	OSEVA PRO Ltd. Grassland Research Station 756 54 Zubri Tel: (42-651)583195/6 Telex: 529 32 TRAVA C Fax: (42-651)583197	Yes
6	DEU001	BGRC	DEUBGRC	Institute of Crop Science, Federal Research Center for Agricult.(FAL) Bundesallee 50 38116, Braunschweig Tel: (49-531)596307/5961 Fax: (49-531)596365	Yes
7	ESP009	CSICMBG	ESPCSICMBG	Biological Mission of Galicia Apartado de Correos, 28 36080, Pontevedra Tel: (34-86)854800 Fax: (34-86)841362	Yes
8	ESP119	CIAMLCO		Centro de Investigaciones Agrarias de Mabegondo Apartado 10 15080, La Coruna Tel: (34-81)673000 Telex: 86021 INIA E Fax: (34-81)673656 Email: valenzu@siagal.inia.es	Yes
9	FRA051	GEVES	FRAINRAMAG	Annick Le Blanck Unite experimentale du Magneraud GEVES Saint Pierre-d'Amilly - BP 52 F-17700, Surgeres Tel: (33)46683000 Telex: 790737 F Fax: (33)46683087	Yes

No.	Inst. code	Acronym	ECPAcronym	Person and Institution	Resp.†
10	GBR004	RBG	GBRRBG	Seed Bank, Seed Conservation Sect., Royal Botanic Gardens, Kew Wakehurst Place, Ardingly Haywards Heath, W.Sussex RH17 6TN Tel: (44-181)3325000 Telex: 296694 KEWGAR G Fax: (44-181)3325069 Email: CGI702	Yes
11	ITA015	PERUG	ITAPERUG	Dr M. Falcinelli Istituto di Miglioramento Genetico Vegetale, Universita di Perugia Borgo XX Giugno 74 I-06122, Perugia Tel: (39-75)5856206 Fax: (39-75)5856224 Email: imgvsas@ipguniv.unipg.it	Yes
12	ITA034		ITALONIGO	Dr F. Bozzo Inst. of Plant Breeding and Agric. Research "Nazareno Strampelli" Via Marconi 1 I-36045, Lonigo (VI) Tel: (39-444)830088 Fax: (39-444)835540	Yes
13	NLD037	CGN/CPRO-DLO	NLDCGN	Centre for Genetic Resources, the Netherlands (CGN) Droevendaalsesteeg 1 - PO Box 16 6700 AA, Wageningen Tel: (31-8370)77045/77001 Fax: (31-8370)18094 Email: CGN@CPRO.AGRO.NL	Yes
14	NOR019	VOLBU		State Agricultural Experimental Station Loken N-2940, Heggenes Tel: (47)61340205 Fax: (47)61340665	Yes
15	POL003	IHAR	POLIHAR	Plant Breeding and Acclimatization Institute 05-870 Blonie, Radzikow near Warsaw Tel: (48-2)7252611 Telex: 812914 IHAR PL Fax: (48-2)7254714	Yes
16	POL022	BYDG	POLBYDG	Botanical Garden of Plant Breeding and Acclimatization Institute Jezdziecka 5 85-687, Bydgoszcz Tel: (48-52)721407 Fax: (48-52)224454	Yes
17	PRT084	ENMP		Ing. J.P.Goncalves Carneiro Sector de Pastagens e Forragens Dept Past., Forrag., Proteaginosas Apartado 6 7351, Elvas Codex Tel: (351-68)622844 Telex: 40189 ENMP P Fax: (351-68)629295	Yes
18	ROM003	ICPCP	ROMBRASOV	Grassland Research Institute Str. Cucului, 5 2200, Brasov Tel: (40-92)142232 Fax: (40-68)142119	Yes
19	ROM007			A. Raibuh Genebank of Suceava Bulevardul 1 Decembrie 1918 nr.17 5800, Suceava, Judetul Suceava Tel: (40-30)227087 Telex: (987)23296 Fax: (40-30)227087	Yes

No.	Inst. code	Acronym	ECPAcronym	Person and Institution	Resp.†
20	SVK012	SLOVOSIVO		Plant Breeding Station Levocske Luky 054 01, Levoca Tel: (42-965)27771	Yes
21	SVN019	AISLJ	YUGAISLJ	Dept. of Field Crops & Seed Prod., Agricultural Institute of Slovenia Hacquetova 2, PO Box 53 61109, Ljubljana Tel: (386-61)1375375 Fax: (386-61)1375413	Yes
22	SWE002	NGB	SWENGB	Mr Morten Hulden Nordic Gene Bank PO Box 41 S-230 53, Alnarp Tel: (46-40)461790 Telex: 32717 NGB S Fax: (46-40)462188 Email: nordgen@ngb.se	Yes
23	TUR001	AARI	TURARARI	Dr Ayfer Tan Plant Genetic Resources Dept., Aegean Agricultural Research Inst. PO Box 9, Menemen 35661, Izmir Tel: (90-232)8461009 Telex: 51293 AARI Tr Fax: (90-232)8461107	Yes
24	BEL004	RVP	BELCLOGRVP	D. Reheul Government Plant Breeding Station Burg. Van Gansberghelaan 109 B-9820, Merelbeke (Lemberge) Tel: (32-9)2521981 Fax: (32-9)2521150	No
25	DEU007	STEIN	DEUSTEIN	Saatzucht Steinach GmbH Wittelsbacher Str. 15 94377, Steinach ueber Straubing Tel: (49-9428)8715 Telex: 65569 Fax: (49-9428)8648	No
26	GRC006	FCPI	GRCFCPI	Constantin Iliadis Fodder Crops and Pastures Institute Theophrastou St.1, PO Box 1262 411 10, Larissa Tel: (30-41)239711 Fax: (30-41)232827	No
27	LTU001	LIA		Lithuanian Institute of Agriculture LT-5051 Dotnuva-Akademija, Kedainiai Dist. Tel: (370-57)37289 Fax: (370-57)56996	No
28	PRT001	BPGV - DRAEDM	PRTNUMI	Ing. Violeta Rolim Nunes Lopes Banco Portugues de Germoplasma Vegetal (BPGV) Quinta dos Peoes - Gualtar 4700, Braga Tel: (351-53)676758 Telex: 33506 NUMI P Fax: (351-53)677328	No
29	ALB011			S. Karadumi Forest and Pasture Research Inst. Tirana	0
30	DEU012	BHERSF	DEUBHERSF	K. Reinhardt Agricultural Research Institute Eichhof 36251, Bad Hersfeld Tel: (49-6621)92280 Fax: (49-6621)51921	0

No.	Inst. code	Acronym	ECPAcronym	Person and Institution	Resp.†
31	DEU146	IPK	DDRGAT	Dr H. Knuepffer Genebank, Inst. for Plant Genetics and Crop Plant Research (IPK) Corrensstrasse 3 06466, Gatersleben Tel: (49-39482)5280 Telex: 351868 ipk d Fax: (49-39482)5155	0
32	DEU189	BORNVEG	DDRBORNVEG	N. Kronseder Saatzucht Steinach GmbH Station Bornhof Klockower Strasse 11 17219, Bornhof-Bocksee Tel: (49-39921)228/29/31 Fax: (49-39921)234	0
33	DEU358	IPK		Dr P. Hanelt Dept. of Taxonomy, Inst. for Plant Gen. and Crop Plant Research (IPK) Corrensstrasse 3 06466, Gatersleben Tel: (49-39482)5272 Telex: IPK 351868 Fax: (49-39482)280	0
34	DEU366	ILFU		Inst. for Agricultural Research Merseburger Str. 41 06112, Halle/Saale Tel: (49-345)120216 Fax: (49-345)50094-30	0
35	ESP022	INIAFOR	ESPFORMADR	Gregorio Montero Centro de Investigaciones Forestales / INIA Autov. Noroeste, km 7.5, Apdo 8111 28080, Madrid Tel: (34-1)3476854 Fax: (34-1)3572293	0
36	FIN020			Dr Voitto Koskenmaki Boreal Plant Breeding Myllytie 8 FIN-31600, Jokioinen Tel: (358-16)41871 Fax: (358-16)4187715	0
37	FRA001	INRA-POITOU	FRAINRALUS	Claude Mousset Station d'Amelioration des Plantes Fourrageres, INRA F-86600, Lusignan Tel: (33)49556000 Telex: INRALUS 791191 F Fax: (33)49556044	0
38	FRA040	INRA-CLERMON	FRAINRACLF	Dr Francois Balfourier Station d'Amelioration des Plantes, INRA Domaine de Crouelle F-63039, Clermont-Ferrand Cedex Tel: (33)73624000 Telex: 392207 F Fax: (33)73624453	0
39	GBR016	WPBS-IGER	GBRWPBS	Mr Ian D. Thomas Welsh Plant Breeding Station, Inst.of Grassland and Environ. Res Plas Gogerddan Aberystwyth, Dyfed SY23 3EB Tel: (44-1970)828255 Fax: (44-1970)828357 Email: HAMILTONS@AFRC.AC.UK	0

No.	Inst. code	Acronym	ECPAcronym	Person and Institution	Resp.†
40	GRC005	GGB	GRCGGB	A. Zamanis Greek Genebank, Agric. Res. Center of Makedonia and Thraki, NAGREF PO Box 312 570 01, Thermi - Thessaloniki Tel: (30-31)471544/471439 Fax: (30-31)471209	0
41	HUN053	PUAK-IA		Prof. Istvan Ecker Pannon University of Agriculture, Institute of Agronomy Deak F. u. 16 H-8361, Keszthely Tel: (36-82)11140 Telex: 35-242 Fax: (36-82)19105	0
42	IRL001	AFT	IRLAFT	V. Connolly Oak Park Research Centre, Nat. Centre for Arable Crops Res. Teagasc, Carlow Tel: (353-503)70200 Telex: 60610 AFTO EI Fax: (353-503)42423	0
43	ITA004	IDG	ITAIDG	Dr Giulio Scippa Istituto del Germoplasma, Consiglio Nazionale d. Richerche Via G. Amendola 165/A I-70126, Bari Tel: (39-80)5583400/463 Fax: (39-80)5587566 Email: RICERCA@VM.CSATA.IT	0
44	LTU003			Dr G. Almantas Voke Branch of the Lithuanian Institute of Agriculture LT-4002, Traku Voke, Vilnius reg. Tel: (370-2)629775 Fax: (37-2)629775	0
45	NLD015	ZWAANW	NLDZWAANW	G.Y. Berthe Limagrain Genetics B.V. Stationsstraat, 124 - PO Box 2 9679 ZG, Scheemda Tel: (31-5979)1233 Telex: 53146 Fax: (31-5979)3030	0
46	PRT025	UTAD		Prof. H. Guedes-Pinto Dept. de Genetica e Biotecnologia, Univ. Tras-os-Montes e Alto Douro Apartado 202 5001, Vila Real Codex Tel: (351-59)320501 Telex: 24436 Fax: (351-59)74480	0
47	ROM002	ICPCPT	ROMICCPT	Dr Doc. A.V. Vranceanu Genetic Resources Dep. – Research Inst. for Cereals and Ind. Crops R-8264, Fundulea, Judetul Calarasi Tel: (40-1)6150805 Fax: (40-1)3110722	0
48	RUS001	VIR	SUNWIR	Dr S.M. Alexanian N.I. Vavilov Research Institute of Plant Industry Bolshaya Morskaja Street 42-44 190000, St. Petersburg Tel: (7-812)3144848/19901 Telex: 121414 ALEX SU Fax: (7-812)3118762 Email: vir@glas.apc.org	0

No.	Inst. code	Acronym	ECPAcronym	Person and Institution	Resp.†
49	SVK022	SEMEX	SVKPOTVOR	Dr Anna Jakabova Research and Breeding Institute of Ornamental Plants 916 25, Potvorice Tel: (42-834)97131 Fax: (42-834)97260	0
50	SWE013	DFBBAL	SWEDFBBAL	Lars Bjork Dept. Horticultural Plant Breeding, Swedish Univ. of Agric. Sciences Fjalkestadsvagen 123-1 S-291 94, Kristianstad Tel: (46-44)75041/75042 Fax: (46-44)75049 Email: balsgard@hvf.slu.se	0

† Response: YES = data were transferred to Botanical Garden; NO = donor is unable to transfer data; 0 = no response.

Genus *Dactylis*

In total, 10 taxa were identified in this genus (see Table 2). Most accessions belong to the most popular species *Dactylis glomerata* L. (98.8%), and they are wild ecotypes and landraces (88.5%).

Only 81.7% of all accessions are original (i.e. accessions collected and conserved in the same country) (Table 3). Most of them are ecotypes (87.6% of all accessions from Format 3). More than 21% of advanced cultivars and breeders' lines are also original accessions but, on the other hand, 44.9% of them are duplicated in one or more genebanks.

Regarding the storage of original accessions, four groups of genebanks can be distinguished:

- storing only (100%) original accessions – genebanks from Spain, Italy, Slovenia, Sweden and Turkey,
- storing mainly (79-95.7%) original accessions – genebanks from Bulgaria, Germany, Spain, Poland, Portugal and Romania,
- storing both original and foreign accessions (near 50% of original accessions) – genebanks from Switzerland and the Netherlands;
- storing mainly foreign accessions (less than 50% of original) – genebanks from Czech Republic, France, United Kingdom, Poland, Romania and Slovakia.

Genus *Festuca*

In four basic formats 27 taxa were recognized, and in the botanical gardens collections next 42 taxa from the European flora as well as 21 from Asiatic flora were also recognized (Tables 4 and 5). Most of the accessions recorded in the Catalogue were ecotypes and landraces (82.8%) from two species: *Festuca pratensis* (71% of all accessions) and *Festuca arundinacea* (17.9% of all accessions). Other species were *Festuca rubra* s.l. (4.9%), *Festuca rubra* subsp. *rubra* (1.63%), *Festuca nigrescens* [= *F. rubra* subsp. *fallax*] (1.33%) and *Festuca ovina* (0.98%). Only a few accessions per taxon were recorded for other fescue species.

Table 2. List of identified species of the genus *Dactylis* and number of accessions in each format

Species name, authority, comments	FORMAT 1	FORMAT 2	FORMAT 3	FORMAT 4	Total	%
glomerata L.	587	146	7686	175	8594	98.78
glomerata L. subsp. *aschersoniana* (Graebner) Thell. (Syn.= *D. polygama* Horvatovszky)		3			3	0.03
glomerata L. subsp. *glomerata*			63		63	0.72
glomerata L. subsp. *himalayensis* Domin			1		1	0.01
glomerata L. subsp. *hispanica* (Roth) Nyman			17		17	0.20
glomerata L. subsp. *ibizenzis* Stebbins & Zohary			4		4	0.05
glomerata L. subsp. *maritima* [taxon not recognized]			3		3	0.03
glomerata L. subsp. *parthiana* [taxon not recognized]			1		1	0.01
glomerata L. subsp. *phyllose* [taxon not recognized]			1		1	0.01
marina Borill.			13		13	0.15
Total number of accessions	587	149	7789	175	8700	100.00
In formats:	6.7%	1.7%	89.5%	2.0%	100.0%	

Less than 70% are original accessions. Most of the original accessions were recorded in Format 3 (80.5%) and Format 2 (94.9%) (Table 6).

As for *Dactylis*, four groups of genebanks are identified according to the storage of original accessions:

- storing only (100%) original accessions – genebanks from Spain, Italy, Slovenia, Sweden and Turkey;
- storing mainly (85-86%) original accessions – genebanks from Germany, Poland, Romania;
- storing both original and foreign accessions (near 50% of original accessions) – genebank from Poland;
- storing mainly foreign accessions (less than 50% of original) – genebanks from Bulgaria, Czech Republic (2 genebanks), Switzerland, France, United Kingdom, Romania and Slovakia.

The percentage of duplicated accessions of advanced cultivars and breeders' lines exceeds 55%.

Recommendations

1. To improve future action in updating of the European Catalogues of *Dactylis* and *Festuca* it is necessary to update each year or as quickly as data increase.
2. Identification of duplicates should be added to future activities.
3. It is essential to collect information about other European species of the above genus. The genus *Festuca* contains an estimated 450 species (Aiken and Darbyshire 1990). More than 170 species are listed in 'Flora Europea' (Tutin *et al.* 1980). It means that in the above Catalogue only 44.7% of all European species were noted.
4. There is a great need to standardize taxonomy, especially in the genus *Festuca*. For example in the case of *Festuca rubra* one accession could have different taxonomic names and all of them are correct. For example: *Festuca rubra* L. = *Festuca rubra* L. subsp. *fallax* (Thuill.) Hayek = *Festuca rubra* L. var. *commutata* Gaudin. = ***Festuca nigrescens* Lam.** The last name is correct according to 'Flora Europaea'. It should be strongly recommended to use the mentioned source of taxonomic descriptions.

Table 3. Accessions from the genus *Dactylis* by genebank and format

Genebank code	FORMAT 1 No. of access.		FORMAT 2 No. of access.		FORMAT 3 No. of access.		FORMAT 4 No. of access.		Total by gene-banks	Total original accessions	%
	Total	Original	Total	Original	Total	Original	Total	Original			
BGROO1	33	6	119	119	8	7	7		167	132	79.0
CHEOO1					11	6			11	6	54.5
CZEO82	128	19	2						130	19	14.6
DEUOO1	112	9			669	660			781	669	85.7
ESPOO9			4		333	326			337	326	96.7
ESP119	1	1			22	22			23	23	100.0
FRAO51	57				190	68			247	68	27.5
GBROO4					58	12	7		65	12	18.5
ITAO34	1	1							1	1	100.0
NLDO37							28	15	28	15	53.6
POLOO3	28	2			1				29	2	6.9
POLO22	102	47			5827	5148	134	5	6063	5200	85.8
PRTO84	7				136	136	1		144	136	94.4
ROMOO3	32				17	17			49	17	34.7
ROMOO7	3	3	25	23	19	19			47	45	95.7
SVKO12	48	1			111	13			159	14	8.8
SVNO19	1	1			27	27			28	28	100.0
SWEOO2	34	34			177	177			211	211	100.0
TUROO1					180	180			180	180	100.0
Total no. access.	587	124	150	142	7786	6818	177	20	8700	7104	81.7
In formats:		21.1%		94.7%		87.6%		11.3%			

Total number of duplicates = 264 from 587 accessions in Format 1. It is 44,9% of all accessions from above format.

Table 4. List of identified species of the genus *Festuca* and number of accessions in each format

No.	Species name, authority, comments	FORMAT 1	FORMAT 2	FORMAT 3	FORMAT 4	Total	%
1	*alpina* Suter.		17	2		19	0.26
2	*altissima*			1		1	0.01
3	*arundinacea* Schreb.	279		898	139	1316	17.87
4	*cinerea* Vill.	3				3	0.04
5	*drymeja* Mert. & Koch.			1		1	0.01
6	*gigantea* (L.) Vill.		2	8		10	0.14
7	*heterophylla* Lam.	2	1	1	2	6	0.08
8	*indigesta* Boiss.			1		1	0.01
9	*lemanii* Bast. (= *F. longifolia auct.* non. Thuill)	30		2		32	0.43
10	*longifolia* Thuill. (= *F. caesia* Sm.)			1		1	0.01
11	*nigrescens* Lam. (= *F. rubra* L. subsp. *fallax* (Thuill.) Hayek, *F. rubra* L. var. *comutata* Gaudin.)	98				98	1.33
12	*nipicola* [species name not recognized in accessible sources of taxonomic terms]			1		1	0.01
13	*ovina* L.	29		43		72	0.98
14	*paniculata* (L.) Schinz & Thell.			1		1	0.01
15	*petraea* Guthnick et Seub.			1		1	0.01
16	*pratensis* Huds. subsp. *pratensis* (?) (= *F. elatior* L. taxonomic name by data donor)			9		9	0.12
17	*pratensis* Hudson	330	10	4856	35	5231	71.03
18	*pseudovina* Hackel ex. Wiseb	2				2	0.03
19	*rubra* L. (subspecies not specified)	104	9	234	12	359	4.88
20	*rubra* L. subsp. *rubra* (= *F. rubra* subsp. *vulgaris* (Gaudin) Hayek)	105		15		120	1.63
21	*scariosa* (Lag.) Ascherson & Graebner			1		1	0.01
22	*sibirica* Hack. ex Boiss. [species not from European flora]			1		1	0.01
23	*tenuifolia* Sibth. (= *F. capillata* Lam, *F. ovina* L. subsp. *tenuifolia* (Sibth.) Peterm)	2				2	0.03
24	*trachyphylla* (Hackel) Krajina	3		1		4	0.05
25	*trichophylla* (Ducros ex Gaudin) K. Richter (= *F. rubra* L. subsp. *trichophylla* Ducros ex Gaudin)	46		6		52	0.71
26	*vaginata* Waldst. & Kit. ex Willd.				1	1	0.01
27	*valesiaca* Schleicher ex Gaudin	2		2		4	0.05
28	not recognized	1		14		15	0.20
	Total number of accessions in each format:	1036	39	6100	189	7364	100
	Percentage:	14.1	0.5	82.8	2.6	100.0	

Table 5. *Festuca* species in botanical gardens collections

No.	Genus, species, subspecies, authorities
	I. Taxonomy according to 'Flora Europea' Vol. 5
29	*airoides* Lam.
30	*amethystina* L.
31	*amethystina* L. subsp. *orientalis* (donor name: *F. inarmata* Schur.)
32	*ampla* Hack.
33	*arvernensis* Augier, Kerguelen & Markgr.- Dannenb.
34	*borderi* (Hackel) K.Richter
35	*bosniaca* Kummer et Sendtner
36	*brigantina* (Markgr.-Dannenb.) Markr.-Dannenb.
37	*capillata* Lam.
38	*carpatica* F.G.Dietr.
39	*circummediterranea* Patzke
40	*costei* (St-Yves) Markgr.-Dannenb.
41	*cretacea* T.Popov & Proskorj.
42	*curvula* Gaudin subsp. *curvula*
43	*curvula* Gaudin subsp. *cagiriensis* (Timb.-Lagr.) Markgr.-Dannen. (donor name: *F. cagiriensis* Timb.-Lagr.)
44	*dimorpha* Guss.
45	*durandii* Clauson
46	*durissima* (Hackel) Kerguelen
47	*durissima* (Hackel) Kerguelen subsp. *bellettii* Hackel
48	*duvalii* (St-Yves) Stohr
49	*elegans* Boiss. (donor name: *F. elegans* Nogfuera)
50	*eskia* Ramond ex DC.
51	*gautieri* (Hackel) K.Richter (former name: *F. scoparia* Kermer)
52	*glauca* Vill.
53	*halleri* All. (donor name: *F. halleri* Augier (Olden))
54	*henriquesi* Hackel (donor name: *F. henriquesii* Alef.)
55	*herivieri* Patzke
56	*juncifolia* St-Amans
57	*koritnicensis* Vetter ex Hayek
58	*pallens* Host.
59	*polesica* Zapal.
60	*pseudeskia* Boiss
61	*pulchella* Schard.
62	*pumila* Vill
63	*rupicarpina* (Hackel) A.Kerner
64	*rupicola* Heuff.
65	*rupicola* subsp. *rupicola* Heuff. (donor name: *F. sulcata* Hack.)
66	*stricta* Host.
67	*tatrae* (Czako) Degen
68	*varia* Haenke
69	*varia* Haenke subsp. *brachystachys* Ekel.
70	*violacea* Schleich. ex Gaudin
	II. Non-European species, taxonomy according to 'Poaceae Urss' (Tzvelev 1976)
1	*dolichophylla* J. et Preslii
2	*duriotagana* Kerguelen
3	*extremadura* Sylvanes
4	*extremorientalis* Ohwi
5	*filiformis* (Ankart) Pourr
6	*jampetii* St. Yves
7	*kirilovii* Bast.
8	*liviensis* Verguin
9	*longifolia* Auquier
10	*magellanica* Lamb.
11	*mairei* St. Yves
12	*mathewsii* Cheesem
13	*patrae* Rodrig.
14	*punctoria* Ronald
15	*rubi* Voldavik
16	*rusca* Vavil.
17	*scirpifolia* Kunth.
18	*semilusitanica* Tr. Poldens
19	*sibirica* Hack.
20	*skvortsovii* E.Alexeev
21	*tuberulosa* Norman

Table 6. Accessions from the genus *Festuca* by genebank and format

	FORMAT 1[†] No. of access.		FORMAT 2 No. of access.		FORMAT 3 No. of access.		FORMAT 4 No. of access.		Total by genebank	Total original accessions	%
	Total	Original	Total	Original	Total	Original	Total	Original			
BGROO1	13						14		27		0
CHEOO1					37	18			37	18	48.6
CZEO79	3								3		0
CZEO82	316	19	1		2	2			319	21	6.6
DEUOO1	132	40			529	527			661	567	85.8
ESP119					22	22			22	22	100.0
FRAO51	59				116	46			175	46	26.3
GBROO4					75	23	3		78	23	29.5
ITAO34	1	1							1	1	100.0
POLOO3	134	17			106	106			240	123	51.3
POLO22	110	17			4097	3729	159	8	4366	3754	86.0
ROMOO3	93	9			320	71	1	1	414	81	19.6
ROMOO7	2	2	38	37	35	35	13		87	74	85.1
SVKO12	98	8			491	65			589	73	12.4
SVNO19	3	3							3	3	100.0
SWEOO2	72	72			242	242			314	314	100.0
TUROO1					28	28			28	28	100.0
Total no. access.	1036	188	39	37	6100	4914	190	9	7366	5148	69.9
In formats		18.1%		94.9%		80.5%		4.7%			

[†] In Format 1 (varieties and breeder's lines) only 564 accessions are unique. Fourteen accessions were recorded with wrong species name and 472 are duplicates of above 578 accessions. Percentage of duplicated accessions: 55.8%.

Annex 1. Structure of the computerized inventory of forage grasses collections in the Botanical Garden of IHAR in Bydgoszcz

Format 1. Location (*) and passport data [one set of data for each plot]

- Number of field *
- Number of row *
- Number in row *
- Number of plot *
- Replication number
- Number of accession
- Genus, species
- Subspecies
- Name of variety
- Accession status
- Breeder name
- Breeding method
- Collection date
- Location of collection
- Province/region
- Country of origin

Habitat specification:

- Grassland type
- Plant community
- Management data (grazed or abandoned etc.)
- Site specification (pH, soil type, N, P_2O_5, K_2O, Mg, Ca, etc.)
- Elevation
- Longitude
- Latitude
- Aspect
- Slope
- Donor name
- Donor country

Format 2. Management data [one set of data for each field]

- Date of planting into the field collection
- Fertilization doses (in kg per ha) before planting:
  - N
  - P_2O_5
  - K_2O
- Organic fertilization (in kg per ha) before planting
- Forecrop (species or mixture)
- Fertilization doses (in kg per ha) during vegetation of plants
  - N
  - P_2O_5
  - K_2O
- Herbicide (optional, in case of heavy weed cover):
  - Name or names, doses per ha, date of application
- Cutting frequency (number of cuts and dates of cutting)
- Other manipulation (specify)

Format 3. Evaluation data - data collected in metric units, then transferred into a 1-9 scale [one set of data for each plot]

- Number of plants per plot
- Uniformity (1-9 scale)
- Percentage of vernals (heading at the year of sowing)
- Mean heading date (expressed as number of days from 01.04.)
- Growth habit (expressed as tiller angle)
- Height of plants at heading phase (cm)
- Length of flag leaf (cm)
- Width of flag leaf (mm)
- Length of inflorescence (cm)
- Seed harvest date
- Seed yield (after cleaning and drying procedures - in grams per plot)
- Germination
- Other (notes depend on species)

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The European databases of *Medicago* spp. (annual species) and *Trifolium subterraneum*

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Updating

At the fifth ECP/GR Forages Working Group Meeting held in April 1995, our commitment was to update and publish the *Medicago* (annual species) and *Trifolium subterraneum* European Catalogues by the end of 1996.

We requested updates of the databases from all the seed bank Institutions holding collections or accessions of medics or *T. subterraneum* (Table 1). Data were received from the following:

BGRIIPGR	Institute of Introduction and Plant Genetic Resources "K. Malkov", Sadovo, District Plovdiv, Bulgaria	
DEUBGRC	Institute of Crops Science, Federal Research Center of Agriculture, Braunschweig, Germany	
GBRRBG	Royal Botanic Gardens Kew, Haywards Heath, W. Sussex, United Kingdom	
GBRWPBS	Institute of Grassland and Environment, Aberystwyth, United Kingdom	The database needs to be converted to a compatible version
ITAPERUG	Istituto di Miglioramiento Genetico Vegetale, Univ. Perugia, Italy	The database is being computerized at this moment

Except for the last two institutes, the database is updated and only needs the search for duplicates and the edition of the new catalogue. Our task has been hindered because of staff departure.

Software

All the data are recorded in dBaseIII and Access v. 2.0.

Databases contents

The *Trifolium subterraneum* database contains 3077 records (Tables 2 and 3) and the *Medicago* database contains 1776 records (Tables 4 and 5).

Databases availability

All data are freely available to any institution upon request.

Table 1. Institutes holding databases with accessions of *Trifolium subterraneum* and *Medicago* (annual species)

Institute code	Institute acronym	City, State	Country name
BGR 001	BGRIIPGR	Sadovo	Bulgaria
DEU 001	DEUBGRC	Braunschweig	Germany
DEU 146	DDRGAT	Gatersleben	Germany
FRA 056	FRAINRAMPG	Mauguio	France
GBR 004	GBRRBG	Haywards Heath	United Kingdom
GBR 016	GBRWPBS	Aberystwyth	United Kingdom
GRC 005	GRCGGB	Thessaloniki	Greece
GRC 006	GRCFCPI	Larissa	Greece
HUN 003	HUNRCA	Tápiószele	Hungary
ISR 002	ISRIGB	Bet Dagan	Israel
ISR 006	ISRHUJ	Jerusalem	Israel
ITA 004	ITAIDG	Bari	Italy
ITA 015	ITAPERUG	Perugia	Italy
PRT 005	PRTENMP	Elvas	Portugal
RUS 001	SUNWIR	St. Petersburg	Russian Federation
TUR 001	TURARARI	Izmir	Turkey
UKR 003	–	Kiev Region	Ukraine
UKR 020	–	Vinnitsa	Ukraine

Suggestions

In some of the databases received, the Institute name is not written within the file. Please write it down with the address and person responsible.

In the *Medicago* Catalogue published in 1988, the ECP number of each accession was assigned by species. In a genus like *Medicago,* which includes many species, this number leads to confusion. We think that it would be better to assign the ECP by order, under the field "Medicago List". Would it be possible to change the ECP number of the old catalogue (1988) for the order number in the new catalogue, explaining this in the introductory chapter?

Table 2. European *Trifolium subterraneum* Database accessions classified by contributing Institute

Institute	Advanced cultivars	Breeders' lines	Status unrecorded; named accession	Semi-natural, ecotypes	Wild	Status unrecorded; unnamed accession	Total
AUSCSIRO	1	1	–	–	26	–	28
BGRIIPGR	13	–	–	–	–	4	17
DDRGAT	5	–	–	–	–	–	5
DEUBGRC	28	–	–	403	–	–	431
ESPINIALO	35	115	5	–	2249	18	2422
GRCFCPI	11	–	–	–	–	–	11
ITAIDG	–	–	–	–	–	10	10
ITAIMGV	–	–	–	–	–	2	2
TURARARI	–	–	–	–	12	–	12
USAPIO	1	5	–	–	133	–	139
Total	94	121	5	403	2420	34	163077

Table 3. European *Trifolium subterraneum* Database accessions classified by country of origin

Origin country	Advanced cultivars	Breeders' lines	Status unrecorded; named accession	Semi-natural, ecotypes	Wild	Status unrecorded; unnamed accession	Total
Australia	47	8	4	1	–	–	60
Bulgaria	–	–	4	–	–	–	4
Cyprus	–	–	–	–	18	–	18
Algeria	–	–	–	–	11	–	11
Spain	7	90	–	–	1605	14	1716
France	–	–	–	–	42	–	42
Greece	1	6	–	–	75	–	82
Israel	–	1	–	–	1	–	2
Italy	–	1	–	–	60	2	63
Morocco	–	2	–	373	52	–	427
Portugal	–	6	–	6	213	–	225
Tunisia	–	2	–	–	44	3	49
Turkey	–	–	–	–	6	–	6
Unknown	39	5	–	23	292	15	375
Total	94	121	8	403	2420	34	3080

Table 4. European *Medicago* Database (annual species) accessions classified by contributing Institute

Institute	Advanced cultivars	Breeders' lines	Status. unrecorded; named accession	Semi-natural, ecotypes	Wild	Status unrecorded; unnamed accession	Total
AUSCSIRO	–	–	–	–	18	–	18
DDRGAT	1	–	2	–	79	–	82
DEUBGRC	1	–	1	370	–	–	372
ESPINIALO	13	2	1	–	480	11	507
GBRRBG	–	–	–	–	95	–	95
GRCFCPI	1	–	2	–	26	–	29
ISRIGB	–	–	–	–	349	–	349
ITAIDG	–	–	–	–	14	–	14
ITAIMGV	–	–	–	–	2	–	2
ITAPERUG	–	–	–	122	–	–	122
TURARARI	–	–	–	–	186	–	186
Total	16	2	6	492	1249	11	1776

Table 5. European *Medicago* Database (annual species) accessions classified by country of origin

Origin country	Advanced cultivars	Breeders' lines	Status unrecorded; named accession	Semi-natural, ecotypes	Wild	Status unrecorded; unnamed accession	Total
Australia	7	1	–	–	4	4	16
Bulgaria	–	–	9	–	7	–	16
Cyprus	2	–	–	–	170	–	172
Algeria	–	–	–	–	–	–	–
Spain	–	–	–	–	194	–	194
France	–	–	–	–	7	–	7
Greece	–	–	1	–	115	–	116
Israel	–	–	1	–	356	–	357
Italy	–	–	–	–	24	–	24
Morocco	–	–	–	370	6	–	376
Portugal	–	–	–	–	57	–	57
Tunisia	–	–	–	–	2	–	2
Turkey	–	–	–	–	191	–	191
Unknown	7	1	–	122	116	7	253
Total	16	2	11	492	1249	11	1781

The European *Phleum*, *Phalaris* and *Agrostis* databases

Manager: Merja Vetelainen
Nordic Gene Bank, Alnarp, **Sweden**

Updating

Updating of the *Phleum, Phalaris* and *Agrostis* databases started in 1995 and is still ongoing. Information of some of the largest collections is not yet included in the central databases.

Computerization

The database management system is dBase for Windows.

Availability of the databases

These three databases are available on the Internet and they can also be delivered on diskettes upon request.

Phleum database

URL: http://www.ngb.se/Databases/ECP/Phleum

The database contains information from 19 institutes and for 4268 accessions. In Table 1 accessions are classified by contributing institute and accession type. In Table 2 they are classified by country of origin and in Table 3 by taxa. Duplications and other gaps will be screened in the database and this information will be delivered to the respective institutions.

Table 1. Accessions classified by contributing institute (*Phleum* spp.)

Institute	Advanced cultivar	Breeders' lines	Primitive cultivar	Semi-natural ecotype	Wild	Unrecorded	Total
BELCLOGRVP	1	0	0	1	0	0	2
BGRIIPR	7	0	1	0	0	1	9
CZEZUBRI	102	11	0	0	0	0	113
DEUBGRC	69	4	0	459	42	46	620
DEUGAT	12	0	1	0	5	6	24
FRAINRAMAG	28	0	0	0	0	0	28
GBRRBG	0	0	0	0	71	0	71
GBRWPBS	52	1	45	1	30	1	130
GRCFCPI	0	0	0	0	0	9	9
HUNRCA	78	0	0	0	10	20	108
IRLAFT	0	0	0	0	32	0	32
ITAIDG	0	0	0	0	13	0	13
ITAPERUG	0	0	0	0	0	11	11
POLIHAR	3	0	0	0	2529	0	2532
REGNGB	44	4	23	0	346	0	417
ROMGBSV	0	0	21	13	0	0	34
SLOVOSIVO	32	1	0	0	33	22	88
SVN019	1	0	0	0	5	0	6
TURARARI	0	0	0	0	21	0	21
Total	429	21	91	474	3137	116	4268

Table 2. Accessions classified by country of origin (*Phleum* spp.)

Country of origin	Advanced cultivar	Breeders' lines	Primitive cultivar	Semi-natural ecotype	Wild	Unrecorded	Total
Not registered	77	2	50	1	181	62	325
BEL	5	0	0	1	13	0	19
BGR	1	0	0	0	1	0	2
CAN	12	0	0	0	0	0	12
CHE	0	0	0	0	1	1	2
CHN	0	0	3	0	0	3	3
CSK	7	11	0	0	3	0	21
DDR	3	0	1	0	4	3	10
DEU	30	0	1	458	201	47	736
DNK	36	0	4	0	15	5	56
ESP	0	0	0	0	2	0	2
FIN	16	5	1	0	144	1	166
FRA	10	0	0	0	21	3	35
GBR	35	0	1	0	17	2	54
GBW	0	0	0	1	0	0	1
GRC	0	0	0	0	11	0	20
HUN	39	0	0	0	17	3	59
IRL	0	0	0	0	34	0	34
ISL	3	1	0	0	0	0	4
ITA	3	0	0	0	30	11	44
JPN	7	0	0	0	0	0	7
NLD	60	1	0	0	2	0	63
NOR	20	0	17	0	167	18	205
NZL	1	0	0	0	0	0	1
POL	14	0	0	0	2133	8	2155
PRT	1	0	0	0	1	0	2
ROM	2	0	12	13	3	12	30
RUS	1	0	0	0	0	0	1
SUN	2	0	0	0	29	2	33
SVK	3	0	0	0	2	11	18
SVN	1	0	0	0	5	0	6
SWE	26	1	1	0	77	1	105
TUR	0	0	0	0	21	0	21
USA	9	0	0	0	0	0	9
YUG	5	0	0	0	2	0	7
Total	429	21	91	474	3137	193	4268

Phalaris database

URL: http://www.ngb.se/Databases/ECP/Phalaris

In the database, information from 8 institutions and 231 accessions is included. As for the *Phleum* database, duplications and other defects will be screened in the database and this information will be delivered to the respective institutions.

Agrostis database

URL: http://www.ngb.se/Databases/ECP/Agrostis

The *Agrostis* database includes passport data from 8 institutions and 271 accessions. The database will be managed as the other central databases at the Nordic Gene Bank.

Table 3. Accessions classified by taxa (*Phleum* spp.)

Institute	*alpinum*	*arenarium*	*graecum*	*hirsutum*	*montanum*	*paniculatum*	*phleoides*	*pratense*	*serrulatum*	*subulatum*	Not recorded	Total
BELCLOGRVP	0	0	0	0	0	0	0	2	0	0	0	2
BGRIIPR	0	0	0	0	0	0	0	9	0	0	0	9
CZEZUBRI	0	0	0	0	0	0	0	113	0	0	0	113
DEUBGRC	0	0	0	0	0	0	0	620	0	0	0	620
DEUGAT	0	0	0	0	0	1	3	20	0	0	0	24
FRAINRAMAG	0	0	0	0	0	0	0	28	0	0	0	28
GBRRBG	6	12	1	3	5	0	7	34	0	3	0	71
GBRWPBS	0	1	0	0	0	0	3	125	1	0	0	130
GRCFCPI	0	0	0	0	0	0	0	0	0	0	9	9
HUNRCA	2	0	0	0	0	0	4	102	0	0	0	108
IRLAFT	0	0	0	0	0	0	0	32	0	0	0	32
ITAIDG	0	0	0	0	0	0	0	2	0	1	10	13
ITAPERUG	11	0	0	0	0	0	0	0	0	0	0	11
POLIHAR	0	0	0	0	0	0	0	2532	0	0	0	2532
REGNGB	18	0	0	0	0	0	0	399	0	0	0	417
ROMGBSV	0	0	0	0	1	0	0	32	0	0	1	34
SLOVOSIVO	0	0	0	0	0	0	0	83	0	0	5	88
SVN019	0	0	0	0	0	0	0	6	0	0	0	6
TURARARI	0	0	0	0	0	0	2	5	0	0	14	21
Total	37	13	1	3	6	1	19	4144	1	4	39	4268

The European *Lolium* and *Trifolium repens* databases

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(see Part I, p. 6)

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(see Part I, p. 7)

Status of National Collections

Collecting and evaluation of wild and cultivated local germplasm of forages in Cyprus

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Introduction

At the Cyprus Agricultural Research Institute research work is carried out on collecting, conservation and evaluation / utilization of native, wild and cultivated forage and pasture crops. Forage taxa are described in the Flora of Cyprus (Meikle 1977, 1985).

The number of taxa (sp. + spp.) of the following forage genera recorded to occur in Cyprus is given in parentheses (Della 1998): *Trifolium* L. (32), *Medicago* L. (20), *Vicia* L. (20), *Pisum* L. (2), *Lolium* L. (5), *Dactylis* L. (1), *Festuca* L. (1), *Bromus* L. (17), *Poa* L. (8), *Phleum* L. (1), *Oryzopsis* Michx. (2), *Cynodon* L. (1), *Hordeum* L. (8), *Phalaris* L. (5).

One of the priorities of the genetic resources programme of the ARI is to collect, conserve and evaluate most of the forage germplasm of both legumes and cereals, with emphasis on cultivated species for which there is a danger of genetic erosion or even extinction, since old varieties are replaced by new ones (Della 1994, 1997).

Collecting done in Cyprus

In the past, several attempts have been made by local and foreign scientists to collect and screen germplasm of forage crops. During 1951, 1963, 1967 and 1970 extensive collections of Cyprus medics and trifolium species were made by the Western Australian Department of Agriculture (WADA). The germplasm was evaluated in Australia (Bailay and Gayfer 1968) and a new variety – 'Cyprus barrel medic' – was released for use by the farmers (Crawford 1963). In 1975 Cyprus agreed to cooperate with the International Board for Plant Genetic Resources (IBPGR) through the ARI. Since then the following collections of forages have been made (Table 1).

Table 1. Forages collecting activities in Cyprus (Della 1994, 1997)

Year	Scientific name	Collecting organization(s)	No. of access.
1978	*Hordeum vulgare* L.	IBPGR/ARI	26
1984	*Lathyrus ochrus* L.	ARI/IBPGR/ICARDA	12
1984	*Lathyrus sativum* L.	ARI/IBPGR/ICARDA	19
1984	*Pisum sativum* L.	ARI/IBPGR/ICARDA	6
1984	*Vicia ervilia* L., wild	ARI/IBPGR/ICARDA	15
1984	*Vicia sativa* L.	ARI/IBPGR/ICARDA	67
1984	*Medicago sativa* L.	ARI/IBPGR/ICARDA	29
1987	*Medicago* species (annual), wild	WADA/ARI	41
1988	Wild forages	IBPGR/ARI	100
1993	Grasses (wild)	ARI	73

Also in 1995 an agreement was signed between the Cyprus Agricultural Research Institute and the FAO Regional Office for the Near East which partially financed the collecting and evaluation of the most important forage crops. Hence eight visits were organized around Cyprus during spring 1995 to locate the crops, determine the time of maturity of each at the various locations and to collect the mature seed. The

species / accessions collected were: *Vicia* sp. (16), *Avena* sp. (13), *Lolium* sp. (6) and *Trifolium* sp. (2).

The seed of each accession was sown in autumn 1995 at the Saittas experimental farm for multiplication. Observations were taken during the growing season on the performance of the crops. The seed was harvested in spring and replicated trials were established in autumn 1996 for those species / accessions whose seed was sufficient.

There is no *Rhizobium* collection in Cyprus. However, the biological nitrogen fixation using introduced *Rhizobium* has been studied at the ARI in cooperation with ICARDA. Results have shown that, in Cyprus, legumes such as common vetch, faba beans, ochrus and medics that respond to *Rhizobium leguminosarum* and *R. meliloti* can fix up to 80% of their nitrogen requirements without inoculation. Other legumes, however, such as chickpea, peanut, soyabean and field bean, which respond to other *Rhizobium* species, have nodulation problems and inoculation is needed to ensure good biological nitrogen fixation. In rotation studies in the rain-fed areas of Cyprus it was found that the inclusion of common vetch, which fixes nitrogen, results in higher protein output. Also, grain yield from subsequent cereal crops was higher even though receiving less nitrogen fertilizer (Papastylianou 1986) compared with a continuous cereal production system.

Genetic conservation

Ex situ

All the collected forage germplasm is stored in the CYPARI Genebank under controlled conditions (0-4°C and 50% RH). Germplasm is hermetically sealed in laminated foil packets. Top priority on genetic conservation is given to the cultivated forage legumes, most of which have already been collected, as mentioned earlier. The collected forage species were also sent to ICARDA (Syria) and Bari (Italy) for storage and evaluation (Della 1994, 1997). Collecting of wild forages has started and will continue at a slower pace since these species are less endangered than the cultivated ones. Priority is given mainly to barley, lolium, vetches, peas, medics, clovers and lucerne.

In situ

No direct measures have been taken until now by the Government of Cyprus for conserving the wild relatives of the most important cultivated forage crops such as *Lolium* spp., *Hordeum* spp., *Avena* spp., *Vicia* spp., *Medicago* spp., *Trifolium* spp., *Lathyrus* spp. and others in their natural habitat. *In situ* conservation of these species for the time being is rather unlikely.

Screening/utilization of collected germplasm

Since 1970 great emphasis has been given in Cyprus on the use of genetic resources for improving field crops.

Vicia sativa *(common vetch)*

In the early 1970s seeds of *Vicia sativa* local populations were evaluated for several years and it was observed that the variety 'Local' was a mixture of different types of seed size, seed shape and seed colour. As a result of a purification programme carried out at the ARI, a selection with uniform seeds of large size was recommended for release (Agricultural Research Institute 1972-77). The forage yield of this line was not higher than that of the mother variety, but its uniform seed type satisfies the seed market.

Annual Medicago *species*

In 1951, 1963, 1967 and 1970 Australian scientists collected medic and trifolium germplasm that was used in their programmes. As a result of those collections a new variety, namely 'Cyprus barrel medic', was released to Australian farmers (Crawford 1963). The advantages of this variety were its earliness and resistance to drought.

A main seed-collecting tour in July 1986 organized by the Western Australian Department of Agriculture and covering all the occupied area of Cyprus, yielded 91 accessions of various *Medicago* species. These accessions, together with 113 other accessions collected in 1967, mostly from the occupied area, are listed in Table 2.

Table 2. Distribution of medics and trifolium species collected during two collecting tours in Cyprus (1967, 1986)

Species	Rainfall (mm)	Altitude (m)	Occurrence (%)
Medicago blancheana Boiss.	300-400	305	0.97
Medicago constricta Durieu	400-450	300-670	1.94
Medicago disciformis DC.	400-500	5-305	1.45
Medicago doliata Carmign.	350-500	3-20	0.97
Medicago intertexta (L.) Miller	350-400	60-305	1.45
Medicago laciniata (L.) Miller	500	175	0.49
Medicago littoralis Rohde ex Loisel	250-580	1-400	18.93
Medicago marina L.	500	30	0.49
Medicago murex Willd.	450	300	0.49
Medicago orbicularis (L.) Bartal	250-500	6-305	4.37
Medicago polymorpha L.	250-450	300	1.94
Medicago rigidula (L.) All.	450	300	0.49
Medicago scutellata (L.) All.	300-500	50-300	3.40
Medicago truncatula Gaertner	250-650	3-400	48.54
Medicago turbinata (L.) All.	250-900	30-1210	5.34
Trifolium angustifolium L.	500-600	10-200	3.40
Trifolium cherleri L.	375-600	2-250	1.94
Trifolium purpureum Loisel.	500-550	8-250	3.40

The seeds of the above accessions were sent to ARI by WADA and were evaluated. The evaluation involved herbage yield, winter growth, protein content, digestibility, plant height and characteristics related to persistence, such as flowering time and seed yield. A more complete evaluation is in progress at WADA. A minor collecting tour covering the free areas of Cyprus was made in 1987 again, in cooperation with WADA. This tour yielded 41 accessions of various *Medicago* and *Trifolium* species. The seed of this collection is stored in the CYPARI Genebank and at the moment there is no programme in progress at the ARI to evaluate annual medics.

However, it is interesting to note that testing of medics either selected from local populations or introduced from Australia or ICARDA was not successful whether medics were used in rotation with cereals on arable land, or for pasture improvement on marginal land. The main reasons for that failure were (a) the extremely slow growth of medics during the winter (December-February) resulting in severe weed competition and late availability of forage for grazing, (b) the much lower dry matter yield compared with that of other legumes (common vetch and Lana vetch) and barley, and (c) the unsatisfactory regeneration of medics for establishing a good pasture stand in the following season.

Medicago sativa *(lucerne)*

Lucerne is considered to be the most nutritious and profitable perennial forage crop grown in Cyprus. Since the results from the introduction and testing of new varieties were disappointing it was decided in 1984 to select populations belonging to the 'Local' variety from farmers' fields with the aim to select the most productive ones. There were 29 populations evaluated in replicated trials for 4 years. The results showed that, among the various locally selected populations, there were large differences in the various parameters examined. The dry matter yield over the whole experimental period (May 1985 - December 1988) ranged from 68 to 116 t/ha while herbage yield of the control (variety 'Local') was 108 t/ha.

It appears, therefore, that selection of local germplasm holds more promise in the search for improved material than the introduction of foreign varieties (Droushiotis 1994).

Hordeum spontaneum *(wild barley)*

Observations in Cyprus have shown that wild barley behaves as a pasture crop (Hadjichristodoulou 1988), and it was thought that with proper management it may be used for pasture development. Wild barley, *Hordeum spontaneum* and *H. agriocrithon* (natural outcrosses of *H. spontaneum* with *H. vulgare*) are found in abundance in the WANA region and are distinguished from *H. vulgare* by a brittle rachis, shrunken kernels and other seed-dispersing mechanisms. Owing to these characteristics both species of wild barley are able to regenerate naturally, except where overgrazing is practised. In addition, wild barley also has a certain level of seed dormancy. About 20% of the seeds do not germinate in the first year, but do so in the following year, thus safeguarding the survival of the species. The nitrogen concentration of the wild barleys at the grazing stage is 3-5%. Taking advantage of the pasture characteristics of wild barleys, Hadjichristodoulou (1990, 1995b) established pastures in Cyprus to test the performance of these crops and their crosses with *H. vulgare* under grazing conditions. In those trials it was shown that there were no adverse effects on crop growth when the herbage was grazed by sheep two or three times from mid-December to mid-April depending on weather conditions, particularly rainfall. However, by the end of April the crop must be left to produce seed. After seed maturity the dry herbage can also be grazed (July). By applying this procedure, reseeding is not required in the following years. Since barley is not a nitrogen-fixing crop, ample amounts of nitrogen fertilizer are necessary for maximizing forage production. Research work is now under way to study the possibility of using mixtures of barley with either medics or with *Vicia amphicarpa*, so that the legume component will provide mainly the nitrogen and the cereal the herbage production.

Genes of wild barley were also used to produce grain barley varieties tolerant to heat and drought stress (Hadjichristodoulou 1992, 1993, 1995a).

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Status of the national forages collections in Greece

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Two Institutes hold forages collections in Greece: the Macedonia-Thraki Agricultural Research Center, Greek Gene Bank (MTARC/GGB) in Thessaloniki and the Central Greece Agricultural Research Center, Fodder Crops and Pastures Institute (CGARC/FCPI) in Larissa. Both these Institutes are affiliated with the National Agricultural Research Foundation (NAGREF), a primary state-funded legal entity of the Ministry of Agriculture.

CGARC/FCPI has a national responsibility for fodder crop and pasture improvement. Breeding forage species is the main job. On the other hand collecting and maintenance of forage germplasm is a subsequent task, to support plant breeding. Collecting activities resulted in a considerable forage collection including 2683 accessions as shown in Tables 1 and 2. A large number (1991) of these accessions is stored in tin boxes in natural room conditions. Almost all material is currently documented only for passport data using the characters of the standard collecting form of FAO/IBPGR. Computerization of the passport data of the accessions in Larissa is in progress and will be concluded by the end of 1997. Only a limited number of accessions has undergone regeneration, characterization and preliminary evaluation.

Owing to lack of funds and staffing, progress on forage germplasm collection activities has not been up to our expectations.

MTARC/GGB has a national responsibility for plant genetic resources. Medium-term (0 to +5ºC) and long-term (–18 to –21ºC) storage facilities have a capacity of 80 m³ and can hold approximately 10 000 samples (Table 3). GGB maintains, in medium-term conditions, 1168 seed samples of forages accessions (Table 1). Most of the accessions kept in Thessaloniki were collected or created by CGARC/FCPI and donated to GGB. All this material is documented and fully computerized in a database using dBaseIV.

Lolium perenne core collection

Owing to the absolute lack of funds and personnel available for genetic resources only the populations from Greece, Bulgaria, Italy, France and Spain have been included in our *Lolium* core collection trial. Varieties 'Ariïn' and 'Olympion' have been included as control varieties. Young seedlings were transplanted in the field in March 1996. Heading tendency and drought damage in the sowing year have been scored. Winter damage and winter bulk in the first year after establishment have been scored also, in mid-February 1997. All plots were cut and fertilized 1 March 1997. Collected data have not been analyzed yet, because of the lack of resources mentioned above.

Table 1. Forages collections in Greece

Genus	Number of accessions		
	1. Larissa	2. Thessaloniki	3. Total[†]
Medicago	533	118	573
Trifolium	463	356	553
Dactylis	175	150	252
Festuca	160	41	183
Lolium	138	74	182
Phleum	2	12	12
Vicieae	480	107	578
Others	40	310	350
Total	1991	1168	2683

[†] Not the sum of columns 1 and 2 but the number of unique accessions per genus.

Table 2. Details on forages collections in Greece

Genus and species	Advanced cultivars	Landraces	Wild or semi-natural	Breeders' lines	Total
Agropyron canicum (L.) Beauv.	–	–	1	–	1
Agropyron elongatum (Host.) Beauv.	–	2	2	–	4
Agropyron repens (L.) Beauv.	–	–	2	–	2
Agropyron spp.	–	–	16	–	16
Aristella bromoides (L.) Bertol.	–	–	4	–	4
Brachypodium spp.	–	–	8	–	8
Briza media L.	–	–	1	–	1
Dactylis glomerata L.	25	–	157	70	252
Ervum ervilia L.	–	12	–	–	12
Festuca arundinacea Schreb.	30	–	34	110	174
Festuca ovina L.	–	–	2	–	2
Festuca spp.	–	–	7	–	7
Hedysarum coronarium L.	1	–	–	2	3
Hordeum bulbosum L.	–	–	25	–	25
Hordeum spontaneum	–	–	50	–	50
Hordeum vulgare L.	31	26	1	–	58
Lathyrus cicera L.	4	?	–	?	20
Lathyrus ochrus (L.) DC. in Lam. & DC.	–	?	–	?	17
Lathyrus sativus L.	–	?	–	?	20
Lathyrus spp.	–	?	–	?	8
Lolium perenne L.	24	–	57	80	161
Lolium spp.	4	–	16	–	20
Lolium temulentum L.	–	–	1	–	1
Lotus spp.	1	2	19	–	22
Lupinus albus L.	–	3	–	–	3
Lupinus angustifolius L.	–	–	70	–	70
Lupinus luteus L.	–	–	1	–	1
Lupinus spp.	–	–	2	–	2
Medicago arborea L.	2	–	36	55	93
Medicago coronata (L.) Bartal.	–	–	1	–	1
Medicago falcata (L.) Arcangeli	–	–	5	–	5
Medicago lupulina L.	–	–	6	–	6
Medicago minima (L.) Bartal.	–	–	1	–	1
Medicago orbicularis (L.) Bartal.	–	–	48	15	63
Medicago sativa L.	101	30	3	200	334
Medicago spp.	–	–	70	–	70

Genus and species	Advanced cultivars	Landraces	Wild or semi-natural	Breeders' lines	Total
Melilotus alba Medicus	–	–	4	–	4
Melilotus spp.	–	–	5	–	5
Onobrychis spp.	1	–	3	11	15
Oryzopsis spp.	–	–	15	–	15
Phacelia tanacetifolia Benth.	1	–	–	–	1
Phalaris tuberosa L.	–	–	8	3	11
Phleum pratense L.	–	–	2	–	2
Phleum spp.	–	–	10	–	10
Poterium sanguisorba	1	–	12	–	13
Poterium spp.	–	–	2	–	2
Sorghum sudanense (Piper) Stapf	10	–	–	–	10
Trifolium alexandrinum L.	11	4	55	20	90
Trifolium angustifolium L.	–	–	1	–	1
Trifolium arvense L.	–	–	9	–	9
Trifolium aureum Pollich	–	–	2	–	2
Trifolium campestre Schreb.	–	–	13	–	13
Trifolium cherleri L.	–	–	13	–	13
Trifolium dubium Sibth.	–	–	1	–	1
Trifolium echinatum Bieb.	–	–	1	–	1
Trifolium fragiferum L.	1	1	3	–	5
Trifolium hirtum All.	5	2	23	–	30
Trifolium hybridum L.	5	2	1	–	8
Trifolium incarnatum L.	3	1	5	–	9
Trifolium obscurum Savi	–	–	5	–	5
Trifolium pratense L.	35	7	57	20	119
Trifolium repens L.	15	3	74	15	107
Trifolium resupinatum L.	8	3	9	15	35
Trifolium scabrum L.	–	–	9	–	9
Trifolium spp.	–	–	64	–	64
Trifolium spumosum L.	–	–	3	–	3
Trifolium stellatum L.	–	–	4	–	4
Trifolium striatum L.	–	–	2	–	2
Trifolium subterraneun L.	7	3	3	–	13
Trifolium tomentosum L.	–	–	2	–	2
Trifolium vesiculosum Savi	2	1	5	–	8
Trigonella foenum–graecum L.	1	1	–	–	2
Trigonella spp.	–	–	2	–	2
Vicia sativa	6	?	2	?	500[†]
Vicia spp.	–	–	1	–	1
Total	**335**	**103**	**1076**	**616**	**2683**

[†] Of the total 500 accessions, the number of landraces and breeders' lines has not yet been determined.

Table 3. Quality status of national forages collections in Greece

Institute	Type of accession	No. of access.	Storage conditions	Accessions need urgent regeneration (%)	No. access. regenerated/ year	Avail-ability (%)
***Medicago* (incl. shrubs)**						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	103	Room temp.	40		20
	Landraces	30	Room temp.	25		20
	Semi-natural	40	Room temp.	10		10
	Wild species	90	Room temp.	40		?
	Breeders' lines	270	Room temp.	10		0
NAGREF/GGB, Thessaloniki	Advanced cultivars	2	100% Mterm[†]	0	0	100
	Landraces	8	100% Mterm	0	0	50
	Semi-natural	5	100% Mterm	?	?	?
	Wild species	103	100% Mterm	?	?	?
Trifolium						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	92	Room temp.	40	?	30
	Landraces	27	Room temp.	50	?	30
	Wild species	274	Room temp.	40	?	10
	Breeders' lines	70	Room temp.	20	?	0
NAGREF/GGB, Thessaloniki	Advanced cultivars	12	100% Mterm	0	0	100
	Landraces	17	100% Mterm	?	?	?
	Wild species	327	100% Mterm	?	?	?
Dactylis						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	25	Room temp.	75	?	IOU
	Wild species	80	Room temp.	80	?	5
	Breeders' lines	70	Room temp.	20	?	0
NAGGER/GAB, Thessaloniki	Wild species	*150*	100% Mterm	*?*	*?*	*?*
Festuca						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	30	Room temp.	80	?	10
	Wild species	20	Room temp.	80	?	10
	Breeders' lines	110	Room temp.	25	?	0
NAGREF/GGB, Thessaloniki	Wild species	41	100% Mterm	?	?	?
Lolium						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	28	Room temp.	90	?	4
	Wild species	30	Room temp.	75	?	20
	Breeders' lines	80	Room temp.	10	?	0
NAGREF/GGB, Thessaloniki	Wild species	74	100% Mterm	?	?	?
Phleum						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	2	Room temp.	?	?	?
NAGREF/GGB, Thessaloniki	Wild species	12	100% Mterm	?	?	?
Vicieae						
NAGREF/ CGARC-FCPI, Larissa	Advanced cultivars	10	Room temp.	0	0	100
	Other types[‡]	470	Room temp.	?	?	?
NAGREF/GGB, Thessaloniki	Advanced cultivars	9	100% Mterm	0	0	100
	Landraces	95	100% Mterm	?	?	?
	Wild species	3	100% Mterm	?	?	?

[†] Mterm = medium-term storage.

[‡] Mainly Breeders' lines and Landraces. Most of this material has not been regenerated since 1982.

Genetic resources of perennial grasses and legumes in Lithuania

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Lithuanian Institute of Agriculture, Kedainiai, Lithuania

Conservation priorities

The conservation of perennial grasses and legumes is a continuous process and should cover areas of activity such as collecting, evaluation and characterization of plant genetic resources in the field, regeneration, documentation of samples and other issues (Tyler 1987).

In Lithuania this programme is still in its initial phase: estimation of priorities to determine what breeding material and wild species should be collected and stored in the genebank.

Genetic resources of perennial grasses and legumes consist of the following main groups in Lithuania.

Registered varieties and valuable breeding material

A list of Lithuanian varieties which in the near future have to be described and placed in the genebank storage was established. Twenty-eight varieties of the most important species of grasses and legumes were named, which had a status of registered varieties or were excluded from registration. For example such varieties as 'Pievis' and 'Perlas' (timothy), 'Rausviai' (alsike clover), 'Velyviai' (red clover) have been tested in state variety testing trials but have never been registered. In spite of that, all these varieties have to be placed in the genebank for storage.

All the breeding material developed through the use of seeds of Lithuanian and foreign origin was attached to the Lithuanian breeding material. This breeding material should be sufficiently evaluated (for example in productivity trials), stable, uniform and have at least one agronomically valuable characteristic to be accepted for storage. Therefore the inventory of our old seed samples was undertaken to check the seed viability of the samples and the coverage of the related information. If seed viability is decreased or if a sample is insufficiently described, it should be regenerated.

Semi-natural and wild ecotypes.

(see section on Collecting activities, page 109)

References

Tyler, B.F. (ed.). 1987. Collection, characterization and utilization of genetic resources of temperate forage grass and clover. IBPGR Training Courses: Lecture Series 1. International Board for Plant Genetic Resources, Rome.

Current status of CGN forages collection

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Centre for Plant Breeding and Reproduction Research (CPRO-DLO), Centre for Genetic Resources The Netherlands (CGN), Wageningen, the Netherlands

The collection

The forages collection consists of 465 accessions of eight different species (Table 1). The grass species were mainly received from the former Foundation of Agricultural Plant Breeding and some private breeding firms (van Soest and Boukema 1995). The pasture legumes were mainly collected by CGN in the Netherlands from 1985 to 1986 (van Soest and Dijkstra 1986). In the next few years, CGN will broaden the collection with original Dutch material of *Lolium perenne* L., *Dactylis glomerata* L., *Festuca pratensis* Huds., *Phleum pratense* L. and *Trifolium repens* L. In 1997, a joint plant exploration mission is planned to Uzbekistan in cooperation with VIR (St. Petersburg) and IGR of Uzbekistan. This mission will also collect some forages including grasses.[17]

Table 1. Forages collection of CGN

Grasses	No. of samples	Legumes	No. of samples
Lolium perenne L.	126	*Trifolium pratense* L.	140
Lolium multiflorum Lam.	67	*Trifolium repens* L.	1
Lolium x *hybridum* Hausskn.	1		
Phleum pratense L.	96		
Phleum bertolonii DC.	6		
Dactylis glomerata L.	28		
Total	324		141

Grasses

The collection mainly includes material of economically important forage grasses of northwest Europe. The genus *Lolium*, including perennial and Italian ryegrass, is with 194 accessions the most important group (Table 1). The *Lolium perenne* collection will be extended with about 100 accessions, mainly cultivars developed in the Netherlands. The *Phleum* collection includes two species and was recently enlarged with more than 60 mainly old Dutch cultivars and presently consists of 102 accessions. The small collection of *Dactylis glomerata* L. (28) will be soon enlarged to approximately 50 accessions, mainly old cultivars from The Netherlands.

Besides Dutch cultivars the forage grass collection includes several ecotypes collected in the Netherlands, Czech Republic, Turkey, United Kingdom, Hungary and several other European countries.

In the near future old Dutch cultivars of *Phleum pratensis* and *Festuca pratensis* Huds. will be included in the collection. It is expected that around the year 2000 the forage grasses collection of CGN will be enlarged with some 250 new accessions of different grass species and will consist of approximately 715 accessions. After the enlargement, the collection will include a broad variation of material produced in Dutch breeding programmes from 1935 to 1990.

[17] A collecting expedition to Uzbekistan was completed in August 1997. Details can be requested from L. van Soest.

Forage legumes

This collection consists of 140 accessions of red clover (*Trifolium pratense*) and one of white clover (*T. repens*). During the first meeting of the ECP/GR Working Group on Forages held in 1984 in Larissa, Greece, several West European countries were requested to collect material of red clover. In most countries red clover cultivation has seriously declined over the past 30 years and this may result in extinction of this fodder crop. In the Netherlands red clover cultivation had virtually disappeared since 1975 and a rescue operation started in 1985 (van Soest and Dijkstra 1986). In 1985 and 1986 collecting trips were organized in all 11 provinces of The Netherlands (Fig. 1) and 126 accessions were collected. Sampling was particularly conducted along roadsides and occasionally in meadows. Seed balls were normally collected from 50 to 100 plants. Areas where red clover cultivation was of some importance in the past were more intensively sampled, taking into account that escapes of former cultivation could be collected.

Besides the collected ecotypes, another 16 red clover accessions, including cultivars, landraces and tetraploid breeding lines, are present in the collection. Four old Dutch landraces ('Groninger', 'Roosendaalse', 'Gendringse' and 'Rode Maasklaver') are included in the *Trifolium pratense* collection. The only accession of white clover is the 'Vermont' polyploid.

The forage legume collection will be enlarged with some old Dutch cultivars of *T. repens*.

It should be mentioned here that the grain legume collection of CGN, with the species *Pisum sativum, Vicia faba* and *Lupinus* spp., also includes some forage types.

Regeneration

All forage crops are regenerated in field plots, isolated in rye fields. The distance between the plots is at least 50 meters. Material that needs vernalisation is kept in unheated greenhouses during the winter. After sowing, during the end of the summer, some 50 plants are planted in the isolation plots in April of the following year. To prevent lodging, the grasses have to be staked. Harvest of the seeds is carried out in July/August.

Documentation

Except the newly introduced 60 accessions of *Lolium multiflorum*, the 465 accessions of the different forage species are documented for passport data in GENIS, the CGN information system, based on the database management system ORACLE (van Hintum 1987). However, the passport data of some of the grass ecotypes from different European countries are incomplete.

So far no characterization/evaluation data of the forage collections are included in GENIS.

Storage

After the seeds have been dried to a moisture content of approximately 5%, they are packed in laminated aluminium foil bags and stored at –20ºC for long-term storage. The users' samples are, however, stored at medium-term storage conditions of 4ºC.

Utilization

Since 1988 some 150 accessions of different forage crops have been distributed to users in the Netherlands and abroad. Both for grasses and legumes, users are supplied with 100 seeds and, on request, with information about the material.

Fig. 1. Collecting sites of *T. pratense*, sampled in the Netherlands in 1985 and 1986.

Future activities

The activities planned for the next 5 years can be summarized as follows:

- to broaden the forage collection particularly with original Dutch material, it is foreseen that in the next 5 years the collection will be enlarged to approximately 900 accessions
- to collect forages in some CIS countries such as Uzbekistan
- to regenerate some 300 accessions
- to update the passport data
- to obtain evaluation data from users and to include the information in GENIS.

References

van Hintum, Th.J.L. 1987. GENIS: A fourth generation information system for the database management of genebanks. Plant Genet. Resour. Newsl. 75/76:13-15.

van Soest, L.J.M. and H. Dijkstra. 1986. Red clover collecting in The Netherlands. Internal report CGN/SVP.

van Soest, L.J.M. and I.W. Boukema (eds.). 1995. Diversiteit in de Nederlandse Genenbank [Diversity in the genebank of The Netherlands] CPRO-DLO/CGN, Wageningen, The Netherlands.

Forages national collections in Poland

I. Status of the national collection of forage grasses at the Plant Breeding and Acclimatization Institute, Poland

G. Žurek [1] ***and W. Podyma*** [2]

[1] Botanical Garden, Plant Breeding and Acclimatization Institute (IHAR), Bydgoszcz, Poland

[2] Centre for Plant Genetic Resources, Plant Breeding and Acclimatization Institute, (IHAR), Radzików, Poland

	Type of accession			
Genus, species	**Advanced cultivars and breeders' lines**	**Status unknown**	**Wild or semi-natural**	**Total per species**
Agrostis alba Auct.			4	4
Agrostis tenuis Sibth.			11	11
Alopecurus pratensis L.			2	2
Bromus inermis Leysser	91		3	94
Dactylis glomerata L.	5401	128	97	5626
Festuca arundinacea Schreb.	711	130	36	877
Festuca heterophylla Lam.			1	1
Festuca ovina L.			3	3
Festuca pratensis Huds.	3396	32	78	3506
Festuca rubra L.	39		20	59
Lolium x *hybridum* Hausskn.			8	8
Lolium multiflorum Lam.			23	23
Lolium multiflorum Lam. var. *westervoldicum*			5	5
Lolium perenne L.	2100	55	112	2267
Phalaris canariensis L.			1	1
Phleum pratense L.	2340		87	2427
Poa compressa L.			1	1
Poa palustris L.			4	4
Poa pratensis L.	1238	208	49	1495
Total by type of accession	15316	553	545	16414

For the whole collection: availability is 100%; storage conditions are long term.

Statistically significant decreases of seed viability were observed in some accessions harvested in 1977-82. The estimated amount of accessions with strong regeneration need is close to 10% of the whole collection.

II. Computerized inventory of the field collections of forages held in the Botanical Garden of the Plant Breeding and Acclimatization Institute in Bydgoszcz

G. Žurek
Botanical Garden, Plant Breeding and Acclimatization Institute (IHAR), Bydgoszcz, Poland

Introduction

In 1972 one of the biggest European grass collections was established in the Botanical Garden of the Plant Breeding and Acclimatization Institute in Bydgoszcz to undertake conservation of forage grasses genetic resources. Since then nearly 20 000 accessions were collected, evaluated and gathered in the form of seed samples. Large numbers of data require simple, quick and precise processing. The most effective way to do so is to establish a computerized inventory of the living forage grasses collection as it was decided during the fifth meeting of the Working Group on Forages (Gass *et al.* 1995).

Materials and methods

The database structure is partly similar to the structure used in European Catalogues of *Dactylis* and *Festuca.* The basic software for data input is dBaseIII+ and the whole inventory works on Excel. The following steps of data input were accepted:

- 1st step: reception of seed or plant accession (input of all available passport data)
- 2nd step: plantation data (date of sowing, date of planting into the field)
- 3rd step: plot location data (number of field, number of row, number of plot in row)
- 4rd step: field management data (fertilization before and after plantation)
- 5th step: evaluation data (data from evaluation protocol)
- 6th step: seed data (day of harvest, drying procedure specification, seed weight, germination percentage in year of harvest).

For each of the above steps a separate sheet (or database structure) was prepared to enable all staff members of the Botanical Garden to perform simple and clear data input. Input sheets / databases for steps 1, 3, 5 and 6 were prepared for each accession, while for steps 2 and 4, only one per field. After completion of the required data, all are entered in the computerized inventory.

Results

Numerous location, passport, management and evaluation data were gathered during 1996. For three fields planted in 1994, 1995 and 1996 a total number of 2875 plots for 1058 accessions was described (Table 1). Evaluation data will be completed for the above accessions during 1997, 1998 and 1999, respectively.

A total of 19 species was identified. Additional accessions of *Festuca* sp., *Koeleria* sp., *Poa* sp. and the *Agropyron* group still require taxonomic identification.

Recommendations

1. It is essential to add other grasses collection (i.e. species for ornamental and recultivation purposes) existing in the Botanical Garden of IHAR to the computerized inventory.

Table 1. Accessions documented in 1996 in the Computerized Inventory of Forage Collections held in the Botanical Garden of IHAR in Bydgoszcz

			Planting year						Total no. of accessions	
			1994		1995		1996			
No.	Genus	Species	Ecot.	Var.	Ecot.	Var.	Ecot.	Var.	Ecot.	Var.
1	*Agrostis*	*alba*					1		1	0
2	*Agrostis*	*stolonifera*	18		3		2		23	0
3	*Agrostis*	*tenuis*					8	4	8	4
4	*Agropyron* sp.						22		22	0
5	*Dactylis*	*glomerata*	32	2			49	1	81	3
6	*Dactylis*	*aschersoniana*	2						2	0
7	*Deschampsia*	*cespitosa*	29	2	29		52		110	2
8	*Deschampsia*	*flexuosa*					2		2	0
9	*Deschampsia*	*media*					2		2	0
10	*Deschampsia*	*wibeliana*					2		2	0
11	*Festuca*	*arundinacea*	22	3	12	1	14	4	48	8
12	*Festuca*	*pratensis*	10	1	16	1	22	3	48	5
13	*Festuca*	*rubra*	55	9	33	2	29	3	117	14
14	*Festuca*	sp.	3				103	1	106	1
15	*Koeleria*	sp.	21		33		29		83	0
16	*Lolium*	*perenne*	49	5	16	11	16	12	81	28
17	*Lolium multifl.* ×	*Fest. arund.*'Perun'						4	0	4
18	*Phleum*	*pratense*			18	1	33	2	51	3
19	*Poa*	*compressa*	8		8				16	0
20	*Poa*	*nemoralis*	4			1	4	1	8	2
21	*Poa*	*palustris*	4				1		5	0
22	*Poa*	*pratensis*	70	10	43	3	29	5	142	18
23	*Poa*	sp.					4		4	0
24	Other species				4				4	0
		Total:	327	32	215	20	424	40	966	92

2. The inventory should have user-friendly functions for people with rather low computer skills.
3. Frequent updating of the above inventory is necessary for effective data processing.

References

Gass, T., R. Sackville Hamilton, K. Kolshus and E. Frison, editors. 1995. Report of a working group on forages. Fifth meeting, 31 March-2 April 1995. Hissar, Bulgaria. European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR). International Plant Genetic Resources Institute, Rome, Italy.

Status of forage collections in Slovakia

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Research Institute of Plant Production, Piešt'any, Slovakia

In Slovakia, attention to collecting, evaluation, and maintenance of plant genetic resources (PGR) has been paid since 1951 in specialized research and breeding centres. Collecting and study of forage crop genetic resources started in the Research Institute of Plant Production (RIPP) in Piešt'any in 1961.

In spite of a long tradition and the need to solve the problems of crop genepools, the united National Programme for PGR, part of the Czech and Slovak Programme, was created and financed only in 1992.

Simultaneously, with the formation of the Slovak Republic as an independent state in 1993, conditions were created for the realization of the Slovak Republic National Programme oriented toward collecting, study and maintenance of PGR. Preparation and implementation of the PGR Programme are financed and supported by the Ministry of Agriculture.

At present, collections are maintained in a decentralized mode, the function of coordination centre being performed by RIPP Piešt'any. Nineteen institutions are involved. The collections contain more than 16 000 samples, including duplicates. In 1996 a new genebank started its operation in Piešt'any. It will ensure the maintenance of the information system and of PGR seed samples for all institutions holding PGR collections.

Slovak institutions dealing with forage genetic resources and/or related activities

1. Research Institute of Plant Production
Piešt'any, Bratislavská 122, 921 01 Piešt'any
Tel. 421-838 722 311, 722 326; Fax 421-838 726 306
Email vurv@bb.sanet.sk

Staff/Position
Dr Timotej Miština, Director
Dr František Debre, PGR Coordinator, Head of PGR Dept.
Dr Jarmila Drobná, Curator, Forages

General activities
Collecting, conservation, documentation, evaluation, and distribution of PGR.

Maintenance of collection
In glass containers with twist
Long-term storage of seeds at –18ºC
Medium-term storage of seeds at 0ºC.

Duplication sites
Not duplicated. In the future, material will be safety-duplicated in the Czech Gene Bank in Prague-Ruzyně.

Availability of genetic resources
Available in limited quantities on exchange basis.

Evaluation status
Characterization and evaluation according to the national descriptor lists.

Documentation status
Passport data and some descriptive data in ISGZS under Fox Pro.

Species	No. of accessions	Species	No. of accessions
Medicago sativa L.	212	*Lotus corniculatus* L.	42
Medicago falcata (L.) Arcangeli	20	*Lotus uliginosus* Schkuhr	2
Medicago × *varia* Martyn	5	*Astragalus cicer* L.	12
Medicago lupulina L.	7	*Onobrychis viciifolia* Scop.	23
Trifolium pratense L.	178	*Anthyllis vulneraria* L.	7
Trifolium repens L.	80	*Melilotus officinalis* (L.) Pallas	5
Trifolium hybridum	8	*Melilotus alba* Medicus	11
Trifolium medium L.	3	*Melilotus dentata* (Waldst. & Kit.) Pers.	1
Trifolium aureum Pollich.	4	*Coronilla varia* L.	1
Trifolium arvense L.	2	*Lathyrus sativus* L.	27
Trifolium dubium Sibth.	1	*Lupinus* spp.	22
Trifolium fragiferum L.	1	**Total**	**674**

2. Plant Breeding Station Levočské Lúky

Breeding station, state enterprise, 054 01 Levoča
Tel. 421-965 427 771; Fax 421-965 427 771

Staff/Position

Dr Vojtech Schwartz, Director
Dr Mária Lorková, Curator

General activities

Collecting, evaluating, documentation, maintenance of genetic resources of grasses and utilization in breeding.

Maintenance of collection

Medium-term storage.

Duplication sites

Not duplicated.

Availability of genetic resources

Available in limited quantity (about 35%).

Evaluation status

Characterization and evaluation according to available descriptors and ongoing for breeding.

Documentation status

Passport data in ISGZS under FoxPro and some descriptive data.

Species	No. of accessions	Species	No. of accessions
Dactylis glomerata L.	197	*Poa pratensis* L.	195
Lolium x *hybridum* Lam.	12	*Poa* spp.	29
Lolium multiflorum Lam.	32	*Agrostis* spp.	79
Lolium perenne L.	228	*Alopecurus pratensis* L.	16
Phleum pratense L.	89	*Arrenatherum elatius* (L.) L. & C. Presl	24
Phleum spp.	7	*Bromus* spp.	1
Festuca arundinacea Schreb.	38	*Cynosurus cristatus* L.	10
Festuca ovina L.	43	*Deschampsia caespitosa* (L.) Beauv.	26
Festuca pratensis Huds.	536	*Trisetum flavescens* (L.) Beauv.	23
Festuca rubra L.	71	Other	12
Festuca spp.	8	**Total**	**1666**

3. Plant Breeding Station Horná Streda

Breeding station, state enterprise, 916 24 Horná Streda
Tel. 421-834 972 21; Fax 421-834 971 67

Staff/Position

Dr Peter Markech, Director

Dr Marta Lazarčíková, Dr Miroslav Vavák, Curator, *Vicia sativa*

Dr Miroslav Vavák, Curator, *Faba vulgaris*

Dr Zdenìk Slaměna, Dr Jozef Štefanka, Curator, *Pisum sativum*

General activities

Collecting, evaluation, documentation, maintenance of genetic resources of legumes and utilization in breeding.

Maintenance and collection

Medium-term storage.

Duplication sites

Not duplicated.

Availability of genetic resources

Available in limited quantity (about 40 %).

Evaluation status

Evaluation according to available descriptors and ongoing for breeding.

Documentation status

Manual passport and some descriptive data.

Species	No. of accessions
Vicia sativa	123
Faba vulgaris	111
Pisum sativum subsp. *sativum* conv. *speciosum.*	103
Total	**337**

4. Grassland and Mountain Agriculture Research Institute Banská Bystrica

Mládežnícka 36, 974 21 Banská Bystrica
Tel. 421-88 732 541; Fax 421-88 732 544

Staff/Position

Dr Stanislav Knotek, Director

Dr Norbert Gáborčík, Curator

General activities

Collecting and maintenance of ecotypes of forages.

5. LEGUMEN, production and commercial company, Piešt'any

Jozefská 14, 921 01 Piešt'any
Tel. 421 - 838 215 23

Staff/Position

Dr L'ubomír Pastucha, Director

General activities

Collecting, maintenance, and breeding of legumes.

Species	No. of accessions
Lathyrus sativus	103
Lathyrus ochrus	2
Lathyrus tuberosus	1
Total	106

6. Slovak University of Agriculture, Nitra

Dept. of Genetics and Breeding, Trieda A. Hlinku 2, 949 67 Nitra

Staff/Position

Dr Ján Brindza, Coordinator

General activities

Collecting and maintenance of ecotypes of *Lotus* spp. and evaluation on chromosome level.

Forage crops genetic resources in F.R. Yugoslavia

Zorica Tomić
Agricultural Research Institute 'Serbia', Forage Crops Centre Kruševac, F.R. Yugoslavia

Yugoslavia is situated between 41°25 and 46°11 N latitude and between 18°26 and 23°01 E longitude. It covers an area of 102 173 km^2, with a population of approximately 11 million people. About 50% of the total area is above 500 m asl while 15% is above 1000 m asl. The country is mainly mountainous with two separate basins, Panonian and Adriatic, and two mountain zones, West and East. Yugoslavia is covered by more than 6 million ha of agricultural land with 60% lowland and 21% pastures. Forage crops on lowland cover very small areas.

Our country is an exceptionally rich source of natural autochthonous genetic resources. This is due to its complex and specific geographical position. It belongs to the Mediterranean basin, which is one of the centres of genetic diversity for a number of plant species. Many cultivated forage crops have their relatives in autochthonous natural meadow communities. All those species show, more or less, a high level of diversity and represent important genetic resources.

Yugoslavia presents a high level of biodiversity and genetic variability. All plant species from temperate and subtropical climate can be grown successfully. As a result of the successful work of the Institutes dealing with the breeding and introduction of foreign cultivars, Yugoslavia possesses rich cultivars of almost all cultivated species. The research work of the Institutes was especially successful with the crops of highest economic importance (maize, wheat, sunflower, sugarbeet). According to the figures of the Federal Commission for the registration of new cultivars, 1055 cultivars with different properties from over 190 cultivated species were registered. From all those species 63 cultivars have been selected, including 23 legumes, 14 perennial grasses, 11 annual legumes and 15 other forage cultivars. So far 917 cultivars of 81 species have been introduced from abroad and released for production, including 44 cultivars of legumes and 54 cultivars of perennial grasses.

The research work on breeding is carried out at the Institute of Agriculture, Novi Sad; the Agricultural Research Institute 'Serbia', Belgrade; the Forage Crops Center, Kruševac; the Center for Agricultural and Technological Research, Zaječar; the Agricultural Faculties of Belgrade and Novi Sad; and the Institute of Agriculture, Podgrorica.

Best results in breeding of forage crops have been achieved in creating cultivars of lucerne, forage beans, sorghum millet and Sudan grass. Less work was dedicated to the breeding of red clover and birdsfoot trefoil, although these two species are most commonly utilized. Fairly modest results have been achieved in the breeding of perennial grasses, in spite of the excellent potential of production and resistance to diseases and pests of autochthonous species.

The Forage Crops Center in Kruševac is one among eight specialized Centers where work on plant breeding, agronomy, utilization and seed production of forage crops was the basic occupation for more than 40 years.

To date, 26 cultivars have been bred: 12 cultivars of legumes (5 lucerne, 5 red clover, l white clover, 1 birdsfoot trefoil), 12 of perennial grasses (3 cocksfoot, 2 tall fescue, 2 red fescue, 2 Italian ryegrass, 1 meadow fescue, 1 timothy grass and 1 tall oatgrass), and 1 cultivar of stock beet. Two cultivars of grasses and two of legumes are being currently tested at the Federal Commission.

Work on the conservation, collecting and utilization of genetic resources of plant and animal species was part of breeding research that has already been conducted on some species.

In 1987 the national policy of ex-Yugoslavia adopted the unique programme establishing the Gene Bank of Yugoslavia. The construction of the Gene Bank started in Belgrade and it is expected to maintain all material from the Institutes that coordinated the work on individual species during the previous breeding periods.

However, after 1992, during the period of economic sanctions, scientific research in Serbia and Montenegro managed to maintain some degree of activity. The conservation and utilization of genetic variability is, however, not possible without a national programme as a strategic, high-priority project. Last year the Federal Institute for plant and animal genetic resources within the Federal Ministry of Agriculture was founded. It covers all activities on genetic resources in Yugoslavia. The construction of the building for the Gene Bank of Yugoslavia will be completed. The unique strategic project, which is to be initiated this year, includes collecting, conserving and characterization of accessions of all plant and animal species of genetic resources in Yugoslavia.

The size of the collection of genetic resources of forage crops, legumes and perennial grasses is presented in Table 1.

Table 1. Status of the National Collections – Gene Bank of Yugoslavia (Agricultural Research Institute 'Serbia', Forage Crops Center Kruševac)

Species[‡]	No. of accessions
Agrostis gigantea Roth.	16
Agrostis stolonifera L.	34
Agrostis capillaris L.	35
Lolium perenne L.	10
Dactylis glomerata L.	5
Trifolium repens L.	49
Trifolium hybridum L.	6
Trifolium pratense L.	19
Medicago sativa L.	63

[‡] For all species: Type of accessions = wild species; Storage conditions = long term; Availability = 100%.

The collection is part of breeding and prebreeding research at the Agricultural Research Institute in Novi Sad (63 accessions of *Medicago sativa*) and at the Center for forage crops Kruševac (49 accessions of *Trifolium repens*, 6 *Trifolium hybridum*, 19 *Trifolium pratense*; perennial grasses: 16 *Agrostis gigantea*, 34 *Agrostis stolonifera*, 35 *Agrostis capillaris*, 10 *Lolium perenne* and 5 *Dactylis glomerata*). Work on germplasm collections for the Gene Bank of Yugoslavia was carried out in the period 1989-92 according to the Descriptor list for forage grasses, CEC/IBPGR 1985. The work included the identification of passport data, collecting data, characterization and preliminary evaluation, multiplication and conservation of samples.

Collecting of autochthonous populations of perennial grasses and legumes was carried out in more than 100 most important localities of the Serbian flora. The characterization included the most important properties: collecting source, status of samples, characterization and preliminary evaluation: site data, plant data; vegetative characteristics: tillering capacity of juvenile plants, vegetative growth habit, leaf width, estimates of herbage yield, winter damage; inflorescence; tendency to form inflorescences, time of 50% inflorescence emergence, uniformity of time of inflorescence emergence, habitat at ear emergence, abundance of inflorescences; site

data; further evaluation, vegetative; total seasonal yield; inflorescence; mean date of inflorescence emergence, leaf width (reproductive), leaf length (reproductive), length of longest culm + inflorescence, seasonal inflorescence production; stress susceptibility; low temperatures, high temperatures, drought, high soil moisture; pest and disease susceptibility; pests, fungi, bacteria, viruses and chromosome number.

Because of high reduction in some accessions, a part of the active collection of the Gene Bank was multiplied last year in the Forage Crops Center in Kruševac. The regenerated seed will be forwarded to the Gene Bank of Yugoslavia.

The strategic project on forage crops that should start this year will be based on new expeditions and collecting of forage crop species which are important for selection. In phytocenoses appearing on large areas of our country, geographic position and climatic conditions resulted in the appearance of large number of associations of different types, from valley, hilly and mountainous to high mountain areas.

In more than 50 plant associations examined, the number of species varies from 19 in association *Caricetum acutiformis-ripariae* to 178 in association *Ononido-Arrhenatheretum elatior*. The greatest number of associations in floristic composition appears with 60-80 species. The largest areas in Yugoslavia are covered with exactly those associations which have about 70 species, and they are: *Festucetum valesiacae, Danthonietum calycinae, Agostio-Danthonietum calycinae, Agrostio-Chrysopogonetum grylli* and *Nardetum strictae - sensu lato*.

In the floristic composition of the mentioned phytocenoses two families are interesting as the initial material in breeding of forage crops, the Fabaceae and Poaceae.

- In the Serbian flora the family Fabaceae has 34 genera among which the most interesting are *Trifolium* with 50 species, *Vicia* 27, *Medicago* 11, with a great variability of subspecies, varieties and forms, and the genus *Lotus* with 4 species.
- In the family Poaceae there are 70 genera among which *Phleum* with 8 species, *Poa* 17, *Agrostis* 6, *Lolium* 5, *Bromus* 14, *Festuca* 21 and *Dactylis* with 3 species are of greatest interest.

The natural ecosystems of meadows and pasture in our country are still conserved. Associations are well developed with stable floristic composition which is confirmed by a large number of species. Such a wide floristic diversity shows the great potential of genetic variability. Very little potential is being used, which makes a good basis for forming a very rich Gene Bank. This potential will be utilized not only by our breeders, but also by ECP/GR.

Finally, our work will in the future depend not only on our wishes but also on how the European Cooperative Programme will accept and involve us in their research and work.

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Duplications in forages collections

On the identification of duplicate accessions

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Introduction

At the fifth meeting of the ECP/GR Working Group on Forages in Bulgaria (31 March-2 April 1995), a subgroup was formed to develop a protocol for identifying duplicate, or at least unduplicated, accessions. The objective is to identify demonstrably unique accessions that are now held only outside their country of origin, so that primary responsibility for their conservation could be assigned. This document presents the conclusions of the subgroup.

We stress that the objective is not to enable rationalization of collections by eliminating duplicates. Although it may seem pedantic to distinguish between identifying duplicate accessions and identifying unique accessions, in fact it is probable that the vast majority of the world's genebank accessions lie between the two states, as we do not have sufficient information to identify accessions unequivocally either as duplicate or as unique, so that 'not demonstrably unique' is quite different from 'duplicate'. The protocol presented here covers only the first step in the expensive, painstaking procedure of identifying duplicates with sufficient precision to permit their elimination.

Historical and biological duplicates

We distinguish between historical duplicates and biological duplicates. Two accessions are historical duplicates if they originated from the same original collected or bred material without undergoing deliberate selection by breeders. They are biological duplicates if they have been demonstrated to have the same genetic composition. Identification of historical duplicates should not normally depend on characterization and evaluation data (except to confirm historical duplicity as discussed below), and relies primarily on passport data. Conversely, identification of biological duplicates requires the most comprehensive possible set of characterization and evaluation data.

Knüpffer (1989) and van Hintum and Knüpffer (1995) have developed a more comprehensive terminology based on the degree of similarity between accessions, and have considered the consequences for rationalization of collections. However, for the purposes of this document the simpler classification is retained, because of the resulting distinction in the roles of passport and characterization data in seeking duplicates.

Historical duplicates may be biologically distinct. During their different regeneration histories, since becoming two accessions they will have undergone different genetic drift; they may have been subjected to different natural selection; one or both may have been contaminated with alien pollen or seed; one or both may even have been incorrectly labelled and so be totally unrelated. They may even have diverged through genetic drift during the initial subsampling to generate two

accessions from one. Biologically distinct accessions should both be maintained in a collection even if they are historically duplicates.

Conversely, biological duplicates may be historically distinct, at least within the history of their conservation in genebanks. For example, different collectors may have collected from the same site, or several samples may have been taken from a region of uniform populations. For maximum efficiency of conservation, identified biological duplicates should be pooled, not maintained in a genebank, regardless of whether they are historically duplicate.

Therefore biological duplication, not historical duplication, is the only acceptable criterion for rationalizing collections by eliminating (pooling) duplicates.

We also distinguish between Possible Historical Duplicates (PHDs) and Confirmed Historical Duplicates (CHDs). Two accessions are considered PHDs if they have identical passport data, or they are at least 'matching' in some sense. Identity of passport data is not sufficient to confirm historical duplication. Mistakes in labelling bags and plots, in interpretation of data supplied, or in data entry can cause the same passport data to be associated with different accessions, and true historical duplicates to have different passport data. Indeed it may be impossible to confirm historical duplication. Detailed tracing of their histories will not detect all errors. Testing whether they are biological duplicates can be suggestive: major qualitative differences between the two accessions would indicate they are not historical duplicates but one or both have been mistakenly labelled, whereas smaller quantitative or zero differences would suggest probable historical duplication.

Identification of biological duplicates is itself costly and time-consuming, particularly as it involves more than conventional characterization for the following reasons:

1. Resource limitations restrict conventional characterization and evaluation trials to a small number of characteristics, and it is probable that most accessions that look similar on the basis of these characteristics do actually differ in other characteristics. Since the need for long-term conservation of genetic resources arises from the need to satisfy unknown future demands for unknown genes, it would not be appropriate to identify accessions as biological duplicates unless they are shown to be identical for many more characteristics than measured usually. A wide range of morphological, physiological, biochemical and molecular characters should be used.
2. The usual approach in statistical analysis, which is to accept that two accessions are the same unless there is strong evidence (usually with 95% certainty) to the contrary, is not appropriate for genetic resources collections: rather, we need more positive evidence that they are the same before accepting them as the same.
3. Most trials need only detect major differences and so need only low replication. To decide whether two accessions are biological duplicates requires higher sensitivity and therefore higher replication than normal characterization trials.

Thus identification of biological duplicates requires considerably more detailed, painstaking characterization than is usually undertaken, and is considered prohibitively expensive.

Scope of the exercise

The above discussion demonstrates that to confirm historical duplication and to identify biological duplicates is extremely laborious and expensive, and would require a major research programme for each crop. On the other hand, preliminary identification of PHDs is more achievable.

It must be stressed that, corresponding to this limitation, the overall objective is not to seek to eliminate duplicate accessions, but rather to identify those accessions that are demonstrably unique. Since primary responsibility for the maintenance of an accession lies with the genebank in the country of origin of that accession unless it no longer exists in that country, the most important and urgent output of the exercise will be identification of unique accessions that are no longer stored in their country of origin and, in particular, demonstrably unique accessions that are held only outside their country of origin.

However, where funds are very restricted this could be used to reduce the current costs of maintaining collections by relegating one of each PHD pair to long-term storage only, where it is 'mothballed' for future use.

Principles underlying identification of PHDs

Ideally, all genebanks would maintain full and correct passport data in the same database format and transfer it electronically on donating seed. Then passport data of all PHDs could be identical. In practice, their passport data are usually not identical.

It is not the purpose of this document to analyze fully what has happened, nor to recommend a protocol for distributing and maintaining passport data. However, to establish a protocol for identifying PHDs, it is necessary to develop criteria for deciding when two sets of passport data 'match' even though they are not identical. To do so we must consider the various ways in which differences could arise in the passport data of PHDs, as follows.

The donor may have:

- corrected or added new passport data since making the donation, or
- failed to supply the donee with all passport data when donating the accession.

The donee may have:

- had to modify passport data to conform with the data format of his own database
- corrected obvious spelling or grammatical errors
- failed to enter all supplied passport data on his database
- translated to another language, possibly including translation of names
- changed the passport data to conform to his own standards for transliterating, abbreviating words, conventions for entering location data
- made unintentional mistakes in data entry. A relatively low error rate may be expected in parts of text fields, where linguistic rules for spelling enable a certain amount of self-validation. This does not apply to entire text fields, and higher error rates occur in punctuation, spacing, names, abbreviations, and words with alternative spellings (e.g. American vs. British spellings). The same higher error rate occurs in coded and numeric fields.

Various procedures can facilitate detection of some of these differences, defining 'matched' accessions even where passport data are not identical. These include lists of synonyms, differences between spelling conventions, differences between transliteration conventions, and cross-referencing similarities of different fields.

However, given the limited value of identifying PHDs in terms of rationalizing collections, it is proposed that we do not even develop a full protocol for identifying PHDs. Instead, we propose a still simpler protocol for partial identification of PHDs using only limited fields from the passport data, which achieves the same objective

of assigning accessions to primary holders but with relatively little investment of time and resources. A suggested protocol is presented in Appendix II of this report.

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Safety-duplication of germplasm collections in Europe

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Introduction

Duplication of accessions for safety reasons is an essential component of rational germplasm management. If safety-duplication is undertaken effectively, it insures against loss from natural disasters, neglect, human error and civil strife (IPGRI 1995, 1997). For the period between 1981 and 1995, the genebanks of the CGIAR report 66 cases where germplasm was restored to a total of 38 countries (SGRP 1996). The Seeds of Hope project in Rwanda (Scowcroft 1996) and the restoration of rice germplasm in Monrovia, Liberia emphasize the value of restoring lost germplasm as part of international efforts to recover agricultural research capacity and agricultural systems in war-torn countries (Richards and Ruivenkamp 1997). In Europe, the restoration of Albanian forages collections, which were recently lost, will depend on the extent to which Albanian material had been duplicated outside the country.

Safety-duplication has received attention during a recent external review of the CGIAR genebank operations (SGRP 1996). The resulting Recommendation 13 reads as follows:

> "Centres should give high priority to the regeneration and multiplication of accessions that have not yet been duplicated off-site and all germplasm designated under the FAO/CGIAR Agreements should be placed for safety-duplication in off-site genebanks as soon as possible"

According to the Report on the State of the World's Plant Genetic Resources for Food and Agriculture, prepared for the International Technical Conference on Plant Genetic Resources (Leipzig, Germany, June 1996), 85% of the countries submitting Country Reports stated that their collections were only partially or not at all safety-duplicated. Lack of data on individual accessions is currently preventing a comprehensive assessment of the degree of safety-duplication or redundancy between collections (FAO 1996a). Consequently, the FAO Global Plan of Action acknowledges the importance of replicating and storing conserved material in long-term facilities, as part of the strategy to sustain existing *ex situ* collections. A recommendation is also made that country formalize agreements to safeguard diversity in *ex situ* collections in conformity with applicable international agreements, since this would allow countries wishing to do so to place collections in secure facilities outside their boundaries (FAO 1996b). This recommendation is particularly relevant to some smaller countries in which full-fledged *ex situ* conservation operations may not be feasible.

Rationalization and safety-duplication of European collections

An important objective of the Priority Activity 5 of the GPA (Sustaining existing *ex situ* collections) is to increase the efficiency of conservation activities and to reduce unnecessary duplication of efforts (FAO 1996b). Sharing of responsibilities for the conservation of strategically important resources requires a great deal of confidence between partners. Europe is a region with large differences between countries and a history including numerous conflicts. Nevertheless, the past collaboration within the European Programme for Crop Genetic resources Networks (ECP/GR), the recent geopolitical changes in Europe, the interdependence between countries and the financial difficulties of genebanks throughout the region would be conducive to the

development of a more comprehensive system for sharing conservation responsibilities for PGRFA within the region.

Generally, the level of duplication existing within and especially between genebanks in Europe is considered relatively high. Besides safety-duplication, such duplication results from exchanges between genebanks, acquisitions of the same accession, joint collecting missions, repeated incorporation of an accession into the same collection, erroneous identification, etc. (Knüpffer *et al.* 1997). Duplication occurring within a collection, if not specifically for safety reasons, is generally undetected and undesirable. The resulting increase in the cost of maintenance and evaluation unnecessarily draws upon the genebanks' scarce resources. Although the undesired and undocumented duplication of collections in Europe is high, many valuable accessions such as landraces and wild relatives of crops have never been safety-duplicated.

The identification of duplicates in a collection is a complex exercise. It first requires the definition of what will be considered as an undesirable duplicate as opposed to what is considered as unique. Detecting the duplicates then involves various steps of passport data analysis followed by verification through morphological and/or molecular techniques (Knüpffer *et al.* 1997). Although laborious, this exercise ultimately contributes to a more rational management of germplasm by reducing redundancies and, in some cases, by identifying the most original sample among a set of duplicates.

This rationalization exercise is obviously more effective if coordinated throughout the existing collections of one or more regions. International efforts can then be directed to the evaluation and utilization of the most original accessions, independently from their storage location. With this in mind, a comprehensive exercise is currently being undertaken within the frame of ECP/GR to update and then analyze the European Central Crop Databases (Gass *et al.* 1997).

The Steering Committee of ECP/GR and a number of ECP/GR Working Groups have begun to develop the concept of an origin-based sharing of conservation responsibilities known as European Collections. This concept is analogous to the decentralized national collections being developed in Spain and France. Such a system of sharing responsibilities is not intended to preempt on the negotiations by the FAO Commission on Genetic Resources for Food and Agriculture leading to a revised International Undertaking on PGRFA nor is it intended to determine the ownership of accessions or germplasm collections. Rather it would promote a regional trusteeship of genebanks over collections and allow national programmes to more effectively prioritize their conservation effort. The regional trusteeship could be extended to a global trusteeship if the relevant international negotiations evolve accordingly.

A key element of the proposed system is confidence among countries regarding:

- the quality of conservation and regeneration procedures applied to germplasm conserved under the Trusteeship Agreements, and
- the access to germplasm maintained under these agreements.

Both of these elements depend to a very large extent on goodwill and on transparency of procedures. ECP/GR could provide a "safety net" to these concerns: (1) by establishing a task force or committee which would peer-review collections in genebanks having accepted trusteeship responsibility, and (2) by ensuring that safety-duplicates of designated material are maintained in a country other then the one where the original genebank is located.

Prioritizing safety-duplication

It may not be possible that a genebank implement all at once the safety-duplication of all its accessions, if this operation has previously been neglected. Although all the accessions worth conserving should be safety-duplicated, it may be necessary to follow

a scale of priorities. In establishing this scale of priorities the genebank or the national programme give consideration to a number of elements:

- known existence or not of duplicates in other genebanks / countries
- the potential value of the material as determined by the data associated with each accession, such as the occurrence of proven or likely sources of resistance and other valuable traits
- the origin of the accession, assuming that each country has the primary responsibility for conserving material originating (collected, bred or selected) on its territory
- the origin of the accession, assuming that the genebank / country wishes to contribute towards holding in trust material originating from another country where the safekeeping or access is uncertain.

Making safety-duplication safe

When safety-duplication is based on a bilateral agreement between two genebanks or between two countries, the storage conditions and other quality criteria are usually mentioned in the agreement signed by the parties. At the regional level, however, safety-duplication is generally monitored on the basis of statements made by genebank curators and is rarely assessed against jointly agreed quality standards.

The following criteria are suggested as elements of an effective safety-duplication arrangement.

Long-term storage conditions

Since the safety-duplicate should 'outlive' the original accession, it should be stored under conditions allowing at least the same duration and quality as the original collection. The event prompting the replacement of the safety-duplicate would in this case be the loss of viability and consequent regeneration of the original sample. International standards for conservation of seed collections have been published by FAO / IPGRI (1994).

Off-site duplication outside the country

While this is not an obligation, it is an important criterion if the original collection is seen as an integral part of the international and multilateral effort to conserve genetic resources. Duplication outside the country constitutes a warranty against disruptions which might occur to the genetic resources programme at the national level. Beyond institution-related disruptions, most countries in Europe have experienced civil strife or war during the past 50 years – a rather short time perspective when dealing with conservation of plant genetic resources. Moreover, important benefits can accrue from the collaboration and mutual trust that is implied in the exchange of services between countries to mutually conserve safety-duplicates of valuable collections.

Duplication under formal agreement

Formal agreements for safety-duplication create longer lasting frameworks for cooperation between the concerned genebanks or national programmes. In this way, standards for conservation can be defined and responsibilities clearly assigned. The agreement allows a registration of the information for the public and the international community. This is also useful for the institutions undertaking the agreement as it clarifies their respective mandates and facilitates a longer-term commitment to honoring the agreement.

A bilateral agreement, recently established between the Nordic Gene Bank (NGB) and the Institute of Biology (IB), Salaspilis, Latvia is given in Annex 1. This agreement places all the responsibility for appropriate management of the accessions on to the

owner of the seed (IB). The NGB makes storage space available for the duplicated seed and covers the cost of conserving it under long-term conditions. Relevant accession-related data are also safety-duplicated under the same agreement. The 'black box' arrangement implies that the seed and related data will not be used or distributed, but simply stocked for safety reasons. The owner (IB) maintains complete juridical control of the 'black box'. The requirement of 6 months' notice before any change can be made to the agreement makes it possible to find alternative solutions in case the two parties decide to denounce their commitment. The safety-duplicates stored under black box agreement are not listed as part of the germplasm holdings or the index seminum of the hosting genebank.

Safety-duplication in the Forages Working Group

The issue of safety-duplication of collections of forage species was addressed by the ECP/GR Forages Working Group in its early stages (IBPGR 1989) . During its fourth meeting it was recommended that database officers identify apparently unduplicated accessions and then contact curators of these accessions, inviting them to start effective duplication by sending as many accessions as seem practical to another long-term storage of their choice (IBPGR 1993).

Members of the Working Group have since regularly reported on the safety-duplication status of the collections in their country. To date the level of documented safety-duplication is still extremely low (Table 1). This is due to:

- the assumption that unintended duplication needs to be identified before safety-duplication is undertaken
- the assumption that exchange of germplasm and sharing of material among partners after a collecting mission constitute sufficient guarantee that the genetic diversity is also conserved in another genebank
- the lack of awareness of the simplicity and low level of cost of 'black box' duplication arrangements
- uncertainty among genebanks with regard to the highly politicized international negotiations on PGR access and sharing of benefits.

A number of European genebanks have expressed willingness to host safety-duplicates of forages collections (see Appendix V of this report).

Conclusion

Although duplication of collections for safety reasons is an essential element of an effective conservation strategy, European genebanks have to date given low priority to this activity. While a number of reasons can be mentioned to explain this situation, the increased awareness and utilization of 'black box' arrangements will probably facilitate more rapid progress in the future.

When applied along with standard long-term conservation conditions, duplication in a different country from the original collection, and under formal agreement, the 'black box' arrangements will contribute to strengthened collaboration and enhanced mutual trust. Such measures also play an important role in a multilateral system of decentralized "European collections" such as the one currently being discussed within the frame of ECP/GR.

Table 1. Level of safety-duplication of forages collections as reported in the ECP/GR Forages Working Group meetings

Belgium	55 *Lolium* accessions sent to RAC, Changins, Switzerland.
Bulgaria	The collections have not been safety-duplicated.
Cyprus	Accessions of forage legumes have been safety-duplicated at ICARDA, Syria and Bari, Italy.
Czech Republic	Accessions of grasses have not been safety-duplicated under long-term conditions. Approximately 30% of accessions of legumes have been safety-duplicated.
France	Safety-duplication is undertaken within the country.
Germany	The collections have not been safety-duplicated
Netherlands	Safety-duplication is being carried when accessions are regenerated. Full safety-duplication is expected to be reached by the year 2000.
Nordic Countries	62 accessions of different forage species have been safety-duplicated in the Svalbard Islands and NGB is formally accepting safety-duplicates from Latvia and Lithuania.
Slovakia	No safety-duplication has been undertaken yet. A reciprocal safety-duplication agreement with RICP, Prague, Czech Republic is in preparation.
Spain	The forages collections are partly duplicated within and outside the country (Australia, USA).
Switzerland	RAC, Changins has sent 10 accessions of *Dactylis glomerata*, 19 of *Festuca pratensis* and 10 of *Festuca arundinacea* for safety-duplication to R.v.P., Merelbeke, Belgium.
Turkey	Safety-duplication is done within the country, at the Field Crops Central Research Institute, Ankara, Turkey.
UK	All IGER collections have been safety-duplicated within the country.

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Annex 1. MEMORANDUM OF UNDERSTANDING

This Memorandum of Understanding (MOU) is entered into and executed by the Nordic Gene Bank (hereinafter referred to as NGB) and the Institute of Biology (hereinafter referred to as IB).

I. Purpose

The purpose of this MOU is to establish, within the framework of the Nordic-Baltic cooperation and in connection to the NGB base collection, a Safety Duplicate Collection (hereinafter referred to as SDC) of seed material of agricultural and horticultural crops originating in Latvia, having obtained the status ACCEPTED in the base collection of the IB.

II. Statement of common interest

The NGB (Alnarp, Sweden) is a Nordic institute under the auspices of the Nordic Council of Ministers with the regional mandate to conserve *ex situ*, on a medium to long-term basis, genetic material of agricultural and horticultural crops particularly adapted to Nordic conditions.

The IB is a research institute which co-ordinates conservation of agricultural and horticultural crops in Latvia as well as managing active, or short- to medium-term, collections of seed material stored *ex situ*.

III. Statements of the agreement

i. Of relevance for NGB:

§1 NGB accepts the responsibility of conserving *ex situ* under long-term conditions, as a 'black box' arrangement within the storage facilities at Alnarp, a SDC to be delivered by the IB.

§2 The SDC will be stored in accordance with standard NGB procedures.

§3 NGB will not use or distribute any seed material to third party from this SDC without a written consent of the IB.

§4 The cost of conserving this SDC will be covered by sources adrninistered by NGB.

§5 In a situation of emergency all measures will be taken by NGB to maintain the safe storage of the deposited material.

§6 In case of accidents or any other event that may inflict upon the viability, germinability, or availability of the deposited seed, NGB will not be liable to pay any damages to the IB.

ii. Of relevance for the IB:

§7 The IB is responsible for all seed management activities (threshing, drying, packing, germination tests, etc.).

§8 The IB accepts to deliver a recornmended number of 5000 high quality seeds per accession to be included in the SDC. All shipments shall be accompanied with a Phytosanitary Certificate issued by the Plant Quarantine Service in the country of the IB.

§9 The IB further accepts the responsibility of supplying NGB with a safety duplicate of computerized passport and relevant management data pertaining to each stored accession.

§10 Decisions regarding the inclusion or removal of accessions from the SDC will be taken by the IB within the scope defined in Section I. Purpose.

iii. Of relevance for both:

§11 The material deposited in the SDC at Alnarp is the property of the sovereign State of Latvia.

§12 Upon notice, the IB has the right to inspect the SDC at any suitable time.

§13 This MOU may be modified or discontinued at the request of either party.

§14 Requests for termination or any change to the MOU shall be submitted to the other party for consideration not less than six (6) months prior to the desired effective date of termination.

§15 This MOU has indefinite duration, but shall be reviewed once every five (5) years for relevancy.

Signed:	Alnarp, 8 January 1997	Salaspils, January 1997
		
	The Director Nordic Gene Bank Currently: Eva Thorn	The Director Institute of Biology Currently: Gunars Andrusaitis

Standards for regeneration

The regeneration of accessions in seed collections of the main perennial forage grasses and legumes of temperate grasslands: background considerations

N.R. Sackville Hamilton
Institute of Grassland and Environmental Research (IGER), Aberystwyth, UK

The main protocol for regeneration is presented at Appendix III of this report. It does not cover annual forage grasses and legumes, or apomicts such as some *Poa* spp., for which no protocol is currently available. The protocol is based on the Decision Guide for Regeneration (Sackville Hamilton and Chorlton 1997), which should be referred to for additional discussion. This section presents some further background details.

Decisions for regeneration protocols represent a compromise between maximizing the number of accessions that can be regenerated each year within available resources, and maximizing the genetic integrity of accessions. The large backlog of accessions in need of regeneration, currently being experienced by most genebanks, suggests a need to relax the stringency of regeneration procedures in order to increase regeneration capacity. However, this will cause a more rapid deterioration of genetic integrity. If stringency is relaxed too far in the attempt to regenerate all accessions as rapidly as possible, the total diversity conserved may be less than if fewer accessions are regenerated under more stringent conditions. Such excessive relaxation of stringency is unacceptable.

An important element of the regeneration protocol is based on the interaction between base and active collections as recommended in FAO/IPGRI Genebank Standards (1994). The base and active collections need not be physically distinct entities, and indeed it has been argued (Linnington and Smith 1987) that they should not be. Nevertheless in the majority of genebanks they are kept as distinct collections under different conditions. The regeneration protocol therefore assumes that they are physically distinct: it will be necessary to revise the protocol in the future if genebank standards are revised to keep base and active collections as a single entity.

According to the above Genebank Standards, the base collection should be maintained under optimal conditions for long-term storage, primarily for conservation. It should not be used for distributing seed. Enough seed should be stored in the base collection to ensure that there is always sufficient quantity to meet demands for its use, so that seed in the base collection should need regeneration only when it loses viability.

Seed stocks in the active collection should be replenished from seed stored in the base collection. Preferably this should always be the case, but according to Genebank Standards an acceptable alternative is to replenish stocks from remnant seed in the active collection for up to three out of every four regeneration cycles. Given the inevitably high rate of loss of genetic integrity of forage species, this 'acceptable alternative' is here regarded as unacceptable. These recommendations have the dual advantage of (a) preventing the accumulation of losses of genetic integrity in the active collection through successive regeneration cycles, and (b) ensuring that the most critical regeneration cycles for conserving genetic integrity (i.e. regenerating the base collection) are limited to one every 100 years (for most forage species) or so.

The second major consideration in developing the regeneration protocol was the impact of loss of genetic integrity on the distinctness of accessions. There are three

primary causes of loss of genetic integrity: drift, selection (natural and artificial, conscious and unconscious), and contamination with alien genes (through alien pollen, alien seed, alien plants, or even through incorrectly identifying and labelling accessions).

Drift tends to increase the distinctness of accessions. Provided random drift is independent of initial population mean, the expected genetic variance among accessions after regeneration is the sum of their genetic variance before regeneration and the variance due to drift. In addition, drift is greatest when population size is small, which tends to reduce genetic variance within accessions and thus further increase the apparent distinctness of accessions.

In contrast, convergent selection in a uniform regeneration environment reduces not only the distinctness of accessions but also the genetic variance within accessions. Contamination further reduces distinctness of accessions. The combined action of convergent selection and contamination together is worse than the sum of their effects, and potentially can eliminate all diversity between accessions. Therefore, drift is considered relatively unimportant compared with selection and contamination. Wherever this requires a compromise, decisions have been made that minimize the effects of selection and contamination even where this means allowing drift to increase.

Most perennial forage grasses and legumes are obligate outbreeders, and so display high genetic variance within populations, high potential for genetic changes by drift and selection during regeneration, and present a high risk for cross-pollination between regeneration plots if they are not adequately isolated. In addition, many of them are conspecific with wild or feral species that may persist naturally on the paths and other habitats in and around regeneration plots, and so present risks for contamination with alien plants, seed and pollen. In addition, they are long-lived clonally propagated perennials: such species typically display exceptionally high variation in fecundity between plants in a single population (Fig. 1). High variation in fecundity implies a corresponding potential for rapid genetic changes in response to selection pressures. All of these factors combine to make the perennial temperate forages present a greater challenge for regeneration than any other crop group. The regeneration protocol reflects this in the recommended high stringency of regeneration conditions.

Manual pollination would be ideal for the maintenance of genetic integrity of these species. However, because of the small seed size of most of the species and the large numbers of seed required, this labour-intensive option is not considered appropriate in relation to the resources available.

The recommended conditions for prevention of contamination with alien pollen are more stringent than currently used by some genebanks. This reflects not only the adverse impact of contamination on genetic integrity, but also a more cautious interpretation of the literature on pollen flow.

The majority of literature on pollen flow describes unidirectional flow from one source of alien pollen to a receptor plot. In a regeneration field, most plots are surrounded on all sides by potential sources of alien pollen. Contamination rates at a given distance from sources of contamination should be expressed as all-directional contamination rates, i.e. the unidirectional contamination rate multiplied by the circumference of the circle. This means real contamination rates are not only higher than usually described, but also decrease less with distance.

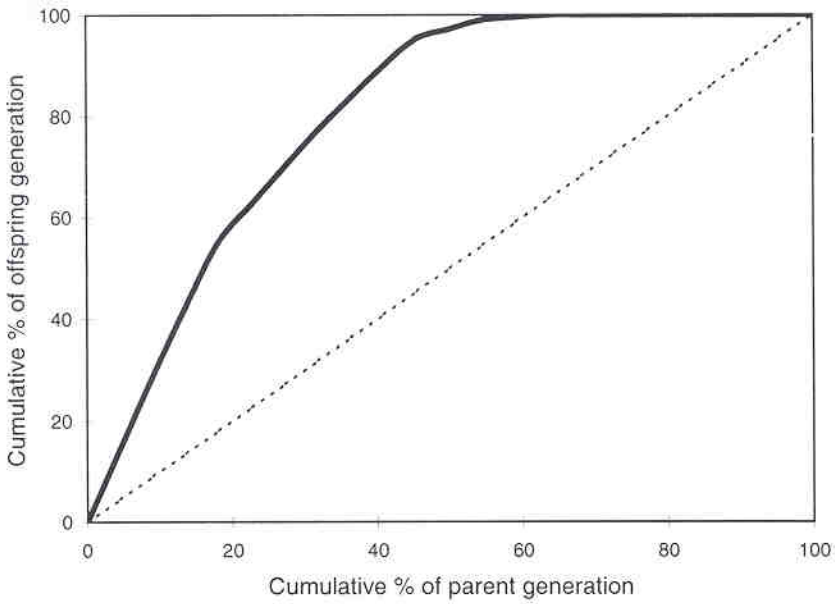

Fig. 1. An example of the inequality of fecundity among plants from a single population of *Lolium perenne*. Plants are ranked in order of fecundity, and the cumulative total fecundity plotted on the y-axis. The dotted line shows the ideal 1:1 relationship where all plants have equal fecundity. The solid line shows actual data from one regeneration plot, and shows that the majority of the offspring generation is produced by a small proportion of the parental generation.

In addition, contamination rates are highly variable, and skewed with the maximum contamination greatly exceeding the mean. Figure 2 shows an example for unidirectional contamination rates in *Lolium perenne* L. (from Giddings *et al.* 1997). Even at 80 m from the source, alien pollen counts can be up to 20% of their value at the source, although the mean is very low. Maximum all-directional contamination is correspondingly higher. It is considered inappropriate to base isolation distances on mean contamination rates when the maximum can be so much higher than the mean.

Contamination in the insect-pollinated legumes shows additional complexities relating to the foraging behaviour of pollinating insects. Goplen *et al.* (1972) found high unidirectional contamination rates in *Melilotus* even 1.5 km from the source in the absence of a barrier crop (Fig. 3). With an intervening barrier crop of oilseed rape in flower, unidirectional contamination was reduced to well under 1%. The presence of a barrier crop was of much greater importance than the isolation distance.

Even with a barrier crop, there was significant contamination. Contamination rate was highest at the near edge of the receptor plot, decaying to near zero at around 15-20 m from the near edge (Fig. 4). The same pattern of contamination was apparent whether the near edge of the receptor plot was located 46 m or 389 m from the source of alien pollen (Fig. 5).

The implication of these results is that insect pollinators fly as far as they need to find a flower but no further. They express preferences for the type of flower they visit, so the most effective barrier crop will have flowers identical to the plot being regenerated.

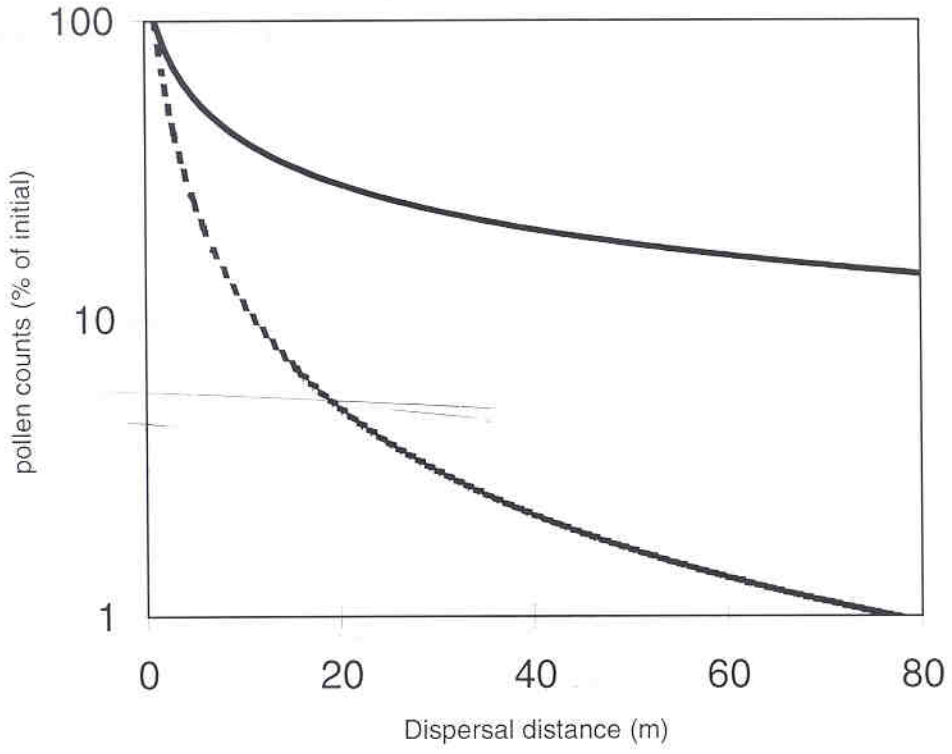

Fig. 2. Pollen dispersal and its uncertainty in *Lolium perenne*. The solid and dotted lines are respectively the maximum and minimum relative pollen counts one direction from a pollen source. Data from Giddings *et al.* (1997).

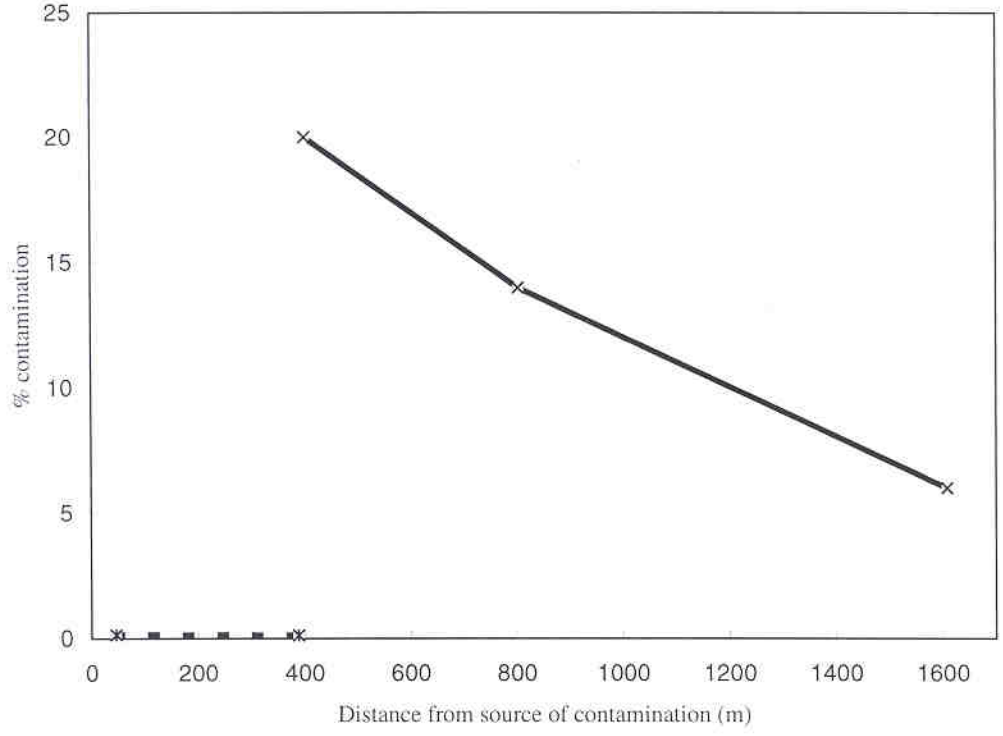

Fig. 3. Effect of isolation distance on pollen contamination in *Melilotus*. Key: dotted line – with intervening rape crop between the test plot and the source of alien pollen; solid line – with no intervening rape crop. Data from Goplen *et al.* (1972).

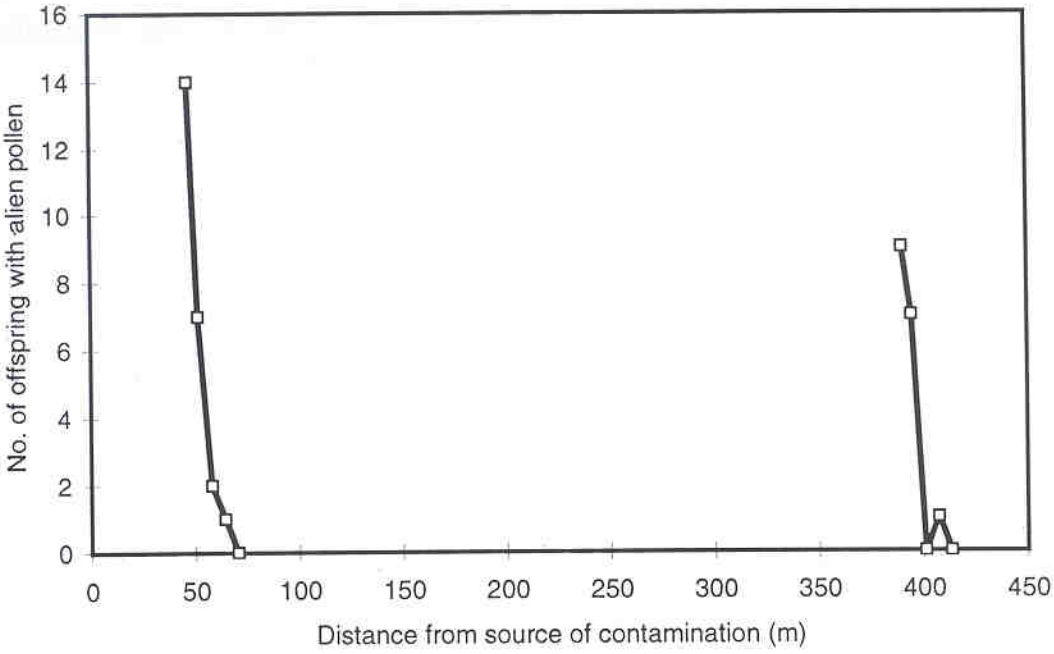

Fig. 4. Effect of isolation distance on contamination in two plots of *Melilotus*, respectively 46 m and 389 m from the source of contamination. Data from Goplen *et al.* (1972).

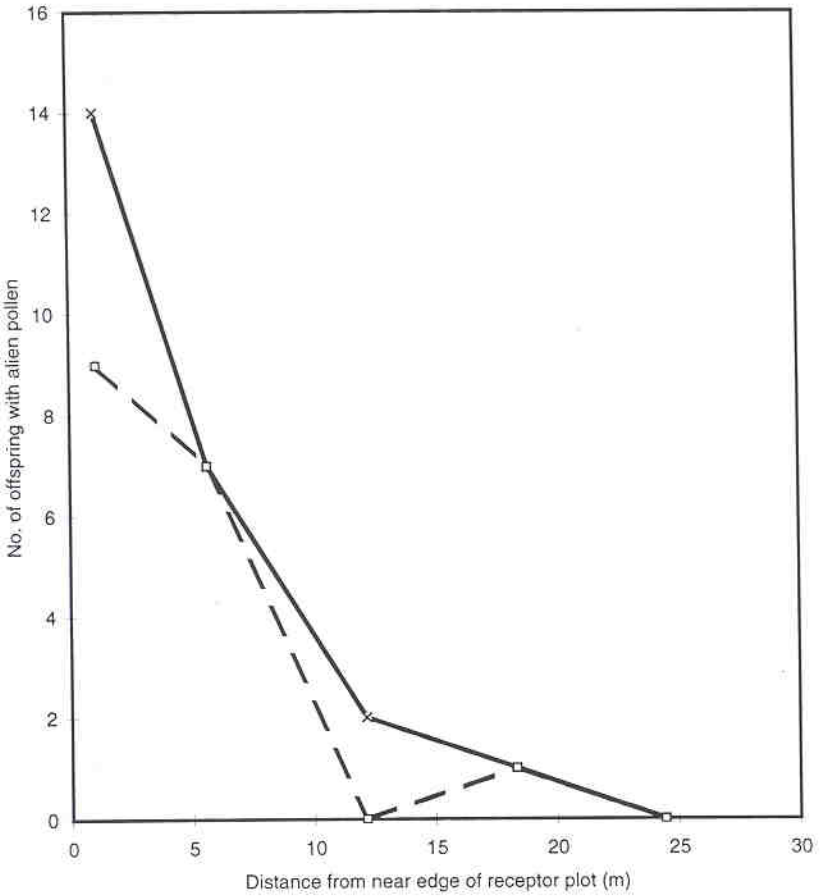

Fig. 5. Effect of isolation distance on contamination in two plots of *Melilotus*. Key: solid line – near plot that is 46 m from source of contamination; dotted line – near edge of plot that is 389 m from source of contamination. Data as for Figure 4.

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Collecting activities

Forage collecting activities in Bulgaria, 1995-96

Siyka Angelova
Institute for Introduction and Plant Genetic Resources, Sadovo, Bulgaria

Year	Region	Type of sward	Collected species	No of items
1995	Northern Bulgaria: Stara planina, Danube plain, Dobrudja, North Black Sea	natural pastures and meadows, forests, pathways, seaside	*Lolium perenne* L.	11
			Dactylis glomerata L.	4
			Agropyron pectinatum (Bieb.) Beauv.	3
			A. cristatum Auct.	2
			A. brandzae PantEu & Solacolu	1
			Medicago falcata (L.) Arcangeli	4
			Trifolium repens L.	6
			Trigonella coerulea (L.) Ser.	2
			Onobrychis arenaria (Kit.) DC.	4
			Vicia lutea L.	3
			V. narbonensis L.	2
1996	Rhodopi mountain eastern/mid, Besaparski hills, Strandja mountain	natural meadows and pastures, pathways	all grass species	48
			Vicia incisa M. Bieb.	2
			V. hybrida L.	2
			Medicago rhodopea Velen.	1
			Onobrychis degenii Dörfl.	1
			Trifolium constantinopolitanum Ser.	1

Forage collecting activities in the Czech Republic, 1995-96

Magdalena Sevcíková
Grassland Research Station, Zubrí, Czech Republic

		Number of collected accessions			
Year	**Region**	**Grasses**	**Legumes**	**Meadow dicots**	**Participation**
1995	Ceske stredohori	149	4		GRS Zubri
1995	S Moravia		246	144	RIFC Troubsko
1995	Krkonose	201	56	47	GB Prague RIFC Troubsko GRS Zubri
1996	NE and SE Moravia	62	2		GRS Zubri 2 Japanese Institutes
1996	S Moravia		137	85	RIFC Troubsko
1996	Orlicke hory	134	60	38	IHAR Radzikow GB Prague RIFC Troubsko GRS Zubri

Collecting activities in Germany, 1995-96

Evelin Willner
IPK-Genebank, Aussenstelle Malchow, Malchow / Poel, Germany

1995:
We collected in Germany in the Altmarkregion at old grassland sites (pastures or meadows), where we could find ecotypes, mainly of the following species:

Species	Number of accessions
Dactylis glomerata L.	34
Festuca pratensis Huds.	23
Lolium perenne L.	47
Phleum pratense L.	19
Poa pratensis L.	16
other species	170
Total	**309**

We sampled mainly clone plants; less frequently, seeds.

In 1996 and 1997 we evaluated this material (primary evaluation); after that we will multiply the valuable genotypes. So we will have next year seeds for delivery to users and some information for our database.

1996: collecting mission in Croatia
A scientific collecting mission for plant genetic resources was undertaken in collaboration with the Croatian genebank (Agricultural University of Zagreb) and the Arche Noah (society of maintenance of crop plant diversity) of Austria.

From 17 September to 1 October 1996 we collected in four different areas (two mountain regions, two levels) of north and east Croatia:

I.	Zumberak	(400-500 m asl)
II.	Slavonien	(80-150 m asl)
III.	Lonsko Polje	(0-80 m asl)
IV.	Zagorje	(150-400 m asl)

With help from local experts and thanks to the good preparation and organization of Ms. Papes-Mokos, we collected old cultivars, landraces or wild materials (438 accessions) of several crop plants:

Cereals	43
Vegetables	128
Legumes	98
Spices	43
Fodder crops (legumes, grasses)	71
Other crops	55

All plant samples will be reproduced in Austria (except grasses) and Germany (in Malchow: grasses: in Gatersleben: cereals, legumes, vegetables, spices and others) and a smaller part of cereals, vegetables and legumes also in the Croatian genebank.

Collecting grass genetic resources in Hungary

Lajos Horváth [1] ***and An Ghesquiere*** [2]
[1] Institute for Agrobotany, Tápiószele, Hungary
[2] Dept. Plant Genetics and Breeding (DvP), Melle, Belgium

The social and economic changes in the beginning of the 1990s had some radical effects on the Hungarian agriculture, and among them a significant decline in the animal husbandry production, the number of livestock – including cattle and sheep – decreasing radically too. These circumstances resulted in very considerable changes in the former ecosystem of the Hungarian pastures and meadows.

Up to the end of the last decade the practical culture of the Hungarian grasslands had been characterized by heavy use or even overgrazing or overmowing. Because of the rapid decrease in the number of livestock this situation changed greatly and a lot of grasslands remained unused year after year. There is no doubt that the lack of grazing or mowing causes irreversible changes within the cultivated plant association of these territories and those elements which have the best adaptation to intensive use disappear from the plant community. Realizing the direct danger of the genetic erosion, the Institute for Agrobotany organized some collecting expeditions in recent years, to rescue the still-available remains of these endangered grass genetic resources. The most important are the two international collecting trips, undertaken jointly with DSV (Germany) and RvP, Merelbeke (Belgium) in 1992 and in 1996. Table 1 summarizes the results of these two trips. The number of accessions is distributed over the different species found during these collecting trips in East Hungary.

Changes in the occurrence of the most important species are shown in Table 2. Although the collecting sites were not the same within the surveyed countryside in the two collecting years, on an average an obvious decrease can be observed in the frequency of the more valuable forage grasses. After regenerating and testing the accessions, the material will be available to interested persons.

Table 1. Number of grass accessions (by species) collected in East Hungary in 1992 (31 collecting sites) and in 1996 (36 collecting sites) by RCA (Institute for Agrobotany, Tápiószele, Hungary)

Species collected	1992	1996
Agrostis alba auct. non L.	1	8
Agropyron pectinatum (M.B.) P.B.	0	1
Alopecurus pratensis L.	15	7
Aegilops cylindrica Host	0	3
Anthoxanthum odoratum L.	1	1
Arrhenatherum elatius (L.) P.Beauv.	3	3
Beckmannia eruciformis (L.) Host	1	2
Briza media L.	1	2
Bromus inermis Leyss.	1	10
Dactylis glomerata L.	24	18
Festuca arundinacea Schreb.	6	8
Festuca pratensis Huds.	16	9
Festuca pseudovina Hack. ex Wiesb.	6	5
Festuca rubra L.	1	10
Festuca sulcata (Hack.) Nym.	1	0
Festuca sp.	41	24
Festuca vaginata W. et K. ex Willd.	1	0
Holcus sp.	0	3
Hordeum hystrix Roth	1	0
Koeleria cristata (L.) Pers.	3	2
Koeleria sp.	0	7
Lolium perenne L.	30	17
Melica ciliata L.	0	1
Phleum pratense L.	2	4
Poa pratensis L.	42	36
Poa sp.	0	3
Poa trivialis L.	0	1
Puccinellia distans (L.) Parl.	0	1
Puccinellia limosa (Schur.) Holm.	0	5
Pholiorus pannonicus (Host) Trin.	0	2
Thypoides arundinacea (L.) Dum	6	5
Total accessions	**203**	**198**

Table 2. Changes in the occurrence of the most important grass species

Species	1992†		1996‡	
	Total occurrences	Frequency (total/31 sites)	Total occurrences	Frequency (total/36 sites)
Alopecurus pratensis L.	15	0.48	7	0.19
Bromus inermis Leyss.	1	0.03	10	0.28
Dactylis glomerata L.	24	0.77	18	0.50
Festuca pratensis Huds.	16	0.52	9	0.25
Lolium perenne L.	30	0.97	14	0.39
Poa pratensis L.	42	1.35	36	1.00

† 31 collecting sites.
‡ 36 collecting sites.

Collecting of semi-natural and wild ecotypes in Lithuania

Nijole Lemeziené
Lithuanian Institute of Agriculture, Kedainiai, Lithuania

It is possible to find about 122 species of grasses and 155 species of legumes in Lithuania (Anonymous 1963, 1971). But not all these species have good forage and turf characteristics. The plant breeder J. Šedys made some rational proposals for collecting different wild species of perennial grasses and legumes (Šedys 1995). In support of these proposals in 1996 a long-term programme was prepared (Table 1). According to this programme we are going to collect 54 species of perennial grasses. All these species will be divided into three different groups according to their importance for Lithuanian agriculture.

- First group: species of a major commercial importance for Lithuania (species involved in the breeding programmes), marked by '1' in Table 1. They are: *Medicago sativa* L., *Onobrychis sativa* Scop., *Trifolium pratense* L., *Trifolium repens* L. *Dactylis glomerata* L., *Phleum pratense* L., *Poa pratense* L. These species have to be collected in all natural habitats without any restrictions.

- Second group: species not involved in the breeding process, but widely enough spread in Lithuania (marked by '2'). These are: *Lotus corniculatus* L., *Trifolium hybridum* L., *Trifolium medium* Crufb., *Alopecurus pratensis* L., *Festuca arundinacea* Schreb. etc.

- Third group: sparsely spread species (marked by '3'). The wild ecotypes of the second and especially the third group of species will be collected to a lesser extent.

According to the programme, duties have been shared between different institutions: the Lithuanian Institute of Agriculture (LIA), the Botanical Institute (BI), the Lithuanian University of Agriculture (LUA). For example, plant breeders (nine persons) of the LIA are responsible for collecting all wild species of perennial grasses and legumes and for the evaluation of species which are involved in the breeding process. A scientist from the Institute of Botany is responsible for collecting and evaluation of legumes, and a geneticist from the University of Agriculture for the evaluation of rare species of perennial grasses.

Over the period 1994-96 four expeditions were arranged in the northern and middle part of Lithuania for collecting wild ecotypes. A total of 328 wild ecotypes of perennial grasses and legumes were collected (Table 2).

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Table 1. The conservation programme of genetic resources of forage grasses and legumes in Lithuania

Legumes	Importance†	Grasses	Importance†
Anthyllis vulneraria L.	3	*Agrostis stolonifera* L.	3
Coronilla varia L.	2	*Agrostis tenuis*	2
Lathyrus montanus Bernh.	3	*Alopecurus pratensis* L.	2
Lathyrus niger (L.) Bernh.	3	*Anthoxanthum odoratum* L.	3
Lathyrus pratensis L.	3	*Arrhenatherum elatius* (L.) J.&C. Presl	3
Lotus corniculatus L.	2	*Beckmannia eruciformis*(l) Host	3
Lotus uliginosus Schkuhr	3	*Bromus erectus* Huds.	3
Medicago sativa L.	**1**	*Cynosurus cristatus* L.	3
Medicago falcata(L.) Arcangeli	2	***Dactylis glomerata*** L.	**1**
Medicago lupulina L.	3	*Elymus arenarius* L.	3
Melilotus alba Medicus	2	*Festuca arundinacea* Schreb.	2
Melilotus officinalis (L.) Pallas	3	*Festuca gigantea* (L.) Vill.	2
Onobrychis sativa Lam.	**1**	*Festuca ovina* L. s.s.	2
Onobrychis arenaria (Kit.)DC.	3	***Festuca pratensis*** Huds.	**1**
Trifolium pratense L.	**1**	***Festuca rubra*** L.	**1**
Trifolium repens L.	**1**	***Lolium perenne*** L.	**1**
Trifolium hybridum L.	2	*Phleum arenarium* L.	3
Trifolium elegans (Savi) Ascherson & Graebner	3	*Phleum phleoides*(.) Karsten	3
Trifolium lupinaster L.	3	***Phleum pratense*** L.	**1**
Trifolium medium L.	3	*Phleum pratense* L. subsp. *nodosum* (L.) Peterm. pro parte	3
Trifolium rubens L.	3	*Poa angustifolia* (L.) Hayek	3
Vicia cassubica L.	3	*Poa longifolia* Trin.	3
Vicia cracca L.	2	*Poa nemoralis* L.	3
Vicia villosa Roth.	3	*Poa palustris* L.	3
		Poa pratensis L.	**1**
		Poa trivialis L.	3
		Trisetum flavescens (L.) Beauv.	3
		Trisetum sibiricum	3

† 1 = species of major commercial importance; 2 = species of less commercial importance; 3 = rare species.

Table 2. Collecting activities in Lithuania, 1994-96

Year	Region	Forages/Turf plants	*Ex situ* collection
1994	Northern part	Forage/turf grasses	20
		Forage legumes	10
1995	Northern part	Forage/turf grasses	185
		Forage legumes	65
1996	Middle part	Forage/turf grasses	125
		Forage legumes	23

Forages collecting activities in Poland, 1995-96

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Introduction

An ecotype is an organism whose physical structure has over time recorded local environmental conditions; these records are genetically fixed. Plant ecotypes record the local elevation, latitude, temperature extremes, precipitation, soil fertility, type and moisture, sun/shade conditions, etc. Ecotypes are biological realities known for 116 years in Europe and widely used in breeding.

Collecting wild ecotypes and further evaluation, conservation and utilization are the main topics of interest of numerous genebanks worldwide.

In the scope of the cooperation between the Centre for Plant Genetic Resources of IHAR (Radzików, Poland), the Botanical Garden of IHAR (Bydgoszcz, Poland) and the Research Institute of Plant Production (RIPP, Piešt'any, Slovakia) two collecting missions were organized in 1995 in the West Carpathian mountains – Western Tatras, High Tatras, Bielsko Tatras, Pieniny and Gorce Mountains, and one mission in 1996 in Ukraine and Slovakia. Additionally, staff of the Botanical Garden of IHAR undertook collecting in the southern region of Poland (Słowiński National Park). In total, 664 wild ecotypes of forage species were collected and prepared for further examination during the implementation of the theme 'Gathering and evaluation of selected grass species with particular consideration of ecotypes' and within the scope of the project 'Collecting, study and conservation of cultivated plants genepool'.

Results

Seed samples as well as plants were collected from meadows, pastures, rocks, touristic routes, field borders, roadsides, farmers' gardens, fields, roads and wastelands abandoned for 15-20 years.

In this collecting expedition, named 'Tatry 1995', the following physico-geographical regions were examined:

West Tatra Mountains – Zuberec, Zverovka, Chlebnice, Huty, Tichá dolina, Kôprová dolina, Piekelnik, Podszkle

High Tatra Mountains – Štrba, Spišska Teplica, Klčov, Dreveník, Hodkovce, Huncovce, Wielki Staw, Morskie Oko, Zakopane, Dolina Strążyska, Dolina Malejłąki, Grzęse, Długi Upłaz, Dolina Chochołowska, Skalnaté Pleso, Veľká Svišťovka, Tatranská Polianka, Velická dolina

Podhale – Rzepiska, Niedzica, Zapszanka

Pieniny Mountains – Bańków Gronik, Polana Wyrobek, Trzy Korony, Majerz, Krościenko, Sromowce Niżne, Tylmanova Rzeka, Ochotnica

Belianske Tatry – Javorina, Zadné Meďodoly, Kopské Sedlo, Monkova dolina

Gorce Mountains – Jaworzynka, Przysłop, Polana Chyzikowa, Polana Gorc Kamienicki, Polana świnkówka.

In 1996 collecting missions were carried out in the following regions:

Czech Republic – Orlické Hory (Nevator, Nová Ves, Olešnice, Polom, Rovenské Šediviny, Šerlich, Třechovská Louka, Zelenka)

Ukraine – the Carpathian Region (Bila Cerkva, Jasenija, Kvasy, Nyžne Solotvina, Rachiv, Solotvvyna, Cerkivna, Derevac, Jamna, Lipa, Lužki, Vyškiv)

Slovakia – mountain regions: Bralo, Bukovce, Jalová, Korejovce, Krajná Porúbka, Rumina, Šemetkovce, Stakčínska Roztoka, Topola, Ubla

Poland, northern part – Baltic coast (Słowiński National Reserve) – Będzimierz, Chocielewko, Czerwieniec, Człochow, Czołpino, Gardenia Wielka, Izbica, Kamienica – Młyn, Kluki Lotki, Pobłocie, Rekowo Lęborskie, Retowo, Rowy

Poland, Kłodzka Valley – Batorów, Gołańcz, Jarkow, Jeleniów, Jerzkowice Wielkie, Kulin, Pasterka, Sawanna.

Conclusions

The gathering of rare grass species as well as rare ecotypes (i.e. from extreme site conditions) is the most important goal of collecting missions and conservation of genetic resources.

Grass ecotypes from collecting expeditions are a rich source of initial materials for different breeding and research studies.

Table 1. Collecting activities of the Centre for Plant Genetic Resources, IHAR, Radzików, Poland

	Collecting year		
Genus, species	**1995**	**1996**	**Total per species**
Agropyron repens (L.) Beauv.	0	1	1
Agropyron sp.	1	0	1
Agrostis alba Auct.	1	3	4
Agrostis canina L.	2	0	2
Agrostis capillaris Leers.	0	1	1
Agrostis sp.	1	0	1
Agrostis stolonifera L.	3	0	3
Agrostis tenuis Sibth.	7	6	13
Alopecurus pratensis L.	9	7	16
Alopecurus sp.	1	0	1
Anthyllis vulneraria L.	2	1	3
Arrhenatherum elatius (L.) J.&C. Presl	7	2	9
Bromus inermis Leysser	1	0	1
Bromus sp.	1	1	2
Calamagrostis villosa (Chaix) J.F. Gmelin	0	1	1
Calamagrostis epigeios (L.) Roth	0	1	1
Cynosurus cristatus L.	5	5	10
Dactylis glomerata L.	15	19	34
Deschampsia cespitosa (L.) Beauv.	4	8	12
Festuca capillata Lam.	0	1	1
Festuca gigantea (L.) Vill.	3	0	3
Festuca ovina L.s.s..	4	2	6
Festuca pratensis Huds.	13	21	34
Festuca rubra L.	15	18	33
Festuca sp.	2	0	2
Holcus mollis L.	0	1	1
Lathyrus pratensis L.	1	0	1
Lolium multiflorum Lam.	0	1	1
Lolium perenne L.	6	11	17
Lotus corniculatus L.	11	6	17
Medicago falcata (L.) Arcangeli	2	3	5
Medicago lupulina L.	3	6	9
Nardus stricta L.	1	0	1
Phalaris arundinacea L.	0	1	1
Phleum nodosum Auct.	2	0	2
Phleum pratense L.	6	13	19
Phleum sp.	3	2	5
Poa compressa L.	1	2	3
Poa nemoralis L.	2	2	4
Poa palustris L.	3	2	5
Poa pratensis L.	14	14	28
Poa sp.	1	2	3
Poa trivialis L.	0	1	1
Trifolium alpestre L.	1	0	1
Trifolium aureum Pollich	1	1	2
Trifolium hybridum L.	5	1	6
Trifolium medium L.	1	2	3
Trifolium pratense L.	13	8	21
Trifolium repens L.	16	1	17
*Trisetum flavescens (*L.) Beauv.	8	1	9
Total per year	**199**	**179**	**377**

Table 2. Collecting activities of the Botanical Garden of IHAR, Bydgoszcz, Poland

Genus, species	Collecting year		Total per species
	1995	1996	
Agrostis alba Auct.	1	1	2
Agrostis canina L.	1	0	1
Agrostis rupestris All.	1	0	1
Agrostis stolonifera L.	0	2	2
Agrostis tenuis Sibth.	6	2	8
Aira praecox L.	0	2	2
Alopecurus geniculatus L.	0	1	1
Alopecurus pratensis L.	1	8	9
Ammophila arenaria (L.) Link	0	1	1
Anthoxanthum alpinum A. et D. Löve	1	0	1
Anthoxanthum odoratum L.	0	2	2
Apera spica-venti (L.) Beauv.	0	2	2
Arrhenatherum elatius (L.) J.& C. Presl.	0	7	7
Brachypodium pinnatum (L.) Beauv.	1	0	1
Briza media L.	3	0	3
Bromus inermis Leysser	0	1	1
Bromus mollis L.	0	2	2
Calamagrostis arundinacea (L.) Roth	1	1	2
Calamagrostis canescens (Weber) Roth	0	2	2
Calamagrostis epigeios (L.) Roth	1	0	1
Calamagrostis neglecta auct., non (Ehrh.) P. Beauv.	0	1	1
Calamagrostis varia (Schrader) Host	2	0	2
Calamagrostis villosa (Chaix) J.F. Gmelin	3	0	3
Calamagrostis sp.	0	1	1
Cynosurus cristatus L.	5	3	8
Dactylis glomerata L.	11	11	22
Deschampsia cespitosa (L.) Beauv.	12	6	18
Deschampsia flexuosa (L.) Trin.	2	5	7
Elymus arenarius L.	0	1	1
Festuca arundinacea Schreb.	2	6	8
Festuca capillata Auct.	0	2	2
Festuca gigantea (L.) Vill.	1	0	1
Festuca glauca Lam.	1	0	1
Festuca ovina L. s.s.	0	1	1
Festuca picta Kit.	1	0	1
Festuca pratensis Huds.	12	4	16
Festuca rubra L.	9	14	23
Festuca sylvatica (Pollich.) Vill.	1	0	1
Festuca supina Schur	5	0	5
Glyceria aquatica Wahlenb.	0	2	2
Glyceria fluitans (L.) R. Br.	1	1	2
Glyceria plicata (Fries) Fries	0	1	1
Helictotrichon versicolor (Vill.) Pilger	1	0	1
Holcus lanatus L.	0	4	4
Holcus mollis L.	1	2	3
Lolium perenne L.	3	12	15
Melica transsilvanica Schur	1	0	1
Melica uniflora Retz	0	1	1
Milium effusum L.	0	2	2
Oreochloa disticha (Wulfen) Link	1	0	1
Phalaris arundinacea L.	0	12	12
Phleum alpinum L.	2	0	2
Phleum nodosum Auct.	0	2	2
Phleum pratense L.	3	11	14
Poa alpina L.	1	0	1
Poa alpina L. subsp. *vivipara* (L.) Arcang.	1	0	1
Poa annua L.	1	0	1
Poa compressa L.	0	1	1
Poa palustris L.	0	23	23
Poa pratensis L.	14	0	14
Sesleria tatrae (Degen) Deyl	1	0	1
Sieglingia decumbens (L.) Bernh.	3	2	5
Trisetum alpestre L.	2	0	2
Trisetum flavescens (L.) Beauv.	1	0	1
Total per year	**121**	**165**	**286**

Collecting missions in Portugal, 1995-96

Manuel Tavares de Sousa
Estação Nacional de Melhoramento de Plantas, Elvas, Portugal

National Plant Breeding Station
Curators: João Paulo Carneiro and Luis Fortunato
One collecting mission in the central region, on calcareous soils, to collect annual medics: 135 accessions of annual medics of several species were collected, mainly *Medicago polymorpha* L., *M. murex* Willd., *M. scutellata* (L.) All., *M. doliata* Carmign., etc.

Experimental Station (DRAEM), Braga
Violeta Rolim and her team work on *Lolium* breeding. The following accessions were collected:

1995

Species	No. of accessions
Dactylis glomerata L.	23
Lolium multiflorum Lam.	17
Lolium perenne L.	1
Ornithopus compressus L.	30
Ornithopus sativus Brot.	6
Medicago spp. (annual)	8
Trifolium sp.	3
Avena sp.	15
Secale cereale L.	2

1996

Species	No. of accessions
Lolium multiflorum Lam.	4
Hordeum sp.	6
Ornithopus compressus L.	19
Ornithopus sativus Brot.	1
Medicago spp. (annual)	14
Trifolium subterraneum L.	4
Trifolium pratense L.	3
Trifolium spp.	3
Avena sativa	13

Collecting missions in the Russian Federation, 1995-96

Vladimir Chapurin
N.I. Vavilov Research Institute of Plant Industry (VIR), St Petersburg, Russian Federation

The Vavilov Institute, St Petersburg, organized in 1995 and 1996 collecting missions in Uzbekistan, Kazakstan, Ukraine and along the river Volga. During these missions 982 accessions were collected, of which 327 were forage crops, such as red clovers, white clovers, alfalfa, timothy and others.

Each accession was split in two samples and one was left in the country of origin. Vegetables accessions were multiplied and sent to Seed Savers Exchange, Iowa, USA.

Collecting activities in Slovakia, 1994-96

Jarmila Drobná
Research Institute of Plant Production, Piešťany, Slovakia

Year	Region	No. of items
1994	Central Slovakia (PLA Muránska planina)†	37 (Fabaceae) 76 (Poaceae)
1995 (in collaboration with IHAR Radzikow)	Northern Slovakia and Southern Poland (Tatra National Park in Slovakia and in Poland; NP Pieniny, NP Gorcze, etc.)	754 (including cereals, fodder crops, grain legumes, etc.)
1996	Western and Central Slovakia (PLA Malé Karpaty, PLA Biele Karpaty, PLA Stráovské vrchy, etc.)	43 (Fabaceae) 23 (Poaceae)
	Central Slovakia (PLA Pol'ana, Krupinská planina, etc.)	54 (Fabaceae) 64 (Poaceae)
Collaboration of Slovakia, Poland, Ukraine	Eastern Slovakia (PLA Východné Karpaty) and Eastern Ukraine	179 (Fabaceae) 105 (Poaceae)

† PLA = Protected Landscape Areas.

Collecting activities in Spain

Francisco González López
Servicio de Investigación y Desarollo Tecnológico, Badajoz, Spain

During 1995 the Servicio de Investigación y Desarrollo Tecnológico carried out a mission to collect annual pasture legumes in degraded areas of the southwest of Badajoz and southeast of Caceres (Extremadura region). The species and number of accessions collected were as follows:

Species	No. of accessions
Trifolium subterraneum L.	23
Trifolium glomeratum L.	23
Trifolium campestre Schreb.	1
Trifolium cherleri L.	16
Ornithopus compressus L.	22
Medicago polymorpha L.	18
M. pelecinus	8
Astragalus cymbicarpos Brot.	2
Trifolium striatum L.	11
Medicago maculata Sibth.	4
Medicago minima (L.) Bartal.	1
Medicago orbicularis (L.) Bartal.	1
Medicago doliata Carmign.	2
Trifolium stellatum L.	3
Trifolium angustifolium L.	1
S. vermiculata	3
Total	**139**

Collecting activities in Turkey, 1995-96

Cafer Olcay to Sabanci
Aegean Agricultural Research Institute, Menemen, Izmir, Turkey

Joint expeditions were organized with the Cooperative Research Center for Legumes in Mediterranean Agriculture (CLIMA).

- In 1995, 804 accessions (14 genera, 79 species) were collected in northwest Turkey, consisting of 387 *Trifolium*, 297 *Vicia*, 95 *Lathyrus* and 25 other forage legume species.

- In 1996, two separate collecting trips were made to the Mediterranean and inner parts of the Aegean Region, collecting a total of 1227 accessions belonging to 18 genera and 102 species as follows:

Genus	No. of accessions
Trifolium	577
Medicago	276
Vicia	189
Lathyrus	50
Trigonella	23
Coronilla	21
Lotus	14
Onobrychis	14
Others	63
Total	**1227**

Recent collecting activities at IGER, Aberystwyth (United Kingdom)

Ian D. Thomas
Institute of Grassland and Plant Environmental Research (IGER), Aberystwyth, UK

1995: Portugal

Joint Collecting mission principally with Universidade de Tras-os-Montes, Universidade de Coimbra and ENMP, Elvas.

Principal species collected were *Lolium perenne* L. and *Trifolium repens* L.

The objectives of the mission were to collect a large range of genetic diversity in the target species by sampling from a broad selection of locations, habitats and management systems and at the same time to ascertain the extent to which the target species were present in the extreme southwest of continental Europe.

1996: United Kingdom

Joint collecting mission in collaboration with IGFRI (Indian Grassland and Forage Research Institute), Jhansi, India.

Principal species collected were *Lolium perenne, Trifolium repens* and *Festuca gigantea.* The Genetic Resources Unit at IGER has always been aware of the under-representation of UK accessions in its genebank. As part of our collaborative activities with IGFRI we were able to undertake a number of short UK collecting missions.

The main target areas were established, low-input hay meadows in Environmentally Sensitive Areas (ESAs).

The following areas were sampled:

Southwest England	
Somerset Levels	Flood meadows
Mendip Hills	Grazing pastures on limestone
North England	
Pennine Dales	Reputedly highest hay meadows in England
Mid East Wales	Low-intensity hay meadows.

Collecting activites in F.R. Yugoslavia

Zorica Tomić
Forage Crops Research Centre, Agricultural Research Institute "Serbia", Kruševac, F.R. Yugoslavia

The collecting of autochthonous populations of perennial grasses and legumes was carried out in more than 100 of the most important localities of Serbian flora. The strategic project that should start this year will be based on new expeditions and collecting of forage crop species which are important for selection.

Research activities

Austria: Recultivation of alpine areas with seed of alpine plants

B. Krautzer
Federal Research Institute for Agriculture in Alpine Regions, Department of Forage Crops, Gumpenstein, Irdning, Austria

Introduction

Every year, millions of tourists visit our Alps. This causes a lot of different interventions to build up the infrastructure of summer and winter tourism. These activities and the increasing problem of natural erosion are responsible for thousands of square kilometres of damaged areas all over the Alps. The main problem of recultivation in high altitudes is not so much the sensitivity of these areas but the adequate replacement of the destroyed autochthonous vegetation (Lichtenegger 1994). Up to now only commercial varieties of grasses and legumes for the use of our grassland farmers have been available. Those lowland species do not really tolerate the conditions in high altitudes. To achieve a permanent green cover, many expensive measures have to be taken such as regular fertilizing, overseeding and cutting. If these measures are neglected, the vegetation disappears in a few years, and erosion and other problems can follow. To get a closed sward, a vegetation is required that is adapted to the site as much as possible. Only the use of alpine species in the form of vegetative material (Grabherr 1995) or seed (Krautzer 1993) will lead to a satisfactory solution. Of the different methods available, the use of seeds of alpine species would be the cheapest way to revegetate patches in high mountains.

Material and methods

In a field experiment in St. Martin near Gumpenstein, the suitability of 41 alpine species of well-chosen grasses, Leguminosae and other herbs was tested for commercial seed production in low altitudes. The seed properties and the seed quality (germinative capacity, seed weight) were analyzed, following the preconditions of the International Seed Testing Association (ISTA 1985). The demands for field preparation, maintenance and cultivation as well as the seed productivity were analyzed in field experiments. From each species, a number of different provenances were tested. The following species were suitable for commercial seed production:

Festuca nigrescens (Lam). Asch. et Ev.
Festuca pseudodura Steud.
Festuca supina Schur
Festuca violacea Gand. s.stv.
Phleum alpinum L. emend. Gaudin
Phleum hirsutum Honck.
Poa alpina L.
Trifolium badium Schreb.
Trifolium pratense L. subsp. *nivale* Arc.

Results and conclusions

Up to now, most of the analyzed species did not have great importance. For most of them, it was the first time that some data about the seed properties have been obtained. Table 1 shows a summarized description of the seed of the nine selected species. The results between the provenances of the species differed considerably. For this reason, the table shows the most frequent ranges for length, width and thickness.

Table 1. Length, width, thickness and colour of the seeds of the species (Krautzer 1995)

Species	Length (mm)	Width (mm)	Thickness (mm)	Colour	Shape
Festuca nigrescens	3.5-6.0	0.5-1.0	0.5-0.8	light brown	longish, one side sharpened
Festuca pseudodura	3.5-5.0	0.8-1.2	0.5-0.8	light brown	longish, one side sharpened
Festuca supina	2.5-3.5	0.5-0.9	0.5-0.9	light brown	longish, one side sharpened
Festuca violacea	2.0-4.0	0.6-1.0	0.6-1.0	yellow-brown	longish, one side sharpened
Phleum alpinum	1.5-3.0	0.6-1.0	0.6-1.0	grey to light brown	ovoid
Phleum hirsutum	2.0-3.0	0.5-0.9	0.5-0.9	yellow-brown to brown	
Poa alpina	2.0-4.0	0.6-1.0	0.6-1.0	light brown	
Trifolium badium	1.4-1.8	1.0-1.4	0.4-0.8	green to yellow	ovoid-oval
Trifolium nivale	1.0-2.3	0.8-1.5	0.5-1.0	yellow to violet	heart-shaped

The thousand-seed weight (TSW) was ascertained before and after cultivation. The weight of cultivated and wild species showed a great variation from 15% (*Festuca nigrescens*) to 45% (*Poa alpina*) between the provenances. On average, the TSW increased after cultivation.

Table 2 shows the average TSW of 10 to 25 samples of the nine chosen species after cultivation. Great diversity and variability could also be observed in connection with the germinative capacity of alpine plants. Seeds of plants collected in their natural location showed very different results from year to year, depending on the provenance, the harvesting date and the climatic conditions over the year. After cultivation, the germinative capacity (GC) increased on a level of 15-30%. In commercial production, the water supply and different diseases can have an important effect on GC. The worst average value for GC was 73% for *Phleum hirsutum*, the best 92% for *Festuca nigrescens* and *Poa alpina*. A further reason for the increasing GC could also be a selection of fast-germinating individuals.

The TSW and the GC showed a very close connection. Higher TSW always leads to a higher GC in percentages (Flüeler 1992). The explanation could be that in commercial seed production the plants have much better growing conditions (growing space, nutrients, competition). This leads to stronger, healthier plants with higher TSW and GC. In comparison with commercially produced low-altitude species, the alpine plants showed an equal seed quality after cultivation.

The field experiments showed high demands of the chosen species for field preparation, maintenance and cultivation. Drilling and underseed under summer barley proved to be optimal for most of the species. The seed demand for sowing was between 8 and 20 kg/ha and was 20% above the seed demand for comparable lowland species. Establishment dates after the beginning of July resulted in unsatisfactory seed yields. In comparison with lowland species, alpine plants develop very slowly and show very poor competitiveness against weeds and fungal diseases.

Table 2. Thousand-seed weight (TSW), germinative capacity (GC) and seed yield

Species	TSW average (g)	GC average (%)	Seed yield (kg/ha) Year 1	Year 2	Average of 2 years
Festuca nigrescens	0.900	92	771	302	537
Festuca pseudodura	0.811	86	512	118	315
Festuca violacea	0.374	85	421	143	282
Festuca supina	0.512	89	167	247	207
Phleum alpinum	0.470	77	71	27	49
Phleum hirsutum	0.344	73	78	160	119
Poa alpina	0.490	92	681	110	396
Trifolium badium	0.759	86	98	–	–
Trifolium nivale	1.372	83	136	–	–

The productivity of most of the species was surprisingly high. Table 2 shows the average yield of all locations of the discussed species. With the exception of *Phleum alpinum* and *Phleum hirsutum*, all alpine grasses showed a yield of more than 200 kg/ha in an average of two harvesting years. Some locations of *Festuca nigrescens* and *Poa alpina* showed a yield of more than 1000 kg/ha in the first harvesting year. The plants of the alpine clovers *Trifolium badium* and *Trifolium nivale* died after the first harvest and showed an average yield of 98 and 136 kg/ha. Improvement of the production technique and an adaptation of the best locations to contemporaneous ripening and low susceptibility to diseases will lead to further progress in the seed multiplication of those species. Contrary to a widespread view, the research results clearly showed that seed multiplication of the nine analyzed species in lowland regions is possible, from both biological and commercial points of view.

Using seeds of the presented alpine species, well-adapted seed mixtures for almost all locations and altitudes of our Alps can be determined. Table 3 shows the most important characteristics of the species for recultivation in alpine areas. Mixtures for all different demands on climate, soil, water content as well as on the further use (skiing areas, protection against erosion, recovery after technical interferences, alpine pastures, etc.) can be put together. Most of the species are spread all over the Alps, some (*Festuca pseudodura*, *F. supina, F. violacea*) only partially. To avoid floral falsification the species should only be used in areas of their natural range. In the last 5 years, a lot of recultivation trials in alpine areas have been made, using the discussed material. The results clearly showed the value and the possibilities of the use of alpine seed mixtures for permanent recultivation (Wittmann and Rücker 1995).

What would be the size of the market for alpine seed mixtures? In Austria, an area of about 1000 to 1500 ha has to be recultivated every year in altitudes above 1600 m. All over Europe, the area can be estimated as a minimum of 3000 ha. An amount of more than 300 tonnes of alpine seeds would be needed. In the last 3 years, commercial seed production of alpine plants has been established in Carinthia, in the southern part of Austria. Currently, *Festuca nigrescens, Festuca pseudodura, Festuca violacea, Phleum hirsutum* and *Poa alpina* are produced on an area of 13 ha. Up to now, the user's acceptance of the higher product prices is very low. To achieve a widespread use of alpine mixtures for ecological recultivation in alpine areas, a government-enforced obligation to use them would be useful.

[AustrTbl3.doc] – landscape

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Table 3. Important characteristics of the species for recultivation in alpine areas

	Vegetation stage			Soil material		H_2O content		Susceptibility to:		
Species	**Montane**	**Subalp.**	**Alpine**	**Siliceous**	**Calcareous**	**Dry**	**Moist**	**Fertilizing**	**Cutting**	**Grazing**
Festuca nigrescens	+	+	+	+	+	+	(+)	+	+	+
Festuca pseudodura	–	(+)	+	+	(–)	+	(–)	(+)	–	(+)
Festuca supina	–	+	+	+	(–)	+	(–)	(+)	(–)	+
Festuca violacea	(+)	+	+	(+)	+	+	(+)	+	+	(–)
Phleum alpinum	(+)	+	+	+	(+)	(+)	+	+	+	+
Phleum hirsutum	(+)	+	+	(–)	+	+	(–)	+	+	+
Poa alpina	(+)	+	+	(+)	+	+	(+)	+	+	+
Trifolium badium	(+)	+	+	+	+	+	+	(+)	+	+
Trifolium nivale	–	+	+	+	(+)	(+)	+	(+)	+	+

+ = very good, (+) = good, (–) = bad, – = very bad.

Germany: A knowledge base for disease resistance of selected cultivated plant species[18]

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A knowledge base (Table 1) was set up that reviews the current knowledge on disease resistance of plant species investigated in the genebank of the Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, branch station North, Malchow. Over 350 publications on disease resistance of the last 25 years were considered, concerning 116 host-pathogen combinations of *Brassica napus* L. var. *oleifera, Dactylis glomerata* L., *Festuca arundinacea* Schreb., *F. pratensis* Huds., *F. rubra* L., *Lolium perenne* L., *Medicago sativa* L., *Phleum pratense* L., *Poa pratensis* L., *Trifolium pratense* L. and *T. repens* L (see Table 2). Sixteen priority subject matters are taken into consideration, such as resistant genotypes, methods of checking resistance, genetics of resistance and breeding for resistance (see Tables 1 and 3). The knowledge base can be made topical and complete continuously and can be searched and used generally in the IPK-Genebank branch station Malchow (see Table 4). Through the accession number, a seed sample of the desired species and cultivar can be requested from the genebank branch station Malchow.

In the near future this information will be recorded on the Internet with the support of ZADI / IGR, Bonn.

Table 1. Key words of the knowledge base (main subjects recorded)

1	susceptibility
2	interference
3	correlation
4	pathogenicity (pathotypes)
5	resistant genotypes
6	resistance (general)
7	assessment of resistance pests
8	genetics of resistance
9	character of resistance
10	physiology of resistance
11	resistance test
12	resistance type (extract)
13	resistance breeding
14	stress
15	resistance to vectors or pests
16	virulence

[18] A related article has been published in German in 1997 under the title: Ein Sachspeicher zur Krankheitsresistenz bei ausgewählten Kulturpflanzen-Arten. Arch. Phytopath. Pflanz. 31:121-132.

Table 2. Overview of the major subjects of disease resistance recorded

Crop plant	Disease agent	No. of literature references	Main subjects (see Table 1: Keywords)															
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Brassica napus	turnip mosaic potyvirus	2					x			x					x			
	Leptosphaeria maculans	2					x			x								
	Plasmodiophora brassicae	1						x										
Brassica napus var.	cauliflower mosaic caulimo-virus	3	x				x			x			x					
oleifera	turnip mosaic potyvirus	4	x				x						x					
	turnip yellows luteovirus	1					x						x		x			
	radish mosaic virus	1					x						x					
	various viruses	1					x											
	Albugo candida	3					x			x		x						
	Alternaria brassicae	4					x		x		x	x	x					
	Erysiphe cruciferarum	3					x						x		x			
	Fusarium spp.	1					x											
	Leptosphaeria maculans	55	x	x	x	x	x	x	x	x	x	x	x					x
	Peronospora parasitica	3	x				x	x					x					x
	Plasmodiophora brassicae	9				x	x	x	x	x			x		x			
	Pyrenopeziza brassicae	3	x			x		x				x						
	Rhizoctonia solani	2	x		x		x						x		x			
	Sclerotinia sclerotiorum	8	x		x		x	x					x		x			
	Verticillium dahliae	5	x				x						x		x			x
Dactylis glomerata	barley yellow dwarf luteovirus	1								x								
	cocksfoot mottle sobemovirus	6	x		x		x							x	x			
	cocksfoot mild mosaic virus	1								x								
	Erysiphe graminis	2					x			x								
	Fusarium nivale	1								x								
	Puccinia graminis	5					x			x			x					
	Puccinia striiformis f. sp. *dactylidis*	1					x											
	Rhynchosporium orthosporum	3					x			x			x					
	Stagonospora arenaria	5								x	x		x		x			
	Typhula ishikariensis	4					x			x			x		x			
	Typhula incarnata																	
	Graminelle nigrifrons	1															x	
Festuca arundinacea	*(Acremonium coenophialum)*	2		x				x										

Crop plant	Disease agent	No. of literature references	Main subjects (see Table 1: Keywords)															
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	Puccinia coronata corda var. *coronata*	1	x					x										
	Puccinia graminis ssp. *graminicola*	2					x						x					
	Rhizoctonia solani	2					x						x					
Festuca pratensis	*Drechslera sorokiniana*	1					x											
	Puccinia coronata	3	x				x	x		x					x			
Festuca rubra	*Gaeumannomyces graminis*	1	x															
Lolium perenne	barley yellow dwarf luteovirus	4					x			x					x			
	ryegrass mosaic potyvirus	7					x			x			x		x			
	Xanthomonas campestris p.v. *graminis*	1					x											
	Drechslers siccans	1					x											
	Puccinia coronata	3	x				x			x					x			
	Puccinia coronata ssp. *lolii*	1					x											
	Puccinia coronata ssp. *tritici*	1					x											
	Puccinia graminis	1					x			x								
	Puccinia graminis ssp. *graminicola*	1					x					x						
	Rhizoctonia solani	1					x											
	(Listronotus bonariensis)	2		x														
Medicago sativa	alfalfamosaic alfamovirus	3					x			x			x					
	Corynebacterium michiganense pv. *insidiosum*	9	x	x			x	x		x					x			
	Colletotrichum destructivum	1					x											
	Colletotrichum trifolii	14	x	x			x		x	x			x		x			
	Corticum rolfsii	2					x		x				x					
	Fusarium avenaceum	1		x			x			x			x		x			
	Fusarium oxysporum f. sp. *medicaginis* *Fusarium solani*																	
	Fusarium oxysporum f. sp. *medicaginis*	22	x	x	x		x			x			x		x			
	Leptospaerolina trifolii	2		x	x		x						x		x			
	Phoma medicaginis	1	x															

Crop plant	Disease agent	No. of literature references	Main subjects (see Table 1: Keywords)															
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	Phytophthora megasperma f. sp. *medicaginis*	23	x	x	x	x	x	x	x	x	x	x	x		x	x		x
	Pseudopeziza medicaginis	4	x				x					x						
	Pythium ultimum	1	x															
	Sclerotinia trifoliorum	2	x		x		x	x					x		x			
	Stagonospora meliloti	1					x						x					
	Stemphylium botryosum	2					x			x			x		x			
	Uromyces striatus var. *medicaginis*	2	x		x		x	x				x	x		x			
	Verticullium alba-atrum	31	x	x	x		x	x	x		x	x	x		x	x		x
	Aphids	1					x	x										
	Nematodes	1					x											
Phleum pratense	*Cladosporium phlei*	1					x											
	Puccinia graminis f. sp. *phlei-pratensis*	1								x								
	Sclerotinia borealis	2			x		x						x			x		
	Typhula ishikariensis																	
	Typhula incarnata																	
	Fusarium nivale																	
Poa pratensis	*Drechslera triseptata*	1													x			
	Erysiphe graminis																	
	Puccinia brachypodii	1	x				x											
	Puccinia graminis	1	x				x											
	Puccinia Poarum	1					x											
	Puccinia striiformis																	
	Sclerotinia homoeocarpa	1					x											
	NO_2	1					x											
Trifolium pratense	bean yellow mosaic potyvirus	5	x		x		x			x			x		x			
	bean yellow mosaic potyvirus alfalfamosaic alfamovirus	1	x		x		x											
	red clover vein mosaic carlavirus pea top necrosis virus																	
	red clover vein mosaic carlavirus bean yellow mosaic potyvirus	1								x								

Crop plant	Disease agent	No. of literature references	Main subjects (see Table 1: Keywords)															
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	Fusarium oxysporum	1			x										x			
	Fusarium solani																	
	White clover mosaic potexvirus	1	x				x											
	Erysiphe gramninis	2					x											
	Fusarium avenaceum																	
	Fusarium oxysporum	5	x		x		x	x		x		x						
	Fusarium solani																	
	Fusarium roseum avenaceum	1	x							x		x	x					
	Fusarium spp.	2			x							x	x		x			
	Kabatielle caulivora	2					x			x					x			
	Pseudopeziza trifolii	1					x											
	Sclerotinia trifoliorum	8					x			x	x		x		x			
	Sclerotinia sclerotiorum	1					x			x								
	Sclerotinia trifoliorum																	
	Sclerotinia minor																	
	Sclerotinia trifoliorum	1								x								
	Erysiphe polygoni																	
	Stemphylium sarcinae-forme	1													x			
	Uromyces trifolii var. *fallens*	1					x			x			x		x			
	Aphanomyces euteiches	2	x				x			x				x	x			x
Trifolium repens	alfafa mosaic alfamovirus	1					x											
	white clover mosaic virus																	
	alfalfa mosaic alfamovirus																	
	clover yellow vein potyvirus	2					x			x								
	peanut stunt cucumovirus																	
	peanut stunt cucumovirus	1					x											
	Cymadothea trifolii																	
	Pseudopeziza trifolii	1						x										
	Phytophthora claudestina	1					x											

Table 3. Example of information recorded in the knowledge base: disease resistance

Genus	Species	Pathogen	Keyword	Statement	Literature
Brassica	*napus* var. *oleifera*	turnip mosaic potyvirus	resistant genotypes	several plants of cultivar 'Rafal' were immune; this character will be hereditary; all tested common cultivars were susceptible	Walsh, J.A. and J.A. Tomlinson. 1985. Virus diseases of oilseed rape. 35th Ann. Rep. 1984 Nation. Veget. Res. Sta. Wellesbourne :92
Medicago	*sativa*	*Corynebacterium michiganense* pv. *insidiosum*	resistance genetic	Genepool MSA contained 1 dominant gene (BW1) for resistance; in absence of other R-genes will be classified plants of genotype BW1 ... as resistant, plants of genotype BW1 ... as susceptible; MSA contained probable 2 further R-genes (BW2, BW3) with additive, but minor effects; MSB contained R-alleles BW2 and BW3, but not BW1	Viands, D.R. and D.K. Barnes. 1980. Inheritance of resistance to bacteria wilt in two alfalfa genepools: qualitative analysis. Crop Sci. 20:48-54
Phleum	*pratense*	*Sclerotinia borealis, Typhula ishikariensis*	resistance stress, correlation	*P*. *pratense* is more resistant to both pathogens and more tolerant to frost as *Lolium perenne*; cultivars with winter hardiness of *P. p*. are more resistant to both pathogens as cultivars with not so good winter hardiness; *T. i*.-resistance is increased with further growth	Matsumoto, N. and T. Sato. 1983. Factors involved in the resistance of timothy and perennial ryegrass to *Sclerotinia borealis* and *Typhula ishikariensis*. Res. Bull. Hokkaido Nat. Agric. Exp. Sta. 136:23-30

Table 4. Overview of resistant genotypes of different host-pathogen combinations

Crop plant	Pathogen	Resistant genotypes Name (Accessions number) *
Brassica napus	turnip mosaic potyvirus	Calder (CR 776), Sensation (CR 917), Vogesa, Line 165, Mocomber
	Leptosphaeria maculans	Tina
	Plasmodiophora brassicae	
Brassica napus var. *oleifera*	cauliflower mosaic caulimovirus	no immunity
	turnip mosaic potyvirus	Double Zero, Rafal (CR 870) (individual plants), Samo (CR 902)
	turnip yellows luteovirus	R 54
	radish mosaic virus	Jet-Neuf (CR 662), Lirama (CR 722), Licondor, Mytnitskij 2 (CR 778), Blagodatnyij, Salamander (CR 901)
	various viruses	Erra (CR 318), Rangi (CR 873), Sv 73/15796
	Albugo candida	Regent (CR 881)
	Alter brassicae	CSR-142, RC-781, Tower (CR 1025)
	Erysiphe cruciferarum	Eurol, Falcon, Samourai
	Fusarium spp.	Korina (CR 676), Librador (CR 695), Jet-Neuf (CR 662)
	Leptosphaeria maculans (phoma lingam)	Balko, BOH-1592, BOH 1693, Beryl (CR 180), Brink (CR 267), Crésor (CR 288), Darmor (CR 294), Doral (CR 301), Doublo, Elvira (CR 311), Hungry Gap (CR 647), Idol (CR 241), Jet-Neuf (CR 662), Jupiter (CR 664), Juno (CR 2016), Kid (CR 671, Leo, Libritta (CR 698), Lipora, Lirajet (CR 719), Libravo (CR 697), MAH-1291, Mar (CR 755), OKEG 8, Polo, POH 285 (CR 853), Rafal (CR 870), Rapora (CR 876), R 18, R 51, Rothwell 82/3, Sinus (CR 921), Tamara (CR 1009), Wesro, Zollerngold (CR 955)
	Peronospora parasitica	Cresor (CR 288), Synra (CR 1007)
	Plasmodiophora brassicae	OAC Triton (CR 1027), SV 8525952, SV 8525953
	Rhizoctonia solani	Midas- selected breeding lines (CR 775)
	Sclerotinia sclerotiorum	Doral (CR 301), Girita (CR 580), Librador (CR 695), Lirana, Marian, Perle (CR 841), Seegold, Wilhelmsburger Sator Otofte (CR 905)
	Verticillium dahliae	BOH 1582, Liradette, Norde (CR 799), NPZ Rapora (CR 876), NPZ 17674, WW 766, 3059/88, 3581/88
Dactylis glomerata	barley yellow dwarf luteovirus	
	cocksfoot mottle sobemovirus	Aberystwyth S26 (GR 964), Cambria (GR 709), Okamidori (GR 930)
	cocksfoot mild mosaic virus	
	Erysiphe graminis	Dorisa, Welta (GR 1009)
	Fusarium nivale	

Crop plant	Pathogen	Resistant genotypes Name (Accessions number) *
	Puccinia graminis	Klon 58-65
	Puccinia striiformis f. sp. *dactylidis*	some breeding lines
	Rhynchosporium orthosporum	Baraula (GR 696), Dactimo (GR 719), Dora (GR 734), Gambria, Kay (GR 852), Rosa (GR 959), Sylvan (GR 985)
	Stagonospora arenaria	
	Typhula ishikariensis	Dora (GR 734), Giresum, Montpellier
	Typhula incarnata	
	Graminella nigrifrons	
Festuca arundinacea	*(Acremonium coenophialum)*	
	Puccinia coronata corda vap. *coronata*	
	Puccinia graminis ssp. *graminicola*	Melik (Sektionen), AU-Triumpf, Demeter (GR 1346), Mozark, Penno, Southern Cross
	Rhizoctonia solani	Kentucky-31 (GR 1378)
Festuca pratensis	*Drechslera sorokiniana*	Cosmos (GR 1697), Merbeem (GR 1941), Bundy (GR 1688), Belimo (GR 1680), Mana (GR 1937), Prefest (GR 1979)
	Puccinia coronata	Bodroghalmi, Körösłodangi, Csorodai, Vadnai
Festuca rubra	*Gaeumannomyces graminis* var. *avenae*	
Lolium perenne	barley yellow dwarf luteovirus	Ellet selected breeding lines (GR 2751), Premo (GR 3115)
	ryegrass mosaic potyvirus	Endura (GR 2755), Mascot (GR 3026), R1, R2, S23 (GR 3152)
	Xanthomonas graminis pv. *graminis*	RAH 286
	Drechslera siccans	Belford, Danny (GR 2730), Rally (GR 3126), Solen (GR 3172), Sommora (GR 3173), Variant (GR 2783)
	Puccinia coronata	Lihersa (GR 2944), Limes (GR 2952), Liperry (GR 2958), Lisabelle (GR 2964)
	Puccinia coronata ssp. *lolii*	Grasslands Niu (GR 2782), Kangoroo Valley (GR 2912, 2913)
	Puccinia coronata ssp. *tritici*	Wimenera, Graslands Ruanui (GR 2783)
	Puccinia graminis	tetraploid varieties
	Puccinia graminis ssp. *graminicola*	Birdy II, Linn (GR 2953)
	Rhizoctonia solani	Jorand
	Listronotus bonariensis	
Medicago sativa	alfalfa mosaic alfamovirus	Apica

Crop plant	Pathogen	Resistant genotypes Name (Accessions number) *
	Corynebacterium michiganense pv. *insidiosum*	Spredor (LE 823), Stamm 354
	Colletotrichum destructivum	varieties from Ontario
	Colletotrichum trifolii	Arc (LE 420), Aquarius, Hunter River (LE 561), Saranac AR, Siro Peruvian
	Corticum rolfsii	Aikei No. 4, Moapa
	Fusarium avenaceum	NY 9129, NY 9130 (selected breeding lines)
	Fusarium oxysporum	Agate (LE 389), Moapa 69 (LE 687), Narragansett (LE 698), Voris A 77 (LE 897)
	Fusarium solani	Adalfo, Apollo, Glacier (LE 549), Irognosis, Luxin (LE 610), Maris Sabilt, Prima, Ramsey (LE 779), Ranger (LE 781), Roamer (LE 787), Titan (LE 863), Verneul, Victoria, Björn Gibridnyi Pozdnespelyi, Kvarta, Ottawa, Rüttinova, Start
	Fusarium oxysporum f. sp. *medicaginis*	Algonquin (LE 402), Anchor (LE 408), Angus (LE 410), Beaver (LE 435), Cimarron, Drylander (LE 504), Derby (LE 492), Irognosis, Lada (LE 592), Luxin Sarvashi (LE 610), Maris Sabilt, NCMP 9, NCMP 11, NCMP 13, Nuggett (LE 709), Nutiva, OC 66, Ranger (LE 781), Saranac, Severnaja Gibridna (LE 808), Spredor (LE 823), Titan (LE 863), Veko (LE 885)
	Leptosphaerolina trifolii	Europe (selected breeding lines) (LE 520)
	Phoma medicaginis	
	Phytophthora megasperma f. sp. *medicaginis*	Agate (LE 389), Apollo II, Hayden, Hunter River (LE 561), Lanhontan, NAPB 0310, Nevada Synthetic XX, Oneida (LE 717), Sequel, Trifecta, Vernal (LE 889)
	Pseudopeziza medicaginis	Ci 930-75, Duke (LE 508), Ludigo (LE 604), Mavarick, Roamer (LE 787), Orchesenie (LE 721), Palava (LE 729), Quik, Szarvasi 4 (LE 842), Trumpetor (LE 870, Vencor (LE 882)
	Pythium ultimum	
	Sclerotinia trifoliorum	Flamanda, 5472
	Stagonospora meliloti	UC 129 A, UC 129 B (selected breeding lines)
	Stemphylium botryosum	
	Uromyces striatus var. *medicaginis*	Pioneer 572, Valador
	Verticillium alboatrum	AC Blue J, Apollo II, Barrier, Endure, Excalibur, Glacier (LE 549), Hybride de Grecy, Klon 1079, Maris Kabul (LE 628), Maris Phoenix (LE 629), NAPB 108, NAPB 110, Oneida (LE 717), Pioneer 5444, Resis (LE 784), Sabilt (LE 795), Trumpetor (LE 870), Verneuil (LE 890), Vertibenda (LE 892), Vertus (LE 893), Vela (LE 885), VW 34-2, WL 5, WL 316 (LE 919)
	Aphids	C 3 Composite
	Nematodes	Nematol (LE 705)
Phleum pratense	*Cladosporium phlei*	Heidemij (GR 3864), Kitanu, Senpoku GR 4021)

Crop plant	Pathogen	Resistant genotypes Name (Accessions number) *
	Puccinia graminis f. sp. *phlei pratensis*	
	Fusarium nivale	
	Sclerotinia borealis	Engmo (GR 3837)
	Typhula incarnata	
	Typhula ishikariensis	
Poa pratensis	*Erysiphe graminis*	
	Drechslera triseptata	
	Puccinia brachypodii	Sydsport (GR 4568)
	Puccinia graminis	Bonnieblue, Galaxy, Glade (GR 4370), Fanfare, Majestic, Nugget (GR 4498), Sydsport (GR 4568)
	Puccinia poarum	diverse varieties
	Puccinia striiformis	Geronimo
	Sclerotinia homoeocarpa	Adelphi (GR 4282), Geary, Park (GR 4510), So. Dakota Certified, Ventage
	NO_2	Arina
Trifolium pratense	bean yellow mosaic potyvirus	Do 4, Fanny (LE 1401), Fox (LE 1408), Kvarta (LE 1490), R 104, Radegast (LE 1610), Start (LE 1673), Strugi, N1-17, SE 41, SE 44
	bean yellow mosaic potyvirus	
	alfafa mosaic alfamovirus	Dollard (LE 1389), Florex (LE 1406), Kvarta (LE 1490), Napoca Tetra (LE 1536), Do-DT 1
	red clover vein mosaic carlavirus	
	pea top necrosis virus	
	red clover vein mosaic carlavirus	
	bean yellow mosaic potyvirus	
	Fusarium oxysporum	selected breeding lines
	Fusarium solani	
	white clover mosaic potexvirus	selected breeding lines
	Erysiphe polygoni	Celtic (LE 1363), Elbo (LE 1395), Daehrfeldt Prima IV, Hunsballe (LE 1490), Lakeland (LE 1491), Moravsky, HeraPajbjerg, Orbit (LE 1560), Øtofte III
	Fusarium avenaceum	
	Fusarium oxysporum	Bjursele (LE 1258), Kolstad, Matrai, Redquin, Renova (LE 1622), Do-5, HZ-III, HZ-IV
	Fusarium solani	
	Fusarium roseum avenaceum	selected breeding lines

Crop plant	Pathogen	Resistant genotypes Name (Accessions number) *
	Fusarium spp.	selected breeding lines
	Kabatielle caulivora	Eitan
	Pseudopeziza trifolii	Elezovskij, Luzhskij, Pechorski, Tikhvinskij
	Sclerotinia sclerotiorum	Albatros (LE 1236), Diper (LE 1386), Gera Paiberg, Hermes (LE 1432), Justin, Kustrask, Merkur (LE 1514), Moskovskij (LE 1526), Noe (LE 1546), Oktjabr, Polly (LE 1589), Rea (LE 1614), Resistenta (LE 1624), Severodvinsky, Shultune, Stendski rannespelyj, Tamara, Tammisto (LE 1687), Tetri Lossum (LE 1703), Ultuna (LE 1744), Ulva (LE 1745), Venessa (LE 1752),HG 1102 (LE 1434), SVA 066, WWR 52
	Sclerotinia sclerotiorum	tetraploid varieties
	Sclerotinia trifoliorum	
	Sclerotinia minor	
	Sclerotinia trifoliorum	tetraploid varieties
	Erysiphe polygoni	
	Stemphylium sarcinaeforme	selected breeding lines
	Uromyces trifolii var. *fallens*	Pl 210370 (clone)
	Aphanomyces euteiches	selected breeding lines
Trifolium repens	alfafa mosaic alfamovirus	Graslands Pitau (LE 2043), Kent Wlit White, NFG Gigant (LE 1434)
	white clover mosaic virus	
	alfalfo mosaic alfamivirus	
	clover yellow vein potyvirus	SRVR-Herkünfte
	peanut stunt cucumovirus	
	peanut stunt cucumovirus	selected breeding lines
	Cymadothea trifolii	
	Pseudopeziza trifolii	selected breeding lines
	Phytophthora claudestino	Daliak, Dinminup, Karridale, Larisa, Trikala

*seed samples of desired species and cultivars can be requested through the accession number from the genebank branch station Malchow

Greece: Breeding for drought resistance, persistence and forage productivity

Thomas Vaitsis
NAGREF/ Central Greece Agricultural Research Center, Larissa, Greece

Medicago sativa L.

Medicago sativa (alfalfa) is the most important forage crop in Greece grown in pure stands under irrigation or under rain-fed conditions. Breeding alfalfa was in the first priorities of the research conducted by GARC/FCPI during the last 15 years. Seed samples of alfalfa spontaneous plants have been harvested from different regions to complete the germplasm collection kept in Larissa. Individual plants of alfalfa populations have been evaluated in the field, under rain-fed conditions. A great variability was found and the best plants were selected to create new populations, clones and synthetic varieties. Traditional alfalfa varieties and modern bred varieties, indigenous or introduced, were screened in Larissa. The best of them were tested in a network of experiments in more than four sites in contrasted environments under or without irrigation. The semidormant Greek varieties Dolichi, Hyliki, Hypati and Florina proved to be the most persistent and the most productive varieties under or without irrigation. Cheronia, a nondormant Greek variety, also proved to be a good producer, but only under irrigation.

Medicago arborea L.

Medicago arborea is a drought-resistant shrub, suitable for marginal rocky soil reclamation in Mediterranean dry-hot conditions. A collection of *M. arborea* indigenous germplasm was completed in recent years, which contains 38 accessions. A mass selection variety named Naxos has been registered to the national list of varieties and a large number of clones and lines have been produced by selection for drought and cold resistance, leafiness and forage production.

Dactylis glomerata L., *Festuca arundinacea* Schreb., *Lolium perenne* L.

Cocksfoot, tall fescue and ryegrass are three of the most important cool-season perennial grasses in natural pastures in Greece, although they are less known as crops. No Greek perennial grass variety was available until the last years. Foreign varieties have been proven to be poor producers under Greek dry-hot conditions. A project of collecting wild indigenous germplasm was started in 1977. Wild and bred populations were given preliminary evaluation under irrigated or under rain-fed conditions, as individual plants or in dense sowing, for heading time, drought resistance, persistence and forage production. Large variability was found in all characteristics within and between populations. The existing variability of the wild indigenous germplasm has been used in further breeding work, aimed at creating more productive and more persistent varieties, better adapted to dry-hot conditions. The productivity of Greek varieties, tested in Central Greece, was similar to that of foreign varieties under irrigation, while it was much higher under rain-fed conditions. Metsovo tall fescue and Olympion ryegrass are both suitable for use all over Greece under irrigation, or under rain-fed conditions in cool regions. Perrevia cocksfoot could be grown well under rain-fed conditions even in the dry-hot southeastern Greece.

Italy: RAPD fingerprints as a tool for characterizing the genetic background of lucerne (*Medicago sativa* L.) landraces

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Introduction

In Italy cultivated lucerne (*Medicago sativa* L.) is grown on about 1 million hectares and represents the most important leguminous forage crop. In 1995 the Italian National Register of Varieties included 107 cultivars and 14 landraces. In the same year, governmental regulations established that, to meet EC regulations, landraces will definitely be removed from the Register by the year 2002, despite their large use by farmers (70% of the seed market). Thus, there is a real risk of loss of adapted materials if research institutions do not take care of collecting and conserving this germplasm and, at the same time, evaluate it for agronomic traits and genomic variability. In future the improvement of lucerne will depend on the existence and nature of genetic diversity available for manipulation.

The genetic diversity present in lucerne populations has been largely detected by isozymes (Quiros and Morgan 1981) and RFLP markers (Brummer *et al.* 1991; Kidwell *et al.* 1994).

This study was conducted to assess suitability of RAPD markers in detecting the genetic variability among and within lucerne landraces from central Italy. In a first experiment, genetic variability estimations were based on bulked DNA samples; in a second experiment, on single plant DNA samples.

Materials and methods

Experiment 1

As a sample of the available germplasm present in the Marche region, 16 landraces were evaluated (Fig. 1). The Italian varieties 'Equipe' and 'Itaca' and the registered Italian landraces 'Romagnola' and 'Marchigiana' were used as controls in the RAPD analysis.

A hundred seeds from each accession were sown in jiffy pots in February 1995 and plantlets were grown in the greenhouse during the spring. Apical leaves were collected from 4-week-old plants, and total genomic DNA was isolated from six-bulked plants (using one leaflet per plant) following the procedures described by Edwards *et al.* (1991) and Barcaccia and Rosellini (1996). After washing with 75% ethanol and vacuum-drying, the purified DNA was redissolved in 1/3 X TE buffer (Sambrook *et al.* 1989). Spectrophotometric estimation (DU650 Spectrophotometer, Beckman) was used to quantify the amount of genomic DNA and evaluate its purity.

Each population was represented by six bulks (on the whole, 36 plants per population): individual plants 1 to 6, 7 to 12, 13 to 18, 19 to 24, 25 to 30 and 31 to 36 constituted DNA bulks 1, 2, 3, 4, 5 and 6, respectively.

Five 10mer nucleotide primers (P1 ATCCACTGCA; P2 GGTCGCAGGC; P3 CCTTGACGCA; P4 GGACCCTTAC; P5 CTCACCGTCC; Operon Technologies, Inc.) selected in previous investigations on the basis of their ability to find homologous binding sites among lucerne genomic templates (Barcaccia *et al.* 1994) were used to perform Polymerase Chain Reactions according to Barcaccia (1994).

Banding profiles of DNA bulks were recorded by assigning a number to each polymorphic amplification product identified by comparing sample lanes to 100 bp DNA ladders. Only intense RAPD bands ranging in size from 0.3 to 2.2 kb were included in the analysis. Each amplification product was scored as 1 for presence and 0 for absence. The Genetic Similarity Estimate (GSE) was calculated in all possible pairwise comparisons

between samples, using the index of Dice (1945): GSEij=2Mij/(2Mij+Mi+Mj), where Mij represents the number of shared amplification products scored between the pair of samples/lines (i and j) considered, Mi is the number of products present in i but absent in j and Mj is the number of products present in j but absent in i. An index value of 0 indicates that none of the markers evaluated was common to a pair of samples, whereas a value of 1 indicates that a pair of samples generated identical RAPD profiles for that particular set of markers. Moreover, the mean genetic similarity matrix was calculated as the means of GSEs within and between different bulks from each of the 20 accessions evaluated. The cluster analysis was performed according to the unweighted pair-group arithmetic average method (UPGMA) and dendrograms and plots of bulked samples and single accessions were constructed from individual and mean GSEs. All calculations and analyses were conducted using Numerical Taxonomy and Multivariate Analysis System - personal computer (NTSYS-pc) (Rohlf 1992).

Experiment 2

Six landraces from central Italy were evaluated: Casalina, C. Pieve, Grosseto, Gubbio, L'Aquila and Latina using 60 individual plants per landrace. The analysis of RAPD markers was conducted using three 10mer primers (P3 CCTTGACGCA, P5 CTCACCGTTC, P6 CCCGTAGCAC, Operon Technologies, Inc.) chosen on the basis of previous results. Total genomic DNA isolation, Polymerase Chain Reaction, electrophoresis and cluster analysis were performed as reported in experiment 1. Within accession GSEs were calculated as mean of single plant values. The data were also analyzed by a stepwise discriminant procedure and the best predictor RAPD markers were used to perform a discriminant analysis.

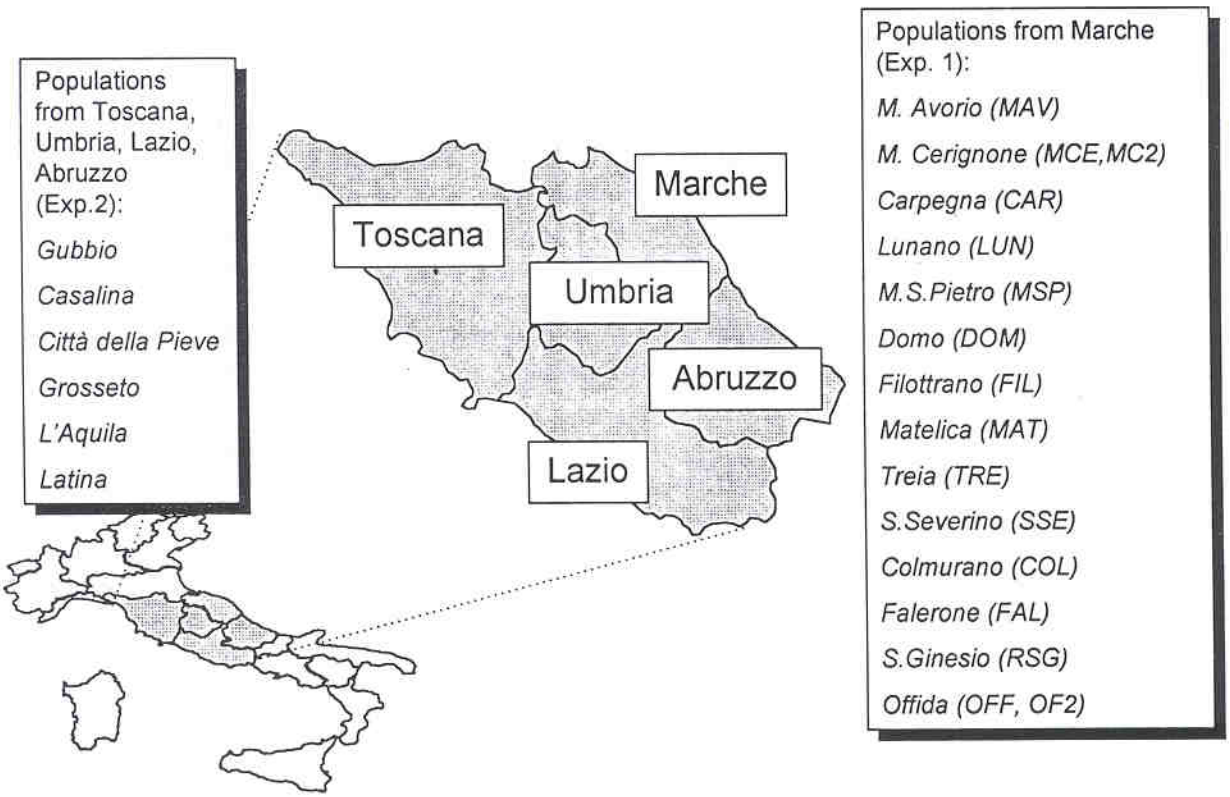

Fig. 1. Landraces examined in the experiments.

Results

In the first experiment, 43 RAPD markers (an average of 8.6 markers per primer) were scored in each accession with the exception of Filottrano and Treia, which both lacked an individual amplification product. Markers specific to a single accession were not detected. On the whole, 25 (58%) polymorphic amplification products were registered as presence or absence characters among the 120 bulks evaluated. RAPD profiles generated from single bulked DNA samples of different landraces were generally monomorphic; however, some amplification products were scorable as polymorphic within and between accessions.

The dendrogram constructed through the cluster analysis illustrates the level of genomic variability detected by RAPD markers among lucerne accessions of the Marche region (Fig. 2). Monte S. Pietro (MSP) was tightly clustered with the landrace Romagnola (ERO) as well as Matelica (MAT) with Lunano (LUN), and Offida (OFF) with Domo (DOM). However, most of the accessions formed a distinct branch on the dendrogram and were clustered from a single branch point showing more than 94% of genetic similarity. This group of accessions included both the control landraces Marchigiana (EMA) and Romagnola (ERO), and the variety Itaca (ITC). The variety Equipe (EQU) and landraces S. Severino (SSE) and Filottrano (FIL) were clustered into a distinct group, showing a consistent genetic diversity from the other accessions (Fig. 2).

On the whole, the results obtained suggest that most of the landraces from Marche belong to a genetically homogeneous population that shares a large part of the genomic traits scored in the registered landrace Marchigiana.

The mean of the genetic similarity estimates within each of the 20 accessions evaluated, calculated as the mean of GSEs between different bulks from the same accession, ranged from 0.911 to 0.977. S. Severino showed the lowest value and Marchigiana the highest one. However mean GSEs of all accessions were very high and indicated a low level of intrapopulation genetic diversity.

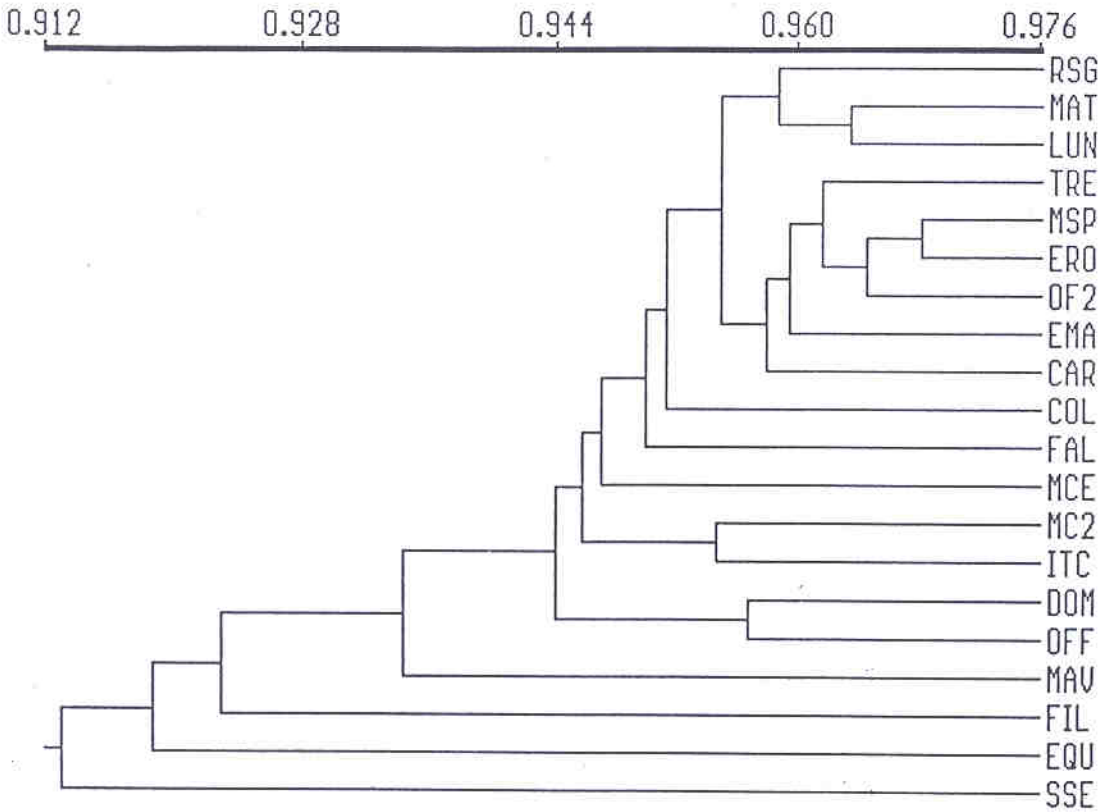

Fig. 2. Dendrogram (UPGMA method) relative to GSEs for landraces from Marche (exp. 1).

In the second experiment, 21 RAPD markers (an average of seven markers per primer) were scored in all landraces. Markers specific to a landrace were not detected, and four different RAPD markers were monomorphic within a single landrace. On the whole, five amplification products were highly conserved among landraces, being shared by from 88.5 to 99.7% of individuals. Most of the amplification products were highly polymorphic, showing presence / absence frequencies rather balanced among landraces.

The mean GSE between pairwise comparisons of different landraces ranged from 0.688 (L'Aquila-Casalina) to 0.769 (Grosseto-C. Pieve).

The dendrogram from mean GSEs clustered five landraces into one distinct group showing a single branch point with more than 73% of genetic similarity. Within such group, C. Pieve, Grosseto and Gubbio on one side, and L'Aquila and Latina on the other side formed two different subgroups, each having more than 76% of genetic similarity (Fig. 3). These preliminary results seem to indicate that five out of six landraces share a large part of the genomic traits, while Casalina is characterized by the presence of a certain amount of unique germplasm.

The results of the cluster analysis were in agreement with those from discriminant analysis, where the centroids were plotted according to functions 1 and 2 (Fig. 4). Using 16 out of 21 RAPD markers scored, five discriminant functions were found, all highly significant with the first three functions, accounting for as much as 89% of the total variation. Function 1 maximally separated the group Grosseto, Gubbio and C. Pieve from Latina and L'Aquila; the best predictors for discriminating these two groups were P5(1) and P6(5). Function 2 maximally separated Casalina from the rest of landraces and the best predictor was P6(3).

The mean GSEs within landraces ranged from 0.690 (Casalina) to 0.777 (Grosseto). The clustering of individuals belonging to Casalina highlighted also three distinct subgroups with a genetic similarity varying between 60% and 75% (Fig. 5).

Discussion

RAPD markers appear to be a useful tool for describing the genetic background of lucerne landraces since their use does not require prior DNA sequence information, they are not affected by developmental stages or environmental conditions, they are quick and cheaper than other molecular markers.

In lucerne RAPD markers obtained from plant DNA bulks of several plants seemed to be an efficient method for quickly assaying the between-accessions variability as in experiment 1, while the within-accession variability was better estimated by using DNA from single plants as in experiment 2. In fact, the bulking procedure used underestimates the level of within-accession genomic diversity when most amplification products are conserved and polymorphic fragments occur at low frequencies as in the material examined. More primers could be evaluated to detect other discriminant RAPD markers and increase the precision of the genetic variability estimates.

Nevertheless, the use of bulked DNA samples could be used as a first approach in screening large germplasm collections: (a) with the purpose of identifying a core collection, (b) when there is urgency for regeneration and not enough resources, and (c) when suitable populations need to be selected for breeding programmes.

Landraces from central Italy could be effectively used as germplasm sources in breeding programmes aimed at the constitution of lucerne varieties since they show dry matter yields significantly higher than cultivars present on the market (Russi and Falcinelli 1997; Veronesi *et al.* 1994, 1997). Choosing among landraces of similar productivity but with different adaptation to find the basic material with which to start the breeding programmes could be assisted by molecular analysis.

The necessity of replacing landraces with improved cultivars to meet EC regulations jeopardizes this precious germplasm with the risk of extinction if research institutions will not collect and conserve such important germplasm sources.

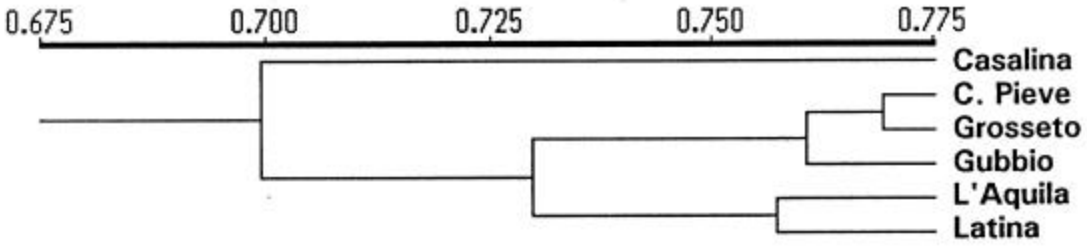

Fig. 3. Dendrogram (UPGMA method) relative to GSEs for landraces from Tuscany, Umbria, Lazio and Abruzzi (exp. 2).

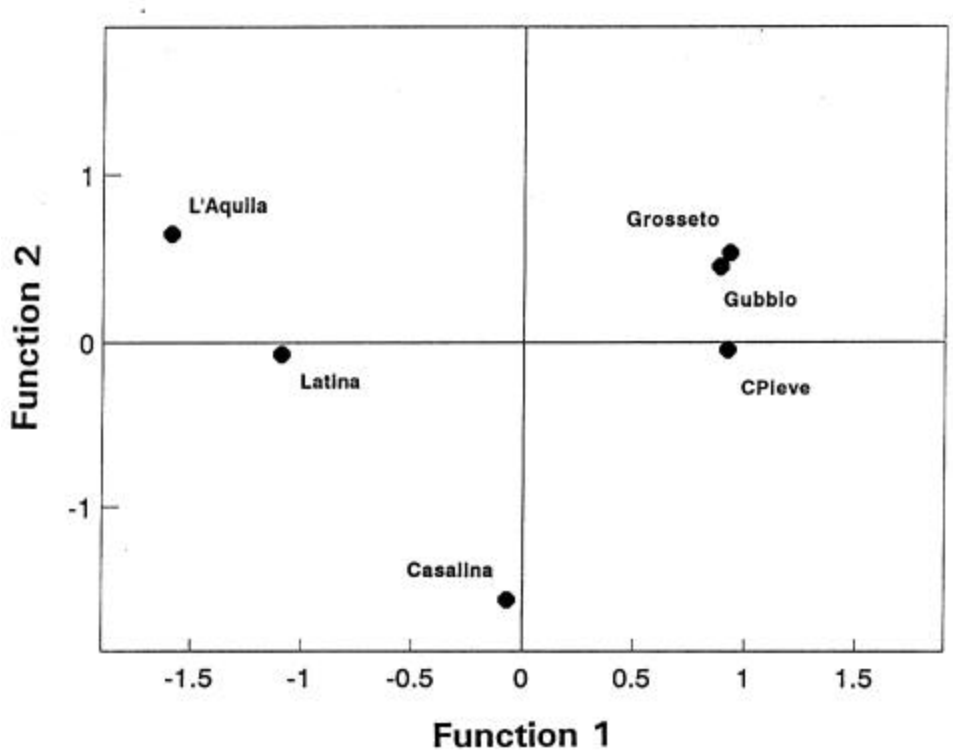

Fig. 4. Centroids of six landraces from Tuscany, Umbria, Lazio and Abruzzi plotted according to the first two discriminant functions (exp. 2).

Acknowledgements
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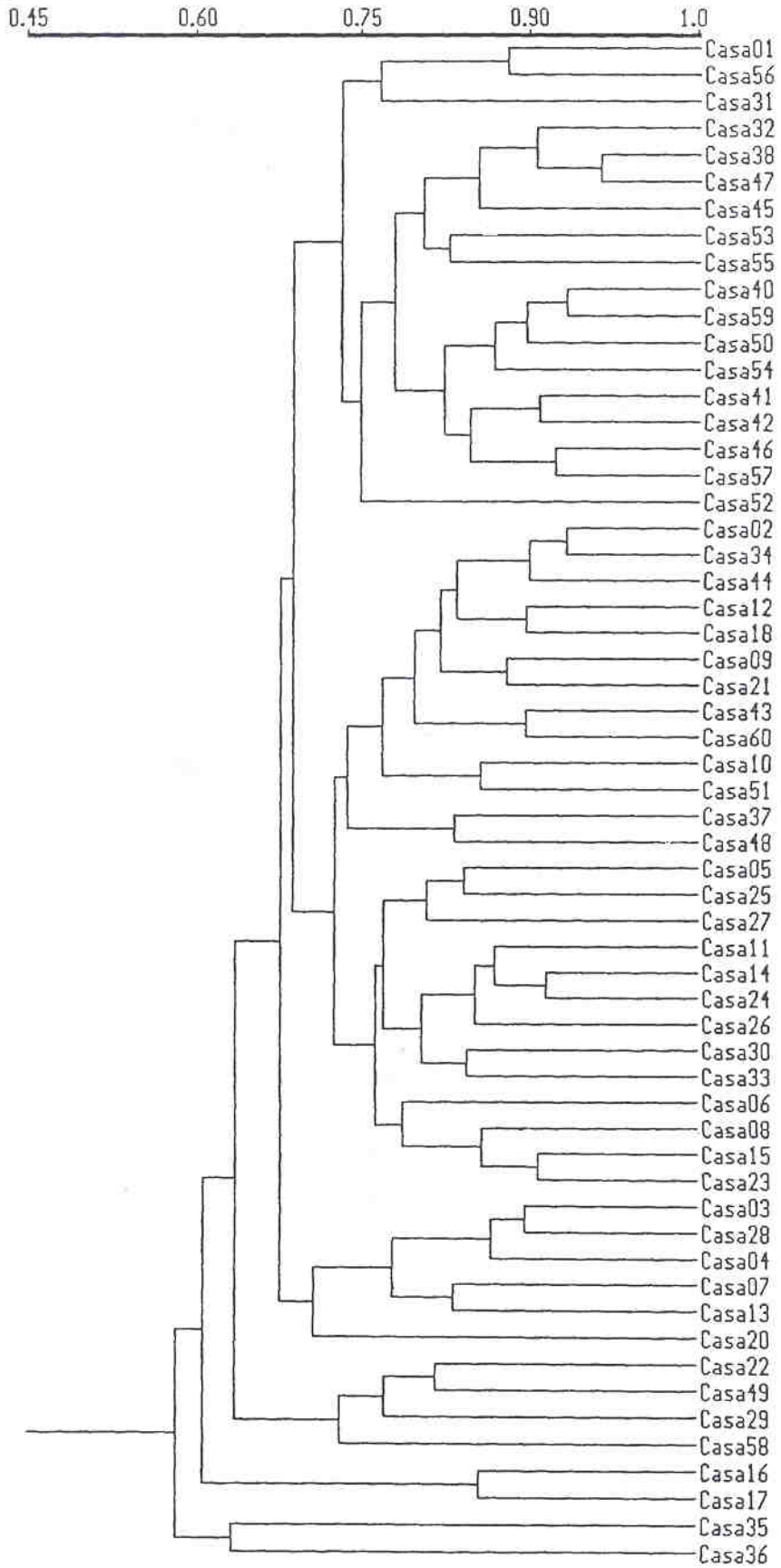

Fig. 5. Dendrogram (UPGMA method) relative to GSEs for plants within the landrace Casalina (exp. 2).

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Turkey: Evaluation of common vetch collections

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Abstract
Common vetch (*Vicia sativa* L.) – 119 accessions – collected from different regions of Turkey was analyzed for 13 characters. There were significant differences among populations for all characters studied. Six principal components were found to express 76% of the total variation. Pod dimensions and seed weight per plant were the major sources of diversity. Main stem length, 1000-seed weight and hay yield per plant had the largest variances.

Introduction

Common vetch (*Vicia sativa* L.) is widely grown in Turkey. There are some high-yielding varieties, but not extensively in use. The landraces or old varieties which have some good characters apart from yield are still being planted in many parts of the country. Additionally, Turkey is the domestication centre of vetches (Harlan 1971). AARI (Aegean Agricultural Research Institute) is the coordination centre of countrywide plant genetic resources activities. As for other plant species, seeds of forages including a great number of common vetch accessions have been collected and maintained in the genebank. Beside conservation of the seeds, multiplication, regeneration and evaluation studies are conducted in coordination with the national forage crops breeding project.

It has been reported that numerical techniques and methods can be effectively used to evaluate a certain number of populations (Veronesi and Falcinelli 1988). Some researchers reported that these techniques could also be applied to different plant species (Goodman 1968; Seiler and Staffort 1985).

The objectives of this study were to specify the characteristics of common vetch populations collected from different regions of Turkey, to find out the relationships among characters, and to classify the populations for the characters studied.

Materials and methods

Common vetch populations (119 accessions) collected from different regions of Turkey were grown at AARI in 1993, and evaluated for 13 characters. The number of accessions was 29, 57, 11 and 22 from central, west, east and south regions, respectively (Fig. 1). Observations and measurements were carried out on 10 plants chosen randomly. The characters were as follows :

Plant height (cm)	Pod length (cm)
Main stem length (cm)	Pod width (cm)
Number of leaves per main stem	Number of seeds per pod
Number of leaflets per leaf	1000-seed weight (g)
Petiole length (cm)	Seed weight per plant (g)
Peduncle length (cm)	Dry matter weight per plant (g)

Morphological characters were recorded at 25% flowering stage which is the optimum time for herbage yield (Soya *et al.* 1988). Earliness was scored by dividing the populations into five groups according to 25% flowering stage with a scale ranging from 1 (very early) to 5 (very late).

Each character studied was analyzed, and statistical parameters such as mean, minimum and maximum values, variance and standard deviation were calculated. Relationships among characters were identified and populations were classified by using Principal Component Analysis.

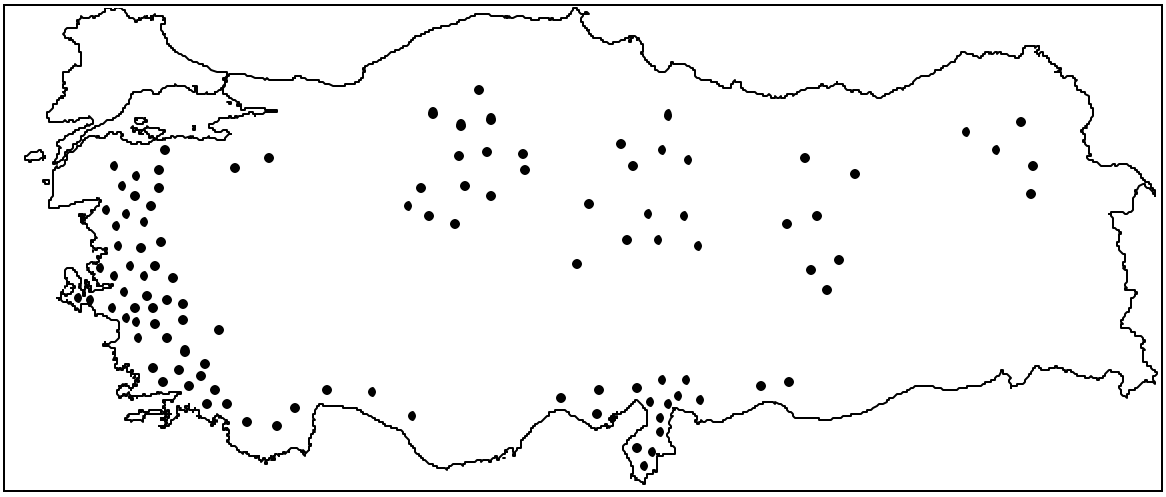

Fig. 1. Distribution of common vetch collections in Turkey.

Results and discussion

There were significant differences among populations for all characters studied. Statistical parameters are presented in Table 1. The largest variances were found for main stem length ranging from 6.8 to 116.0 cm, for 1000-seed weight from 17.2 to 74.7 g, and for dry matter weight per plant from 13 to 94 g. Plant height and seed weight per plant also had a certain amount of variation while pod dimensions, number of leaflets per leaf and seeds per pod were observed as having the least variances.

Figures 2 to 6 show frequency distributions of the characters studied. Plant height ranged from 28 to 60.2 cm with a mean value of 43.1 cm, whereas most populations (69%) were between 40 and 49 cm. Each region was represented in a similar manner for plant height close to the mean value (35-49 cm). There were only 10 populations (0.8%) shorter than 35 cm, and 3 populations taller than 54 cm collected from western and central regions (Fig. 2).

Earliness is an important trait for common vetch production in western and southern regions, especially in the rotation system with cotton. The percentage of early populations, scored as 1 or 2, was 23% of all accessions (Fig. 3), most of them belonging to the west. Late populations were found to occur in every regions.

Table 1. Statistical parameters for 13 characters in common vetch populations

Character	Mean	Min.	Max.	Variance	Standard deviation
Plant height (cm)	43.1	28.0	60.2	37.60	6.13
Main stem length (cm)	55.7	6.8	116.0	918.55	30.30
No. of leaves per main stem	15.3	11.4	22.5	4.37	2.09
No. of leaflets per leaf	14.0	10.2	16.0	0.97	0.98
Petiole length (cm)	6.2	3.4	11.1	2.84	1.68
Peduncle length (cm)	2.9	1.8	5.3	0.52	0.72
Earliness	3.5	1.0	5.0	1.62	1.27
Pod length (cm)	4.8	3.1	6.3	0.21	0.46
Pod width (cm)	0.6	0.4	0.7	0.01	0.06
No. of seeds per pod	7.5	6.0	10.0	0.57	0.76
1000-seed weight (g)	46.1	17.2	74.4	129.03	11.36
Seed weight per plant (g)	16.1	1.8	40.0	57.13	7.56
Dry matter weight per plant (g)	35.9	13.0	94.0	254.20	15.94

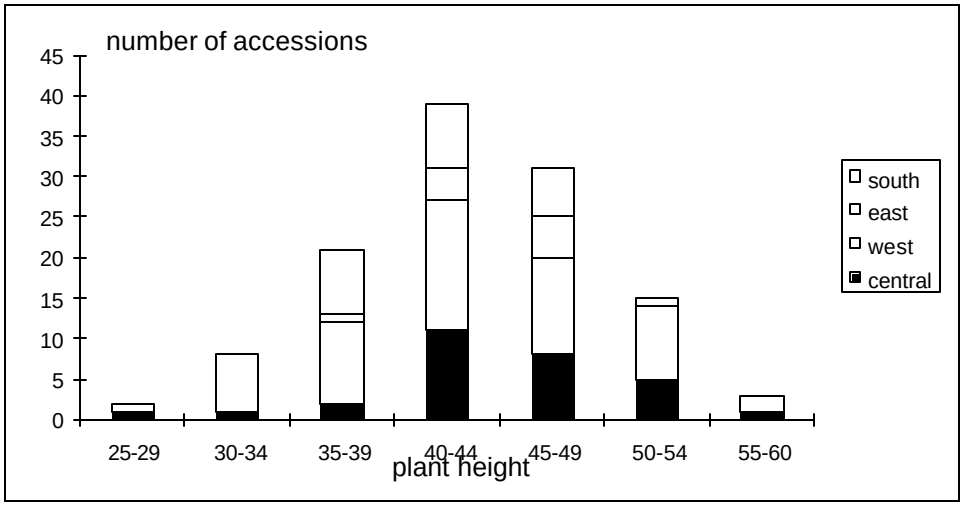

Fig. 2. Frequency distribution of plant height (cm).

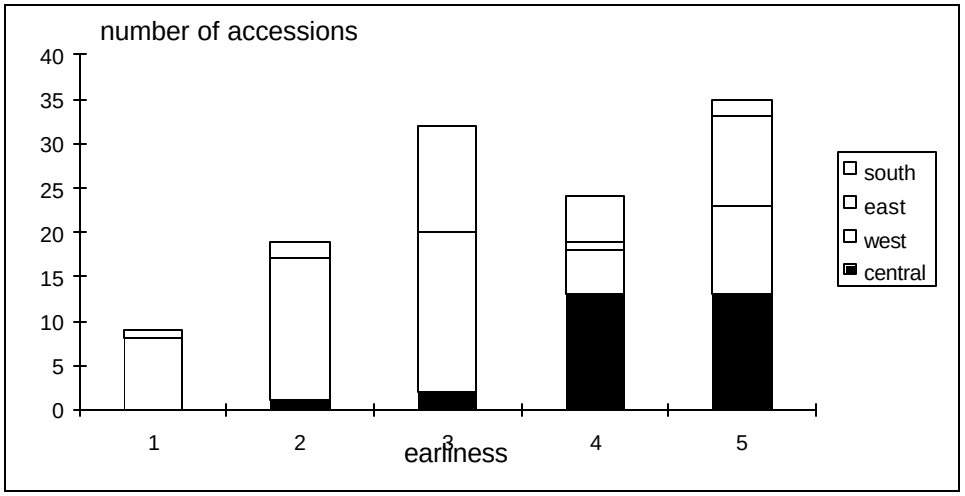

Fig. 3. Frequency distribution of earliness (1=very early, 5=very late).

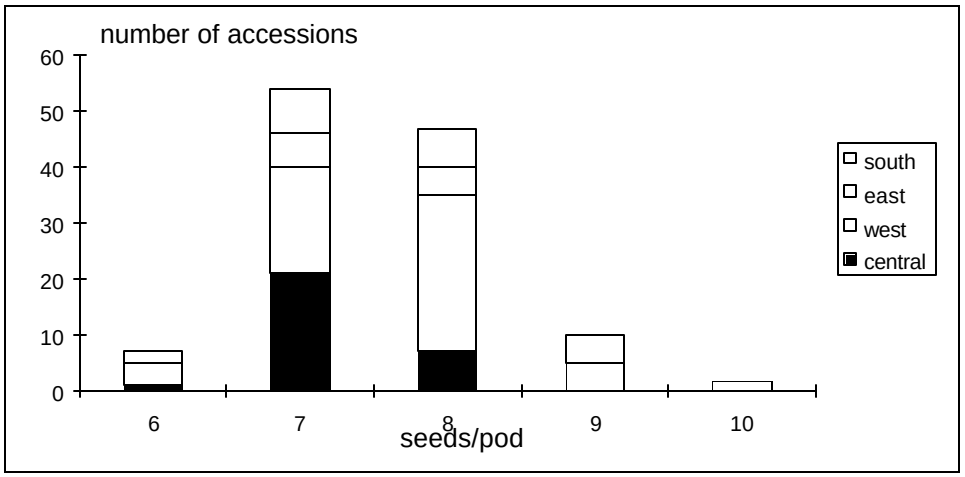

Fig. 4. Frequency distribution of number of seeds per pod.

Eighty-five percent of populations were observed to have 7 or 8 seeds per pod representing every region (Fig. 4). Populations with 9 and 10 seeds per pod (9%) came from the west and south regions. Few populations produced fewer than 7 seeds per pod.

The pattern of 1000-seed weight showed a normal distribution with an average value of 46.1 g, ranging from 17.2 to 74.4 g (Fig. 5). The most prominent group of populations (40%) was between 40 and 49 g.

Seed weight per plant varied between 1.8 and 40 g with an average of 16.1. Only three populations produced seeds greater than 30 g (Fig. 6).

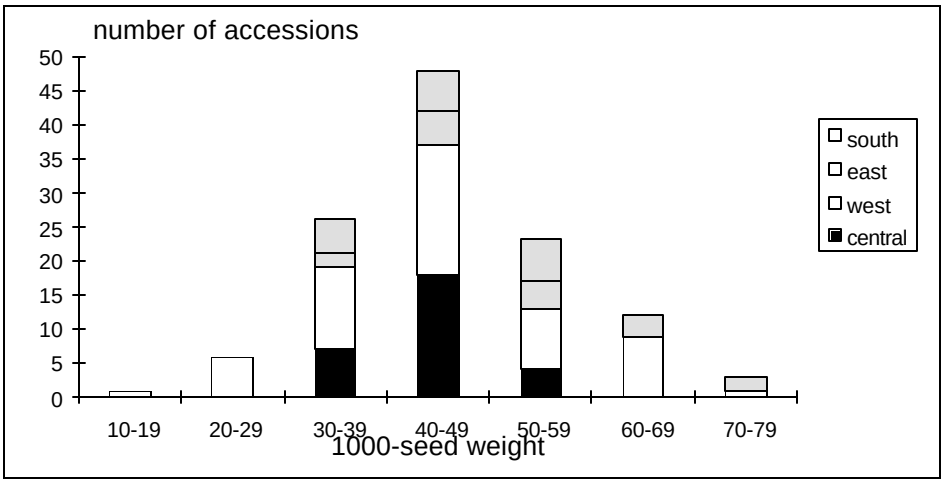

Fig. 5. Frequency distribution of 1000-seed weight (g).

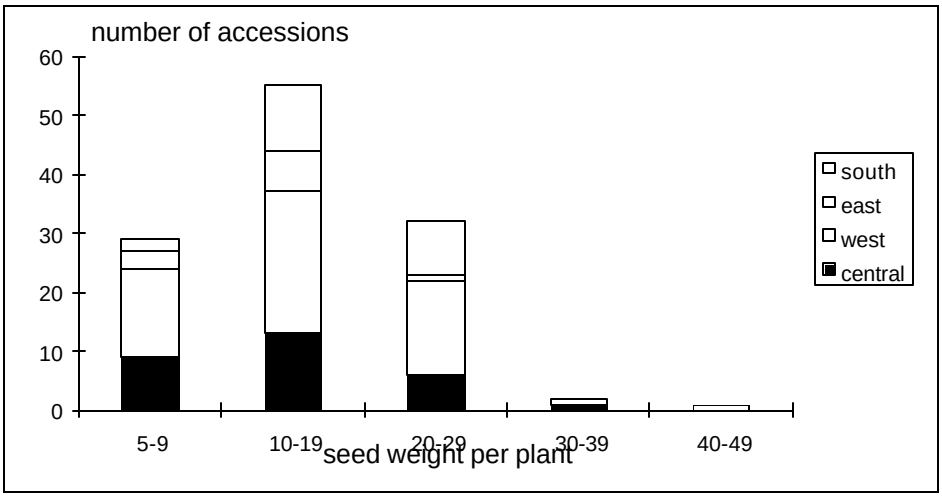

Fig. 6. Frequency distribution of seed weight per plant (g).

Table 2 shows the simple correlation coefficients between the characters. Plant height positively correlated with main stem length, number of leaves on main stem, number of leaflets per leaf, peduncle length and earliness. Main stem length had a significant correlation with only number of leaves on main stem (r=0.64) among morphological characters.

Table 2. Correlation coefficients between 13 characters[†] in common vetch populations

	plh	msl	nms	nll	ptl	pcl	ear	pdl	pdw	nsp	tsw	swp
msl	0.25 **	–										
nms	0.51 ***	0.64 ***	–									
nll	0.25 **	0.14	0.34 ***	–								
ptl	–0.14	0.08	–0.04	–0.02	–							
pcl	0.25 **	0.04	0.30 **	0.23 **	0.15	–						
ear	0.24 **	–0.11	0.09	0.12	0.49 ***	0.49 ***	–					
pdl	0.06	0.11	0.09	0.25 **	–0.11	0.01	0.14	–				
pdw	0.10	0.10	0.12	0.28 **	–0.08	–0.08	–0.05	0.25 **	–			
nsp	–0.21 *	–0.12	–0.22 *	–0.28 **	–0.12	–0.12	–0.14	–0.10	–0.29 **	–		
tsw	0.26 **	0.47 ***	0.31 **	0.30 **	–0.11	–0.11	–0.13	0.30 ***	0.41 ***	–0.26 **	–	
swp	–0.06	–0.12	–0.28 **	–0.14	–0.33 ***	–0.33 ***	–0.20 *	0.05	–0.02	0.08	0.28 **	–
dwp	0.07	–0.64 ***	–0.40 ***	–0.07	0.15	0.15	0.17	–0.09	–0.01	–0.02	–0.43 ***	0.19 *

[†] plh=plant height; msl=main stem length; nms=number of leaves on main stem; nll=number of leaflets per leaf; ptl=petiole length; pcl=peduncle length; ear=earliness; pdl=pod length; pdw=pod width; nsp=number of seeds per pod; tsw=1000-seed weight; swp=seed weight per plant; dwp=dry matter weight per plant.

*,**,*** =Significant at $P<0.05$, 0.01 and 0.001.

There were negative and significant correlations between number of seeds per pod and number of leaves on main stem, number of leaflets per leaf, pod width and 1000-seed weight. The 1000-seed weight was positively influenced by most of the other characters except number of seeds per pod. Pod length and width had large effects on this character (r=0.30 and 0.41). Negative correlations between seed weight per plant and number of leaves on main stem, plant height, peduncle length and earliness showed that an increase in these characters resulted in a decrease in seed weight per plant. Early genotypes have higher seed yields than late ones. Dry matter weight per plant correlated highly and negatively with main stem length, number of leaves on main stem and 1000-seed weight. The significant and positive correlation coefficient between 1000-seed weight and seed weight per plant (r=0.19) indicated that the breeding studies should be focused on both characters to increase common vetch production.

The variation among populations was also observed by using Principal Component Analysis. The first four components with Eigen values greater than 1.0 expressed 62.78% of total variation (Table 3). Component coefficients greater than 3.0 were taken into account as having a larger contribution to the total variation (Brown 1991). Negative values indicate the direction of relationship between the variable and component (Seiler and Stafford 1985; Veronesi and Falcinelli 1988).

Table 3. Principal component coefficients for 13 characters

Character	prin 1	prin 2	prin 3	prin 4
Plant height (cm)	0.320	0.182	0.070	0.326
Main stem length (cm)	0.410	–0.181	–0.354	0.001
No. of leaves per main stem	0.450	0.102	–0.231	0.124
No. of leaflets per leaf	0.315	0.137	0.258	–0.138
Petiole length (cm)	–0.028	0.133	–0.220	–0.670
Peduncle length (cm)	0.142	0.539	–0.045	0.043
Earliness	0.072	0.483	0.167	0.266
Pod length (cm)	0.199	–0.065	0.354	0.028
Pod width (cm)	0.227	–0.118	0.372	–0.423
No. of seeds per pod	–0.245	–0.122	–0.285	0.263
1000–seed weight (g)	0.375	–0.340	0.203	0.015
Seed weight per plant (g)	–0.125	–0.363	0.356	0.287
Hay weight per plant (g)	–0.307	0.289	0.399	–0.077
Eigen values	3.152	2.096	1.636	1.280
Percentage variance	24.24	16.12	12.58	9.84
Cumulative variance	24.24	40.36	52.94	62.78

Plant height, main stem length, number of leaves on main stem, number of leaflets per leaf and 1000-seed weight were the main contributors to the first principal component which covered 24.24% of the total variation. Component 2, accounting for 16.12% of variation, consisted of peduncle length and earliness in positive direction, 1000-seed weight and seed weight per plant in negative direction. Figure 7 shows the distribution of populations over the first two components. Five morphological characters together with earliness, 1000-seed weight and seed weight per plant were found to be major sources of variation in consideration with the first two components. Thirty-six populations made up a distinct group with a major contribution of these characters cited above.

The third component was made of mainly generative characters – pod length, pod width, seed weight per plant and dry matter weight per plant – with the exception of main stem length, with 12.58% of variation. Only two characters – plant height and pod width – were the main contributors to the fourth principal component which accounted for 9.84% of total variation. The distribution of populations defined by the last two components is presented in Figure 8. Populations no. 51 and no. 100 collected from western Anatolia were quite different from all remaining populations. There was no clear grouping, all populations being scattered around the two axes.

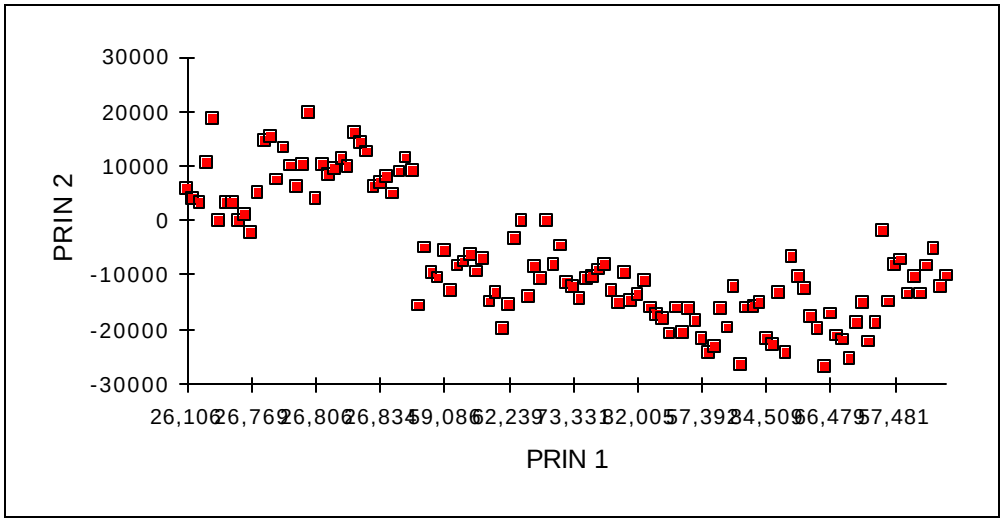

Fig. 7. Distribution of populations defined by principal components 1 and 2.

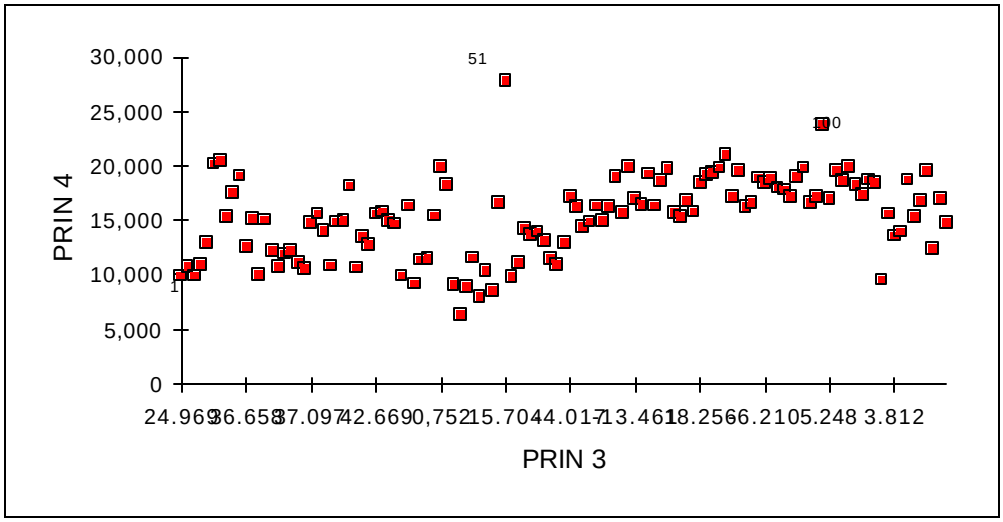

Fig. 8. Distribution of populations defined by principal components 3 and 4.

Principal component analysis together with variance analysis showed that there was a great amount of diversity among common vetch populations. This kind of analysis would help the plant breeders classify the material into groups according to the characters they are studying.

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United Kingdom: Research at IGER on *in situ* conservation of botanical diversity in agricultural grasslands

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A number of regions within the UK have been designated Environmentally Sensitive Areas (ESAs). These areas have high, or at least potentially high, value for *in situ* conservation of biodiversity, which could be at risk from inappropriate management for agriculture, forestry and amenity usage. The aim of the UK government is to reverse environmental deterioration that has already occurred and to promote the continued maintenance and improvement of environmental quality in these areas, through the introduction of guidelines for appropriate management coupled with payment of subsidies to local inhabitants who agree to follow the guidelines. To enable these aims to be achieved, the UK Ministry of Agriculture Fisheries and Food (MAFF) funds several projects at IGER to develop guidelines for the restoration and conservation of biodiversity *in situ* in agricultural grasslands in ESAs.

We are comparing the influence of a range of managements on botanical diversity in different types of grassland. These include varying the amount and type of fertilizer and lime applied, and varying the intensity and timing of grazing and cutting. Management regimes are selected that correspond to traditional local farming practices, intensive management and alternative low-input systems. Effects are measured on productivity, species diversity and soil status.

Different types of grassland have been shown to differ in their potential to increase in species diversity following the implementation of more environmentally sensitive management regimes. Grasslands that, through intensive management over many years, have lost diversity from the seed bank as well as the vegetation, cannot respond quickly to improved management. Natural invasion from surrounding grasslands is too slow to be acceptable under UK government plans.

In such cases, consideration is given to artificially reintroducing species that have been lost. Projects in progress at IGER are determining optimal procedures for introducing seed. An open sward structure needs to be created at critical times to enable seedling establishment, whilst avoiding excessive damage to young seedlings.

The provenance of commercially available seed for re-establishing species-rich grasslands is not currently controlled. We are assessing the importance of using locally provenanced seed. On the one hand, using seed of alien origin risks genetically contaminating local ecotypes. On the other hand, it has been hypothesized that such risks are minimized through a natural 'environmental sieve', by which alien ecotypes are eliminated through being less well adapted. We have shown that this mechanism is not generally effective, and that significant genetic contamination does occur through use of commercial seed mixtures.

Re-establishment of hedges in field margins is being promoted as a valuable component of *in situ* conservation of biodiversity within agricultural landscapes. However, it is undertaken mainly with commercially available hawthorn (*Crataegus monogyna* Jacq.) of eastern European origin. Locally provenanced hawthorn is either not commercially available or expensive. Our studies have shown major ecotypic differentiation between local races and eastern European ecotypes. Local races are superior in terms of adaptation to UK winters, development of a high-quality dense hedge structure, and thorniness. They are therefore superior both in terms of habitat quality for wildlife, and in their effectiveness as a barrier to sheep and cattle. Discussions are in progress with seed companies to promote awareness of the benefits of using local races.

Finally, there is particular concern over the genetic integrity of species that have evolved as dominant or subdominant components of grasslands but have now become rare, existing only as small isolated populations. There is a risk that the remnant populations will become too inbred. There is a corresponding need to address optimal habitat structure when suitable habitats are present only in small isolated pockets. IGER has a project to address this problem, by assessing geneflow between model populations of *Lotus* monomorphic for different isozyme marker alleles and sown in various spatial arrangements.

Appendix I. Forage Passport Descriptors

Based on the FAO/IPGRI Multicrop Passport Descriptors (14 Feb 97) and the main descriptors in the different forages databases

FORAGE PASSPORT DESCRIPTORS
1. Institute code (INSTCODE) Code of the institute where the accession is maintained. The codes consist of the 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym.
2. Accession number (ACCENUMB) This number serves as a unique identifier for accessions and is assigned when an accession is entered into the collection. Once assigned this number should never be reassigned to another accession in the collection. Even if an accession is lost, its assigned number should never be reused. Letters should be used before the number to identify the genebank or national system (e.g. IDG indicates an accession that comes from the genebank at Bari, Italy; CGN indicates an accession from the genebank at Wageningen, The Netherlands; PI indicates an accession within the USA system).
3. Collecting number (COLLNUMB) Original number assigned by the collector(s) of the sample, normally composed of the name or initials of the collector(s) followed by a number. This item is essential for identifying duplicates held in different collections. It should be unique and always accompany subsamples wherever they are sent.
4. Genus (GENUS) Genus name for taxon. Initial uppercase letter required.
5. Species (SPECIES) Specific epithet portion of the scientific name in lowercase letters plus authority.† Following abbreviation is allowed: "sp."
6. Subtaxa (SUBTAXA) Subtaxa can be used to store any additional taxonomic identifier plus authority.† Following abbreviations are allowed: "ssp." (for subspecies); "var." (for variety); "convar." (for convariety); "f." (for form).
A. Collector's name (COLLNAME) The name of the collector.
7. Accession name (ACCNAME) Either a registered or other formal designation given to the accession. First letter uppercase. Multiple names separated with semicolon.
8. Country of origin (ORIGCTY) Name of the country in which the sample was originally collected or derived. Use the ISO 3166 extended codes, (i.e. current and old 3 letter ISO 3166 country codes)
9. Location of collecting site (COLLSITE) Location information below the country level that describes where the accession was collected starting with the most detailed information. Might include the distance in kilometers and direction from the nearest town, village or map grid reference point, (e.g. CURITIBA 7S, PARANA means 7 km south of Curitiba in the state of Parana)
10. Latitude of collecting site (LATITUDE) Degrees and minutes followed by N (North) or S (South) (e.g. 1030S). Missing data (minutes) should be indicated with hyphen (e.g. 10—S).
11. Longitude of collecting site (LONGITUDE) Degrees and minutes followed by E (East) or W (West) (e.g. 07625W). Missing data (minutes) should be indicated with hyphen (e.g. 076—W).

† Authority is only provided at the most detailed taxonomic level.

12. Elevation of collecting site (ELEVATION)

[in meters above sea level]

13. Collecting date of original sample [YYYYMMDD] (COLLDATE)

Collecting date of the original sample where YYYY is the year, MM is the month and DD is the day.

14. Status of sample (SAMPSTAT)

1	Wild	0	Unknown
	– 1A Natural ecotype		
	– 1B Semi-natural ecotype	99	Other (Elaborate in 'Remarks' field)
2	Weedy		
3	Traditional cultivar / Landrace		
4	Breeders' line		
5	Advanced cultivar		

15. Collecting source (COLLSRC)

The coding scheme proposed can be used at 2 different levels of detail: Either by using the global codes such as 1, 2, 3, 4 or by using the more detailed coding such as 1.1, 1.2, 1.3 etc.

1	Wild habitat	2	Farm	3	Market	4	Institute / Research
1.1	Forest /	2.1	Field	3.1	Town		organization
	woodland	2.2	Orchard	3.2	Village		
1.2	Shrubland	2.3	Garden	3.3	Urban	0	Unknown
1.3	Grassland	2.4	Fallow	3.4	Other exchange		
1.4	Desert /	2.5	Pasture		system	99	Other (Elaborate in
	tundra	2.6	Store				'Remarks' field)

16. Donor institute code (DONORCODE)

Code for the donor institute. The codes consist of the 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym.

17. Donor number (DONORNUMB)

Number assigned to an accession by the donor. Letters should be used before the number to identify the genebank or national system (e.g. IDG indicates an accession that comes from the genebank at Bari, Italy; CGN indicates an accession from the genebank at Wageningen, The Netherlands; PI indicates an accession within the USA system)

18. Other number(s) associated with the accession (OTHERNUMB)

Any other identification number known to exist in other collections for this accession. Letters should be used before the number to identify the genebank or national system (e.g. IDG indicates an accession that comes from the genebank at Bari, Italy; CGN indicates an accession from the genebank at Wageningen, The Netherlands; PI indicates an accession within the USA system). Multiple numbers can be added and should be separated with a semicolon

B. Breeding institute (BREEDINST)

Code for the breeding institute. The codes consist of 3-letter ISO country code plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO country code and an acronym.

C. Breeding method (BREEDMET)

If more than one breeding method, enter in the order of breeding development and separate with a semicolon.

1	intrapopulation selection
2	mass selection (interpopulation selection)
3	pair cross
4	polycross
5	backcross
6	polyploidization
7	mutation
99	Other, specify in 'Remarks'

D. General habitat **(GENHABIT)**

1	forest deciduous	8	moorland
2	forest evergreen	9	heath
3	forest mixed	10	arable
4	scrub	11	wasteland
5	parkland	12	macchia
6	orchard	99	Other, specify in descriptor 'Remarks'
7	grassland		

E. Specific habitat **(SPECHABIT)**

1 hedgerow
2 clearing
3 path
4 alongside water, i.e. river, lake, etc.
5 alongside building
6 alongside path, road, track, etc.
99 Other, specify in descriptor 'Remarks'

F. Grassland habitat **(GRAHABIT)**

1 abandoned
2 grazed only
3 conservation only
4 mainly grazed
5 mainly conservation
6 zero grazed
7 lawn
8 sports turf
99 Other specify in descriptor 'Remarks'

G. Aspect **(ASPECT)**

S = south, SW = southwest, SE = southeast, etc.

H. Slope **(SLOPE)**

(degrees)

I. Physiography of site **(SITEPHYS)**

1 plain
2 valley bottom
3 valley slope
4 terrace
5 summit
99 Other, specify in descriptor 'Remarks'

J. Seed availability **(SEEDAVAIL)**

0 Not available
1 Available

K. European forage collection **(EFC)**

0 No
1 Yes

L. Holder of Primary Collection **(PRIMCOLL)**

Code for the institute holding the primary collection of the accession. The codes consist of 3-letter ISO country code plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO country code and an acronym.

19. Remarks **(REMARKS)**

The remarks field is used to add notes or to elaborate on descriptors with value "99" (=Other). Prefix remarks with the field name they refer to and a colon (e.g. COLLSRC: roadside). Separate remarks referring to different fields are separated by semicolons.

FAO WIEWS DESCRIPTORS

1. Location of safety-duplicates (DUPLSITE)

Code of the institute where a safety-duplicate of the accession is maintained. The codes consist of 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym. Multiple numbers can be added and should be separated with a semicolon.

M. Date of safety-duplication (YYYYMMDD) (DUPDATE)

Date of safety-duplication, where YYYY is the year, MM is the month and DD is the day.

2. Availability of passport data (PASSAVAIL)

(i.e. in addition to what has been provided)

0 Not available
1 Available

3. Availability of characterization data (CHARAVAIL)

0 Not available
1 Available

4. Availability of evaluation data (EVALAVAIL)

0 Not available
1 Available

5. Acquisition type of the accession (ACQTYPE)

1 Collected / bred originally by the institute
2 Collected / bred originally by joint mission / institution
3 Received as a secondary repository

6. Type of storage (STORTYPE)

Maintenance type of germplasm. If germplasm is maintained under different types of storage, multiple choices are allowed, separated by a semicolon (e.g. 2;3). (Refer to FAO / IPGRI Genebank Standards 1994 for details on storage type)

1 Short-term
2 Medium-term
3 Long-term
4 *In vitro* collection
5 Field genebank collection
6 Cryopreserved
99 Other (elaborate in 'Remarks' field)

Appendix II. Towards a protocol for designating primary holders of accessions

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Background

The identification of historically unique accessions has attracted considerable interest but presents major technical difficulties (Knüpffer 1989; van Hintum and Knüpffer 1995; Willner *et al.*, this volume). Subsequent identification of historically duplicate but biologically unique accessions presents still further difficulties, especially for accessions of forage species whose genetic composition shows marked changes during regeneration. A major research programme would be required to undertake this for each species. For most species, and especially for temperate forages, it is likely not to be cost-effective in terms of the investment of time and resources relative to the gains to be achieved; moreover, progress in definitively identifying unique accessions cannot be made sufficiently rapidly to achieve the aims of the European Forage Collection programme.

This article suggests an alternative that is considerably easier, is cost-effective and achievable with data in the full ECCDBs (European Central Crop DataBases). It is acknowledged that it may be regarded as conceptually unsatisfactory, since it relies on common donor numbers for detecting duplicates, which can be misleading (see Willner *et al.*, p. 92). It is presented as an economical and rapid solution for improving the organization of genebank collections, not as a definitive means of rationalizing them.

ECCDB managers will be the primary implementors of the protocol, but will need to liaise with relevant genebank curators.

Full resolution of the issues discussed here is beyond the competence of this workshop: this article seeks primarily to suggest a procedure to enable the ECCDB managers to provide relevant information. For ease of reference the suggestions are presented as a practical protocol. However it should not be regarded as a definitive protocol until more widely discussed, revised and approved.

Objective

The objective is to facilitate the development of the European Forage Collection by providing ECCDB managers with a method for (a) selecting member genebanks of the ECP/GR to be recommended as the primary holder of accessions held in the European Forage Collection and (b) identifying the possible need for repatriation.

It is proposed to evaluate the protocol empirically by applying it to the *Lolium* ECCDB for accessions held at IGER.

Principles

According to the Convention on Biological Diversity, each country owns and is responsible for its own biodiversity. Following this principle, the primary holder of each collected accession should normally be a genebank in the country of origin of the accession, provided that that genebank has the facilities and capacity to meet the terms of the European Forage Collection. Notwithstanding this, and recognizing that (a) designating a genebank as primary holder of an accession only concerns curatorship and implies nothing about ownership, and (b) maintenance of genetic integrity is of paramount importance, choice of primary holder should not be constrained by questions of ownership. The primary holder must be able to guarantee storage and regeneration conditions that optimize maintenance of genetic integrity regardless of the origin of the accession. As such, repatriation of a sample of

seed will always be recommended if it has been lost from all genebanks in the country of origin, but this will not necessarily be associated with repatriation of responsibility.

A genebank will in most cases be designated primary holder of accessions it has collected but not of accessions donated to it. Exceptions include:

- it will not be primary holder if repatriation of seed with associated repatriation of responsibility is recommended
- it will not be primary holder if another genebank that collaborated in the same collecting expedition is to be sole primary holder
- it will be primary holder of seed that was donated to it with explicit or implicit transfer of responsibility for maintenance.

Method

The ECCDB manager must first distinguish between accessions **collected** by a genebank and accessions **donated** to a genebank. This is done using the **Source** passport descriptor introduced in the revised Forage Passport Descriptors List (see Appendix I).[19] An accession with no value in this field will not be assigned a primary holder.

Collected accessions

It is assumed that all collecting expeditions conform with the Convention on Biological Diversity and the International Undertaking. In particular, all collecting expeditions include at least one participant from the country in which the expedition is undertaken, and that visiting collectors agree to repatriate samples of seed on request. A collecting expedition undertaken without collaboration may only take place in the collector's own country.

Step 1: identifying "duplicate" collections

For all accessions where **Source = collected by holding genebank**, the ECCDB manager should seek duplicated data in the **Collecting Number** field. The search for duplicates should be based on the parsed components of the data, i.e. separated into groups of letters and numbers with the punctuation marks (space, colon, full stop, etc.) eliminated. This improves detection of accessions with duplicate collecting number even when entered with inconsistent data formats (e.g. with or without a space, colon, full stop, etc. between collectors' initials and number, with or without full stops after each initial, upper or lower case letters, etc.).

It should be emphasized that this does not reliably identify historically duplicate, let alone biologically duplicate, accessions. The approach can be misleading if regarded as identifying duplicates, and is used here only as an easy, fast method of preliminarily identifying potential duplicates.

Step 2: identifying the need for repatriation

In all cases, the ECCDB manager should determine whether there is a need to consider repatriation, which occurs in the following situation:

- none of the genebanks holding accessions with duplicate **Collecting Number** is in the country of origin of the accession (i.e. **first three letters of Institute Code do not**

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[19] The approval of this document would require the inclusion of an additional descriptor to the Forages Passport Descriptors List (Appendix I):
Field name: **Source**
Valid field values: 1=Collected by holding genebank; 2=Donated with transfer of responsibility; 3=Donated without transfer of responsibility; 4= Donated with unknown transfer of responsibility.
(In the case of a genebank that is also a breeding institute, varieties, selections, hybrids, etc. bred by the genebank itself could be recorded as an "internal" donation, as category 2= Donated with transfer of responsibility. We could consider a separate category for such internal donations. However, since the implications for primary holdership are identical to category 2, there is no need for a separate category.)

correspond to Country of Origin for all accessions sharing the same **Collecting Number**) (N.B. Include check for data validity: all accessions sharing the same **Collecting Number** should also share the same **Country of Origin** and identical other passport data on the original collection), and

- the country of origin is an ECP/GR member.

In this situation, the ECCDB manager will contact the genebank in the country of origin with a view to recommending repatriation of the accession.

Step 3: designating primary holder

Step 3a: primary holder of repatriated accession

By mutual agreement between the holding genebanks and the genebank to which the accession is repatriated, one of the following options will be chosen:

1. The genebank receiving the repatriated accession is designated primary holder. This is generally the preferred ultimate option, but only if the genebank is able to maintain genetic integrity to at least the standard achieved by the holding genebank.
2. The original holding genebank (or genebanks if more than one) is designated primary holder, in accordance with the guidelines below. This will be preferred if the holding genebank can regenerate to a higher standard.
3. The genebank receiving the repatriated accession is designated "ultimate" primary holder, but is unable to assume this responsibility immediately. The original holding genebank is designated temporary primary holder as an interim measure. This option is likely to be the most common, since:
   - the receiving genebank will not be able to distribute the accession until enough seed has been regenerated
   - even after it has enough seed to distribute, genetic integrity of the sample held by the receiving institute is likely to be worse than the sample at the original institute.

Thus, the donor of the repatriated material will remain primary holder at least until the repatriated material becomes available for distribution, and probably until the donor runs out of material and also needs to regenerate.

Step 3b: primary holder of "unique" accession without repatriation

(N.B. again it is emphasized that "unique" is merely an abbreviation for an accession without duplicate collecting numbers: this does not imply it is actually unique, either historically or biologically.)

If repatriation of both seed and responsibility is not appropriate and duplicate collecting numbers are not found, the genebank holding the accession is designated primary holder. This will occur under the following conditions:

1. The original collecting expedition was undertaken by the genebank without collaboration.
2. The original collecting expedition was undertaken in collaboration with at least one other organization, but:
   - through failure to enter relevant passport data, or through errors in data entry, or through entering data in incompatible formats, or through following different standards for translation or transliteration, or through failure to provide the ECCDB manager with all relevant data, the search for duplicate collecting numbers fails to detect historically duplicate collections
   - none of the other collaborators is a genebank participating in the ECP/GR
   - all collaborating genebanks that do participate in the ECP/GR have lost their sample of the accession from their collection.

Step 3c: primary holder of duplicate accession without repatriation

If accessions with duplicate collecting numbers are found, the ECCDB manager must determine which, if any, are original duplicates collected by other genebanks collaborating in a joint collecting expedition. This is the case where accessions with duplicate collecting numbers also have **Source=collected by holding genebank**. If there are no such collaborating genebanks, the sole genebank holding the accession with **Source=collected by holding genebank** will be designated primary holder unless repatriation is to be recommended.

If two or more collaborating genebanks do hold original samples of accessions with duplicate **Collection Number** and **Source=collected by holding genebank**, the ECCDB manager may provisionally recommend one of them to be designated primary holder (unless repatriation is recommended). Recommending all original collecting genebanks jointly as primary holders may also be considered an option. Final designation is subject to mutual agreement between the collaborators and the ECCDB manager.

Accessions that have duplicate **Collecting Number** but **Source is different from "collected by holding genebank"** are accepted as having been derived by donation from the original accession. The agreed primary holder of the original collection will be entered as the primary holder of all such donated accessions with duplicate collecting numbers.

Donated accessions

All accessions where **Source is different from "collected by holding genebank"** are considered to have been donated. Varieties, hybrids, selections and other breeders' lines created by a "breeding genebank" are recorded as donations to the genebank, even if this involves no physical donation of seed but only a logical internal donation from breeder to genebank.

The previous section deals with donated accessions that share a duplicate **Collection Number** with original collections, and so that have been assigned a primary holder. This section deals with donated accessions that have not been sourced to an original collection. For these accessions, the ECCDB manager must distinguish between varieties and other accessions.

Step 4: donated varieties

For varieties, the ECCDB manager should conduct a simple search for historical duplicates using only the **Accession Name** passport data field. The search should not involve detailed inspection and correction of similar names, where differences have arisen through errors of transcription, transliteration, translation, etc. Accessions should be regarded as duplicate varieties if parsed components of the accession name are identical. For each distinct name, the ECCDB manager should inspect the origin(s) of accessions with that name. If there appears to be a single origin for accessions sharing the same name, the ECCDB should suggest a primary holder based on that origin. If there appears to be more than one distinct origin for accessions sharing the same name, the ECCDB should suggest a primary holder for each group.

Step 5: other donated accessions

For all other types of accession, the ECCDB must distinguish between donations made **with** or **without** associated transfer of responsibility. This is achieved by reference to the **Source** passport descriptor introduced into the revised Forage Passport Descriptors List.

For accessions where **Source=donated with responsibility**, the genebank will be designated primary holder.

For accessions where **Source=donated without responsibility**, the genebank will not be designated primary holder. No attempt will be made to search for duplicates, so the accessions will not be linked to any primary holder.

For accessions where **Source=donated with unknown responsibility**, transfer of responsibility is assumed in the following situations:

1. The donor is a breeder or other scientist, as identified by (a) a non-missing entry for the **Breeding Institute** passport data field, or (b) a **Donor Institute Code** that refers to an institute that has no genebank. It is assumed that the donation was made by a breeder or other scientist specifically because the genebank provides facilities for guaranteed long-term conservation.
2. The **Donor Institute Code** refers to an institute with a genebank that (a) does not participate in the ECP/GR, or (b) that no longer exists. IPGRI will provide a list of recognized current genebanks participating in the ECP/GR.

For all accessions not meeting the above conditions, the genebank is not designated primary holder.

Discussion and implications

The above protocol will leave many accessions having no primary holder. Their historical uniqueness will be unknown. ECCDB managers may conduct a more elaborate search for potential historical duplicates, but this is not recommended as a priority activity.

Moreover, given the population characteristics of most temperate forage species, each sample of a wild population or primitive variety is likely to be biologically unique because of genetic changes associated with each regeneration and each donation. This applies both to accessions with no designated primary holder, and to accessions where the holder is not the primary holder. It will be particularly true for genebanks that do not follow the highest possible regeneration standards. As such, extreme caution is urged in relation to rationalizing collections based on primary holdings. In particular, no attempt should be made to eliminate an accession from a collection on the basis that it has not been assigned a primary holder.

Rather, the identification of a primary holder should be used as a means of prioritizing characterization, evaluation, regeneration and distribution. A genebank should assign top priority to its accessions for which it has been designated primary holder. It should assign lowest priority to those for which another genebank has been designated primary holder, and will normally refer requests for seed of such accessions to the primary holder unless there is a particular need for seed from its own sample. It should assign intermediate priority to those with unassigned primary holder. We envisage that the primary holder will be the normal supplier for most external users (breeders and other scientists), whilst usage of other seed samples will be restricted mainly to genebank research.

Finally, special consideration must be given to genebanks outside Europe. Since the competence of ECP/GR is restricted to Europe, non-European genebanks cannot be considered candidates for designation as primary holder. This is reflected in the protocol proposed above. To include non-European genebanks as primary holders would require extension of discussion to a global scale.

However, as an interim measure that is within the competence of ECP/GR, the proposals presented here could be extended to include a second designation for a "primary holder without responsibility". If the country of origin is outside Europe, it may be possible to identify a genebank in the country of origin that may hold a sample of the accession. That genebank would then be identified as "primary holder without responsibility". This would not exclude the possibility of that genebank being identified as the primary holder (with responsibility), but that is a matter for agreement with the genebank concerned outside the limits of ECP/GR.

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Appendix III. Guidelines for the regeneration of accessions in seed collections of the main perennial forage grasses and legumes of temperate grasslands

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Contents

1. Introduction

"Timely regeneration must be a priority activity of all genebanks" (FAO 1996). The optimal protocol for regeneration depends on numerous factors, including breeding system and seed storage characteristics of the species concerned, the condition and genetic composition of the original sample, its expected usage and its perceived value within the collection, and operational constraints on genebank activities, such as funds, labour and equipment. It is therefore not possible to lay out a single uniquely optimal protocol. Rather, genebank-specific and even accession-specific decisions have to be made to establish the optimal protocol. In many cases there is not sufficient knowledge on which to determine the optimal solution; it is then necessary to make some pragmatic choices in the short term while undertaking research to enable further improvements in the long term.

A generalized decision guide (Sackville Hamilton and Chorlton 1997) provides help in the decision-making process. However, the choices are complex and multifaceted. It is necessary to progress beyond a general decision guide by providing more specific, prescriptive regeneration guidelines for particular species. This will improve conformity among genebanks by eliminating some of the need for decision-making by individual curators.

This document provides such prescriptive guidelines for the main perennial forage grasses and legumes of temperate grasslands. It is based on the principles presented in Sackville Hamilton and Chorlton (1997), which should be referred to for detailed discussion of the issues underlying the decisions presented here.

2. Background and assumptions

2.1 Taxonomic scope and characteristics

No attempt is made in these guidelines to cover all forage species, because they encompass too wide a range of life cycle characteristics. Taxa covered include those with the following characteristics:

1. Seed are small and sown at high density (typically about $400/m^2$ for dominant grasses, to $40/m^2$ for legumes and other minority components of seed mixtures). The resulting need for large numbers of seed generally rules out manual pollination as a tool for improving maintenance of genetic integrity.
2. Seed are long-lived, with good long-term survival in storage and with relatively well-known storage, dormancy and germination requirements. Seed survival characteristics have not been quantitatively determined as they have for some other species; nevertheless it is clear qualitatively that they are "easy" species for storage. IPGRI-preferred standards for storage and viability are therefore appropriate, there is a high degree of certainty over decisions, and relatively low priority attaches to additional research to improve knowledge of seed characteristics.
3. The species are self-incompatible outbreeders, so that
    a) each accession must be maintained as an interbreeding population
    b) there is a high risk of contamination with alien pollen if appropriate control measures are not taken
    c) genetic variation within populations is high.
4. The species are perennial, able to propagate vegetatively and with an indeterminate growth habit. Therefore there is potentially extremely high variation in fecundity between plants – some plants may produce zero seed, while the majority of the seed produced by a population may be produced by a small proportion of the plants in the population. The combination of this high variance in fecundity with high genetic variance within populations results in an exceptionally high potential for genetic

change during regeneration, even where contamination with alien genes is totally excluded.

5. Many of the species are native and naturally common in the areas where they are most used agriculturally. Sown populations readily become feral, persisting as naturalized populations, spreading out from their original location and introgressing with native populations. Native and naturalized populations may be abundant in paths, verges, fallow land, in the weed flora around experimental plots, and the seed bank in the soil. As such, wherever the species are used commercially or experimentally, there is a high risk of contamination with alien plants, seed or pollen from natural and naturalized populations.

In summary, the species covered by these guidelines present no particular problem in terms of seed storage, but in terms of the maintenance of genetic integrity they are probably the most difficult of all crop groups. The guidelines reflect this by attaching exceptionally high priority to limiting the loss of genetic integrity. Pending further research on alternative methodologies for the improved maintenance of genetic integrity, the guidelines are subject to future revision.

Both wind-pollinated (grasses) and insect-pollinated (legumes) species are covered. These require different protocols for pollination and the prevention of contamination with alien pollen, but otherwise are similar.

Categories of grassland species not covered by these guidelines include:

- inbreeders (mainly the annual species)
- apomicts (such as some *Poa* spp. and many tropical grasses)
- medium- to large-seeded species (including many tropical legumes)
- those with poorly known seed characteristics (including many nonagricultural species).

2.2 Types of collection

The following is assumed in relation to storage conditions:

1. Accessions are maintained in an **active collection** optimized for utilization rather than conservation, and maintained at 0 to 4ºC with 3-7% seed moisture content.
2. A sample of every accession is also held in a **base collection** maintained for conservation, under optimal conditions for long-term storage ("-18ºC or cooler with 3-7% seed moisture content": FAO/IPGRI Genebank Standards 1994) and with genetic integrity as far as possible intact. Seed in the base collection is not used for distribution. The preferred standard for regeneration purposes is to maintain the base collection at the same site as the active. It is acceptable to maintain the base collection at a distant site, although this makes it more difficult to achieve the preferred standard that all samples should usually be regenerated from the base collection (FAO/IPGRI Genebank standards 1994; see also section 3.3).
3. A duplicate sample of every accession is maintained in a **safety-duplicate collection**, also held under optimal conditions but at a distant site from the base collection. Seed in the safety-duplicate collection is not used for any purpose other than replacing accessions that have been accidentally lost from the base collection.

2.3 Units of seed usage

Definition of the fundamental units of seed usage is prerequisite to efficient genebank operation. The three fundamental units are as follows:

1. The **distribution unit** is the mean number of seed distributed with each request. This mean number may be varied in accordance with users' requirements and seed availability. Preferred standard: **mean 250 seeds; range 10-5000 seeds**.

2. The **test unit** is the number of seed required to test seed quality and viability. Preferred standard: **100 seeds**.
3. The **base unit** for regeneration is the number of seed needed to ensure the successful regeneration of a representative sample of the original accession, with genetic integrity maintained as far as possible intact and of sufficient size to meet future demands. The size of the base unit must make full allowance for all possible seed losses during regeneration and storage. Table 1 presents calculations for the preferred and acceptable base unit size.

2.4 Targets for seed production during regeneration

i. Seed quality

New seed produced for storage should as far as possible be free of any pathogen or pest, especially of storage pests and seedborne pathogens, and have ≥ 95% germination rate.

ii. Seed quantity

The target number of seed to be produced depends on whether the regeneration is for the active, base and/or safety-duplicate collections. Targets for number of seed to be stored in the active and base collection are given in Table 2. The target for storage in the safety-duplicate collection is one base unit, i.e. **800** seed preferred, **240** acceptable (Table 1).

iii. Genetic integrity

Genetic integrity deteriorates through two principal routes: (a) contamination with alien genes, and (b) other changes in genotypic composition that occur by random drift and by nonrandom selection even in the absence of contamination by alien genes. Standards for the former are given in Table 3.

Zero change in genotypic composition by drift or selection is not an achievable target. However, it is considered inappropriate to set quantitative targets. We merely set the qualitative target of minimizing changes as far as feasible within the constraints of available funding and infrastructure.

As outbreeders, each accession typically contains high levels of genetic variation among its component plants for many characteristics. Moreover, as perennials with the ability to propagate vegetatively and with an indeterminate growth habit, there is potentially extremely high variation in fecundity between plants. At one extreme, some plants may allocate all resources to vegetative propagation and so produce zero seed. At the other extreme, because of the indeterminate growth habit, some plants may attain a large size and then produce a large number of inflorescences. Typically, most of the seed produced by a population is therefore derived from a small proportion of the plants in the population, while most plants contribute little or nothing. As a result, the potential for degradation of genetic integrity through both drift and selection is exceptionally high in these species. Exceptionally high priority is therefore attached to measures that reduce such changes.

3. Regeneration protocol

The regeneration protocol outlined here highlights aspects, such as the need for uniformity and absolute cleanliness, that are of particular importance to regeneration and that therefore will not feature in agronomy texts. It is assumed that the genebank has background knowledge of general agronomic requirements of the species.

3.1 Selection of location for regeneration

The location selected for regeneration should have the characteristics outlined in Table 4.

Quarantine regulations may also influence the choice of location for regenerating seed from newly imported seed or plants. It may be necessary or preferable to regenerate within quarantine facilities.

Table 1. Preferred and acceptable sizes of a base unit

	Preferred standard	Acceptable standard
Number of parent plants to be used for regeneration	100 plants	30 plants †
Safety factors, guarding against:		
Germination rate < 100%	2	2
Probability of crop failure > 0%	2	2
Other seed losses > 0%	2	2
Total base unit size	**800 seeds**	**240 seeds**

† The figure of 30 should be used with caution. It is lower than usually regarded as acceptable. In part it reflects the higher priority attached here to minimizing selection and contamination than to minimizing drift, and the resulting need for increased effort per parent plant. It is most acceptable for small original samples (e.g. of material collected vegetatively from pasture). It is not acceptable unless the protocol adopts preferred standards in relation to other measures for minimizing selection and contamination, such as regenerating inside isolation chambers. If these other preferred standards are not met, the acceptable standard should be increased to 50 plants.

Table 2. Preferred and acceptable targets for the number of seeds to be stored

(a) in the active collection

Use	Basis of calculation	Preferred standard	Acceptable standard
Viability monitoring	Expected number of tests	5	3
	• test unit size	100	100
	= number of seed required	**500**	**300**
Regeneration	0 if regenerating from base	0	**240**
	1 base unit if regenerating from active		
Seed distribution	Expected number of requests †	10	5
	• uncertainty factor ‡	5	3
	• distribution unit size	250	100
	= number of seed required	**12,500**	**1,500**
Target number of seeds for storage in active collection after regeneration		13,000	2,040

(b) in the base collection

Use	Basis of calculation	Preferred standard	Minimum standard
Viability monitoring	Expected number of tests	20	5
	• test unit size	100	100
	= number of seed required	**2,000**	**500**
Regeneration			
Replenishment of stocks in base collection	1 base unit	800	240
Replenishment of stocks in safety-duplicate collection	1 base unit	800	240
Replenishment of stocks in active collection	Expected number of times	5 §	1 ¶
	• uncertainty factor ‡	4	4
	• base unit size	800	240
	= number of seed required	**16,000**	**960**
Target number of seeds for storage in base collection after regeneration		19,600	1,940

† Standards cannot be set for expected number of requests: determining appropriate values for any genebank is the sole responsibility of the curator. However, it is necessary to enter values here in order

to establish appropriate values for target seed quantities. The values entered are intended to represent approximate figures in the range likely to be adopted by most genebanks.

‡ The uncertainty factor is a factor allowing for uncertainty of usage of seed in relation to the relative costs of producing more or fewer seed than are actually used. See Sackville Hamilton and Chorlton (1997).

§ Assuming adherence to the preferred standard (section 3.3), that samples in the active collection are always regenerated from the base collection.

¶ Assuming adherence to the acceptable standard (section 3.3), that samples in the active collection are regenerated from remnant seed in the active collection for up to three cycles before reverting to the base collection.

Table 3. Preferred and acceptable targets for contamination of accessions with alien genes

Cause of contamination	Preferred standard	Acceptable standard †‡
Misidentification of accessions caused by incorrect juxtaposition of plants and labels at any step during regeneration	0%	0.001%
Contamination with alien plants or seed from any source (other accessions, previous crops, wild or feral populations, seed bank) at any stage (seed preparation, seed-bed preparation, sowing, crop growth, harvesting, all post-harvest seed handling through to seed storage).	0%	0.01%
Contamination with pollen from any alien source (other accessions being regenerated nearby, or crops, wild or naturalized populations in the vicinity) at any stage.	0%	0.1%

† Although values are given for acceptable standards, high priority should be attached to achieving the preferred target instead, because of the detrimental consequences of lower standards in terms of loss of diversity in the collection (Sackville Hamilton and Chorlton 1997).

‡ The differences in values set as acceptable for different causes of contamination reflect the different costs and difficulty of prevention.

3.2 Selection of accessions

An accession needs to be regenerated when it falls below predefined threshold levels for quantity or quality. Thresholds are given in Table 5 for accessions already in storage, and in Table 6 for new material not yet entered into the collection.

Every effort should be made to ensure that enough seed is kept in the base collection to cover all usage, so that they should need to be regenerated only when they deteriorate in quality and never for inadequate quantity. Although Table 5 includes threshold quantity for seed in the base collection, falling below this threshold is regarded as a failure of the regeneration protocol.

Selection of accessions for regeneration involves the following steps:

i. Construct preliminary list of samples that may fall below threshold
ii. Determine which of these are actually in need of regeneration
iii. If necessary, prioritize accessions for regeneration
iv. Select regeneration protocol appropriate to accession status
v. In the event of problems, consider refining future regeneration protocol.

Table 4. Preferred and acceptable standards for the characteristics of the location used for regeneration

Location characteristic	Preferred standard	Acceptable standard
Latitude	Within 5° of site of origin	Within 10° of site of origin
Altitude	Within 300 m of site of origin	Within 500 m of site of origin
Soil	High fertility, permanently moist but well-drained, pH 5-7.5 depending on species	High fertility, permanently moist but well-drained, pH 5-8 depending on species
Method for elimination of alien pollination (grasses)	Plants contained within 100% pollen-proof isolation chambers, at least for the duration of anthesis	Outside, in sheltered site, surrounded by tall crop of densely packed plants ≥2 m high, ≥20 m thick, and with its edge ≤1 m from edge of regeneration plot, ≥50 m from nearest alien pollen source (other regeneration plot, crop, feral population, etc.) (increase distance from alien pollen if quality of barrier crop is reduced)
Method for elimination of alien pollination (legumes)	Plants contained within 100% pollinator-proof isolation chambers, at least for the duration of anthesis	Outside, in sheltered site, surrounded by ≥50 m thick crop with dense canopy of flowers of similar colour, morphology and scent to accessions, preferably conspecific male-sterile ≥50 m from nearest alien pollen source (other regeneration plot, crop, feral population, etc.), near to source of preferred pollinator
Accessibility	Sufficient to enable daily patrols and monitoring	Sufficient to enable biweekly patrols and monitoring

Table 5. Preferred and acceptable threshold levels for the quality and quantity of seed stored in base and active collections, below which seed should be regenerated

Criterion	Basis of calculation	Preferred standard	Acceptable standard
Germination rate		≤ 85%	≤ 70%
Quantity in base collection[†]	1 test unit	100	100
	+ 1 base unit	800	240
	+ 2nd base unit **if** there is an imminent need to regenerate the active collection from the base collection[‡]	0-800	0-240
	= total threshold	**900-1,700**	**340-580**
Quantity in active collection	1 test unit	100	100
	+ 1 base unit **if** the next regeneration cycle is to use residual seed from the active collection [§]	0	0-240
	+ 1 distribution unit	250	250
	* expected number of seed requests before the next possible regeneration cycle	2	1
	= total threshold	**600**	**350-590**

[†] Genebank procedures should aim to ensure that accessions do not fall below this threshold.

[‡] This will be the case if the sample in the active collection is at or below threshold and the genebank adheres to the preferred standard of regenerating active from base.

[§] This will never be the case if the genebank adheres to the preferred standard of regenerating active from base. It will be the case at least one in four cycles if the genebank adheres to the alternative standard of regenerating samples in the active collection from remnant seed in the active collection for up to three cycles before reverting to the base collection.

Table 6. Preferred and acceptable threshold levels for the quality and quantity of newly received seed samples, below which new seed samples should be regenerated before being added to the collection

Criterion	Basis of calculation	Preferred standard	Acceptable standard
Germination rate		≤ 85%	Regenerate regardless of germination rate ≤ 95% ≤ 70%
Health		As far as possible, free of any pathogen or pest	
Quantity	Threshold quantity for regeneration of seed stored in base	900-1700	340-580
	+ Threshold quantity for regeneration of seed stored in active	600	350-590
	+ 1 base unit for safety-duplicate	800	240
	= Total threshold	**2300-3100**	**930-1410**

i. Constructing the preliminary list

Samples to be considered include all seed samples held in the base or active collection, and all newly received samples not yet in any collection. Samples held in the safety-duplicate collection should not normally require separate consideration. Preferred standard is that accessions in the safety-duplicate are held under conditions at least as good as the base collection, and that enough seed are held in the base collection to ensure that they require regeneration only when quality deteriorates. Where this is achieved, samples held in the safety-duplicate collection will need regeneration at the same time as those in the base collection, and regeneration protocol should make this assumption. Where standards fail and seed in the base collection require regeneration because they fall below threshold quantity, regeneration of base and safety-duplicate will fall out of synchrony and a separate regeneration cycle will be needed at some stage for the safety-duplicate collection.

The genebank documentation system should be used to construct the preliminary list, and should indicate the location of the selected samples. The list should include samples that:

- are below threshold for seed quantity (which for newly introduced material will include material received as plants rather than seed), or
- might fall below threshold for seed quality. All seed whose quality has not already been tested fall into this category. This will include all newly introduced materials. It may also include stored seed, if the genebank has failed to meet acceptable standards for testing new seed samples before entering them in the collection.

For seed that has been stored following at least acceptable standards, it can be assumed that quality will not fall below threshold for several years. In the absence of quantitative data on the rate of loss of viability in storage, Table 7 provides an approximate guide based on previous informal experience: it is supposed that seed samples might fall below threshold quality if they have remained in storage longer than the critical number of years given.

Table 7. Critical number of years of storage in base and active collections, after which accessions are considered to be at risk of falling below threshold germination rate and therefore in need of a repeat germination test. It is assumed that the base collection is stored -18°C, and the active collection at +2°C, both at 3-7% seed moisture content.

Germination rate at	Last regenerated in-house using optimal	Collection type

last test	protocol for regeneration and storage?	Base	Active
>95%	Yes	100	20
>95%	No	50	10
>90%	Yes or No	15	5
>85%	Yes or No	5	3

ii. Determining which samples in the preliminary list need regeneration

Germination tests and seed health tests are required to determine which seed samples are actually below threshold for quality. The preferred standard is to assess all accessions identified to be at risk of falling below threshold. If this is not possible, for example if genebank capacity is not sufficient, acceptable standard is to:

1. Identify groups of accessions in the preliminary list that have been previously regenerated in-house at the same time and are likely to show similar germination rates.
2. Test one or two accessions from each such group.
3. Treat all accessions in the group as if they have that germination rate.
4. Raise the quality threshold slightly, to allow for untested accessions having lower quality.

No attempt should be made to group new samples that have not previously been regenerated in-house, as there are likely to be wide variations in germination rate between accessions from the same collecting expedition or in the same batch of seed donated from another genebank: all such materials should have germination rate measured.

With one possible exception, the list of samples in need of regeneration constitutes all those below threshold quantity, plus all those that tests have shown to be below threshold quality.

The possible exception is for new seed samples donated by another genebank. If these fall significantly below acceptable threshold, it may be preferable to reject the accession altogether rather than attempt to regenerate. A decision on whether to reject or regenerate must be taken in conjunction with the donor: if the donor retains a superior sample of the same accession and is therefore able to regenerate to a superior standard, the sample should be rejected and a repeat donation requested. Otherwise, high-priority regeneration should be undertaken and a duplicate sample returned to the donor if requested.

iii. Prioritizing accessions for regeneration

If the number of samples in need of regeneration exceeds genebank capacity, there will be a need to identify which ones are in most urgent need of regeneration. Regeneration may be delayed where it is less urgent. Priorities include:

1. If the list was drawn up on the basis of preferred standards for thresholds, these standards may be relaxed to acceptable standards (Tables 5 and 6), and priority attached to those accessions that fall below acceptable threshold.
2. Regeneration of newly introduced samples and accessions in the base collection takes priority over accessions in the active collection.
3. Regeneration of samples below threshold quality takes priority over those below threshold quantity, with one exception: if a germination test has been conducted on an accession with so few seed that satisfactory regeneration cannot be accomplished using the residual seed, then (a) the sample must be regenerated, and (b) the seed germinating during the germination test must be used as parental plants for regeneration.
4. Rank samples by quality, and regenerate as many as possible of those with lowest quality.
5. Rank samples by perceived value for conservation or utilization, e.g. attach high value to accessions that have been shown to be unique and highly distinctive, or to have particular alleles of research interest, or whose original collecting site has been destroyed.

Regeneration must never be delayed for newly received samples and accessions in the base collection that are below minimum acceptable threshold for quality.

Any accessions in need of regeneration but not selected for regeneration must be immediately put on hold, placed in optimal storage conditions if not already there, and not used for any other purpose until they can be regenerated.

iv. Selecting regeneration protocol appropriate to accession status

The above procedures should identify accessions in need of regeneration before normal regeneration becomes impossible. However, in some cases the process will fail. Where seed quality or quantity is so far below minimum that the normal number and condition of parental plants cannot be established, there will then be a need for some form of 'rescue regeneration'.

At the minimum, this will involve simply recording in the documentation system that a bottleneck has occurred where insufficient plants can be grown from the remaining seed to enable regeneration of a representative sample.

It may be possible also to "rescue" the accession from plants already in use for other purposes, e.g. germination tests, characterization, etc.

If the above fail, the next resort is to retrieve seed from the safety-duplicate collection.

Finally, where quality is so low that normal procedures would result in zero germination even for seed in the safety-duplicate collection, consider using technologies such as embryo rescue.

v. Refining the protocol

There may be a need to consider refining the above procedures if experience shows they are inadequate.

Preferred standard is that accessions in the base collection should need to be regenerated only when they fall below threshold quality. If it is found that more than 5% are being regenerated because they are below threshold quantity, then target quantities for storage in the base collection should be increased (section 2.4).

If germination rates for stored seed are above threshold in most cases (>90%), the number of years between tests may be increased (Table 7). Conversely, if too many (>5%) are too far below acceptable threshold, the number of years between tests should be reduced.

3.3 Selection of parental material

There are three components to the selection of material for use as parental plants: selecting the appropriate source, determining how many plants to grow from that source, and determining how those plants should be sampled from the selected source.

i. Source of parental plants

Samples to be entered into a collection for the first time are received either as living plants or as seed, which provide the only possible source of parental material for regeneration. In contrast, an accession already in a collection is preferably represented by seed samples in the base, active and safety-duplicate collections. Regeneration protocol must define which of these to use as parental material for the next generation of seed (summarized in Table 8).

Preferred standard is normally to use seed in the base collection as parental material for all regeneration, whether for replenishment of stocks in base, active or safety-duplicate collections (FAO/IPGRI Genebank Standards 1994). This preferred standard changes in two situations, both of which represent failures in the system:

1. Replenishing stocks in the active collection from seed in the base collection would cause the latter to fall below threshold quantity (which is against preferred standards). In this case, seed in the active collection must be regenerated from remnant seed in the active collection, for all regeneration cycles until seed in the base collection falls below

threshold quality. The curator should then also consider increasing the number of seed stored in the base collection the next time it is regenerated.

2. The accession either has been lost from the base collection, or has suffered or would suffer an unacceptable loss of genetic integrity. In this case, seed in the safety-duplicate collection should be used to regenerate base, active and safety-duplicate collections simultaneously.

Table 8. Preferred and acceptable sources of parental material for replenishing stocks in base, active and safety-duplicate collections

Source of parental material	Stocks to be replenished		
	Active	**Base**	**Safety-duplicate**
Active	Acceptable for ≤ 3 in 4 regeneration cycles according to Genebank Standards 1994; for perennial forages, regarded as not acceptable unless unavoidable. Preferred if too few seed in base collection	Not acceptable	Not acceptable
Base	Preferred; except: not acceptable if too few seed in base collection	Always, unless exceptional conditions necessitate regeneration from safety-duplicate	Same as for replenishing stocks in base: usually at same time and in same regeneration plot as base
Safety-duplicate	Only in exceptional conditions, where the accession is either completely lost from base or otherwise suffers unacceptable loss of genetic integrity.		

Acceptable alternative standard for replenishment of stocks in the active collection (FAO/IPGRI Genebank Standards 1994) is to alternate between active and base as source of parental material. This can include regenerating from remnant seed in the active collection for up to three successive regeneration cycles before reverting to seed in the base collection for one regeneration cycle. However, this is relatively unacceptable for species with high genetic variance within accessions and high potential rates of loss of genetic integrity. These guidelines are for such species, and therefore it is recommended to adopt the preferred standard wherever possible. This departure from FAO/IPGRI Genebank Standards 1994 is reflected in Table 8.

Preferred standard for replenishment of stocks in the safety-duplicate collection is to regenerate at the same time and in the same regeneration plot as the base collection, using the same set of parental seed from the base collection; regenerated samples for storage in base and safety-duplicate collections should be appropriate random samples of the seed produced in the regeneration plot, which should therefore produce sufficient seed to satisfy requirements of both.

Where seed in the base collection need regeneration because they are below threshold quantity (which is against preferred standard), the seed produced should be used to replace only the base collection, not the safety-duplicate collection as would normally be the case. Consequences of this are that seed in the safety-duplicate collection will then be superior in terms of genetic integrity, but have lower seed quality. The subsequent cycle of replenishment of stocks in the base collection should if possible be undertaken using seed from the safety-duplicate. This will not only resynchronize quality in base and safety-duplicate collections, but also maintain superior genetic integrity.

ii. Number of parental plants

The preferred standard is at least 100 plants established in the regeneration plot (i.e. 100 plants surviving after losses due to <100% germination and establishment). Acceptable standard is 30.

If the number of plants that can be established in the regeneration plots is less than 30, a bottleneck should be noted in the documentation system.

iii. Identity of parent plants

Preferred standard for wild populations is to adopt an integrated strategy for collecting, regenerating and storage that maximizes retention of original population structure and genetic integrity. For regeneration it should be possible to select particular parental plants that best represent the genetic structure of the original population sample. Achieving preferred standard requires use of multiple storage containers for each accession in the base collection. Each container should hold the progeny of one plant (vegetative cutting or seed heads) collected from the original population. For regeneration, an equal number of seed is then sampled at random from each container, to make up the required total number of parent plants.

Acceptable standard is to ignore population structure, thoroughly mix seed of each accession and use a random subsample as parental plants for regeneration.

3.4 Preparation of regeneration plots

Preferred plot size: 100 plants by 20-cm spacing = 4 m^2.

Preferred standard is to use pots, as these provide superior control over soil, weeds, soilborne pests and pathogens, plant growth rate and contamination with alien plants; and the resultant mobility provides superior control of contamination with alien pollen and a means to improve throughput capacity.

Acceptable standard is to use field plots, but this necessitates very considerable care in areas such as follows:

- **Soil.** The regeneration plot must be as uniform as possible in terms of nutrients, soil structure, physical and chemical composition. Consider a physical and chemical analysis of the soil. If necessary, apply soil ameliorative treatments (e.g. fertilizers, lime, drainage, irrigation, ploughing, soil structuring, preheating).
- **Weeds, pests and pathogens.** Determine whether such problems can be reduced during preparation of regeneration plots by the application of appropriate pregermination treatments for elimination of weeds, pests and pathogens. Ensure that any pregermination treatment selected does not adversely affect seed production.
- **Contamination with alien seed and plants.** Preventing contamination involves either:
    - using a novel site with no prior history of the species being present, whether naturally or as part of previous trials or regeneration plots, or
    - rigorous elimination of plants and seed in the soil, e.g. by sterilizing soil, digging out the soil and replacing it with the sterile compost. A single cycle of ploughing to encourage germination followed by spraying or deep ploughing to kill emerging seedlings is not usually sufficient to eliminate all seed from the seed bank.
- **Contamination with alien pollen.** Preferred standard is to erect pollen-proof or pollinator-proof cages over the regeneration plots. Acceptable is to isolate from other regeneration plots and other sources of pollen using a combination of distance and partial barriers (Table 4), eliminating all near sources of pollen. Preparation of the regeneration plot needs to take into account the intended method of control of contamination.

3.5 Preparation of seed

If appropriate or necessary, use seedlings already germinated from previous germination test (section 3.2). Otherwise, start with a new seed sample. The former may be preferred if the germination test produced enough seedlings and used seed from the desired source, or may be necessary when too few other seed remain.

Ensure 100% accuracy in the identification of accessions throughout bagging, labelling and transporting seed. Use built-in cross-checking mechanisms, including labels that stay with the seed wherever possible, dual labelling inside and outside bags, preprinted and pre-ordered sets of labels and labelled bags, and two personnel to cross-check each other.

Ensure zero contamination of seed samples with seed of other accessions. Use only purpose-built seed-preparation facilities (work surfaces, machinery, etc.) containing no crevices or internal lacunae where seed may become lodged. Completely clean all surfaces and implements after preparing each accession.

If necessary, break seed dormancy. Scarification (physically with sandpaper, or chemically with sulphuric acid) is a common requirement for forage legumes.

Avoid use of *Rhizobium* inoculants for legumes, as host-strain specificity is likely to increase variance between individuals. Use mineral nitrogen instead.

Apply proprietary seed dressings to reduce disease incidence or delay the onset of disease.

Sow in seed trays. Transplant seedlings to pots (preferred) or as spaced plants in field plots (acceptable). Preferred pot volume approximately 1-2 L. Preferred spacing in the field approximately 20 cm.

3.6 Crop management

3.6.1 Before anthesis

Inspect plots and plants regularly. As far as possible ensure complete control of weeds, pathogens and pests. Do not thin plants.

As far as possible promote uniform induction of flowering in all plants. Vernalization over winter is a common requirement for flower induction in many temperate forage species.

If using field plots, ensure continued absence of all potential sources of alien pollen both within and near the regeneration plots.

If necessary, prune large plants to reduce variation in size between plants. Prune plants to prevent competition between them. If necessary, restrict growth uniformly by using small pots or low fertilizer application.

Where possible, verify accession identity while the plants are growing, by comparing their phenotype against the documented phenotype of the accession. This will be possible only for accessions with visually distinctive characteristics of high heritability that have been recorded in the genebank documentation system. For some visually variable species such as *Trifolium repens* this may be feasible for a large proportion of accessions. For others such as *Lolium perenne*, it will not be feasible for most accessions.

3.6.2 During anthesis

Ensure no stresses, such as excessive heat or drought, that might interfere with normal meiosis and pollination.

Prune plants at the beginning of anthesis so that all plants have a similar number of inflorescences at a similar stage of development, i.e. remove early inflorescences from plants with many.

If required for the chosen method of elimination of alien pollen, move pots into a pollen-proof or pollinator-proof chamber for the duration of flowering, or erect temporary pollen-proof or pollinator-proof nets around the regeneration plot.

In the absence of sufficient research on pollination patterns within regeneration plots, and given the expense of manual pollination for the large number of seeds required, the preferred standard is currently to permit open-pollination, using the smallest possible size of regeneration plot. For wind-pollinated species in isolation chambers, use an active

air-circulation system to promote pollen dispersal. For insect-pollinated species, introduce pollen-free pollinators at anthesis.

3.6.3 After anthesis

Ensure control of pathogens and pests that reduce the quantity and quality of seed, especially those that are seedborne and potential problems in storage.

Preferably, remove late-forming inflorescences.

3.7 Harvesting and post-harvest management

3.7.1 General procedures

Post-harvest management involves a considerable amount of seed handling and transport, with a correspondingly high risk of contamination with alien seed or even completely misidentifying seed samples. Seed-handling operations must include procedures to eliminate errors in identifying accessions (see section 3.5).

Strict attention must be paid to cleanliness, to ensure clean, high-quality seed and to avoid admixing seed from different accessions, different plants, or other sources. A good seed-handling environment is desirable, preferably in a room dedicated to seed-handling and with the following characteristics:

- good lighting for close and detailed observations of samples
- smooth flat work area, easily cleanable and with no crevices where seed could become lodged
- draught-proof with limited access
- access to all necessary equipment such as sieves, forceps, lens
- controlled temperature and humidity where possible.

Equipment, whether for manual or mechanical seed handling, must be suitable for producing a sample that contains seed only, not chaff, pieces of rachis, dead greenfly, dust, etc. The aim is to produce ‘standard seed’ quality by setting equipment (e.g. column blower, sieves) to a predetermined standard.

Clean machinery and work surface between each seed lot to avoid contamination. Particular attention must be paid to difficult areas, such as inside machinery.

Packets or other containers for seed should be secure, and of appropriate construction. They must at all times be labelled with accession ID, date, location and ID of the regeneration plot.

Handling of seed, plants and accessions must be coordinated with the intended storage method (see section 3.7.7) as follows:

- If seed of each plant are to be store separately (preferred for base and safety-duplicates), then the seed of each plant must be kept in separate containers throughout post-harvest management.
- If seed are to be stored as a balanced bulk (acceptable for base and safety-duplicates; preferred for active), the preferred standard is to form the balanced bulk with clean seed, which necessitates keeping the seed of each plant in separate containers throughout post-harvest management up to the point of producing clean seed.
- If seed are to be stored as a balanced bulk, an acceptable alternative is to form the balanced bulk at some earlier stage in the post-harvest management, prior to seed-cleaning. This will save on handling costs but will result in a less accurate balanced bulk. It is most acceptable when all plants have approximately the same proportion of seed in the harvested material.
- If all seed of one accession are to be stored in the same container as an unbalanced bulk (acceptable for active only), then seed can be bulked at any stage at or after harvesting.

If maintaining the seed of each plant in a separate container, the seed of different plants should be treated as distinct seed lots even if they belong to the same accession. That is:

- each plant must be harvested individually
- the seed produced by each plant must be handled separately
- each container must be separately labelled, and information printed on the label must also include the ID of the parent plant
- the documentation system must provide for individually labelling and tracking progress with each seed lot
- procedures for cleanliness should be extended to include avoiding contamination with seed produced by other plants of the same accession.

At all stages good seed health must be ensured, paying particular attention to storage pests and seedborne pathogens. Known diseased seed lots should be isolated from non-diseased lots. Keep insects out. If possible, filter air to keep out other pests and pathogens. Bags should be kept off the ground or floor of the drying area.

To avoid infection with pathogens such as mildews, harvest in dry weather and store heads in a clean dry atmosphere with good air circulation. Use porous containers such as paper bags or muslin bags, not in waterproof containers such as plastic bags. Keep bags spaced well apart to allow dry air to circulate within and between them.

Fumigants and pesticides should be used if necessary, but with caution and only as a last resort.

To prevent rapid seed deterioration, avoid delays in seed processing after harvesting.

3.7.2 Harvesting

Harvesting must be done at 'optimum' maturity. Optimum here means with as many ripe seed per head as possible, after seed cease to be sensitive to desiccation, and before natural seed dispersal by fruit shattering. Harvest when the first main bulk of inflorescences is ready. Avoid late-developing inflorescences if they have not already been removed.

If regenerating in outside plots (i.e. not following preferred standard), it is also necessary to harvest before excessive losses to bird and other pests, during appropriately dry weather, and before excessive damage by bad weather.

The harvested unit must be suitable for the subsequent threshing method, e.g. for hand-threshing, harvest the peduncle as well as the infructescence to provide a handle.

Bulk harvesting of whole plot by machine is an option only when replenishing stocks in the active collection using the acceptable, not preferred, option of storing an unbalanced bulk (section 3.7.7). In all other cases, plants must be harvested individually.

3.7.3 Initial drying

Seed should be dried as soon as possible after harvest. The initial drying stage aims to dry material to a moisture content low enough for effective threshing. Threshing seed too dry may damage the seed and cause the entire seed head to shatter into the threshing machine along with the seed.

Preferred standard is to dry in loosely packed and widely spaced paper bags, hanging off the ground in a dry room with good ventilation and air circulation. Active fan-assisted drying in a dehumidified chamber is not recommended.

3.7.4 Threshing and cleaning

Thresh manually, using sieves and a column blower to separate seed from chaff. The setting of the column blower must be adjusted differently for each species.

Preferred standard is to use a humidity-controlled room to avoid rehydration.

3.7.5 Final drying

Optimal seed moisture content for final storage is lower than that for threshing, which necessitates a second stage of drying after threshing. Preferred standard is active drying with fan-assisted air circulation in a humidity-controlled room set to dry seed to the 3-7% moisture content.

The alternative is passive drying with self-indicating silica gel in small boxes. As the silica gel absorbs moisture and changes colour from pink to blue, it should be repeatedly replaced with dry silica gel. Drying is complete when the silica gel ceases to change colour. For *Lolium perenne* seed starting at 15% moisture content, the silica gel typically needs replacing after 1, 3 and 6 weeks.

Dried seed can be brittle and easily damaged. Increased care with seed handling is therefore necessary after the drying process is complete.

3.7.6 Initial viability testing

Germination rate should be tested prior to storage and after drying. Depending on seed characteristics, seed may need careful rehydration before the germination test to avoid damage. If genebank capacity is insufficient to test all seed samples, it is acceptable to test a representative sample of accessions, in accordance with overall strategy for monitoring viability.

3.7.7 Seed packaging and storage

Preferred storage medium is heat-sealed foil packs. Seed to be stored in a single container should be thoroughly mixed, to ensure that seed subsequently taken out for testing, distribution or regeneration will be random subsamples.

For storage in the base and safety-duplicate collections, preferred standard is to maintain separately the progeny of each mother plant, and store them in separate containers. All containers for one accession should be placed together in one labelled sealed container. Acceptable standard is to form a balanced bulk by taking an aliquot of seed from each mother plant, mixing thoroughly, and storing in one container. If possible, the size of the aliquot should equal the amount of seed produced by the plant yielding fewest seed. However, the total sample size should not be less than the acceptable target (Table 2), and to achieve this it may be necessary to increase the size of the aliquot. Adherence to the preferred standard is strongly recommended because of the implications for long-term maintenance of genetic integrity.

For storage in the active collection, preferred standard is to form a balanced bulk, in the same way as is acceptable for the base. Acceptable standard is to bulk all seed, but only if the genebank adopts the preferred standard of always regenerating active from base. An unbalanced bulk causes a major loss of genetic integrity: it is considered unacceptable to allow this degradation to cumulate further by repeatedly regenerating active from active.

3.8 Information management

Full records must be maintained, not only of the progress of seed through the regeneration system, but also of the entire regeneration history of each accession. This history starts when the accession enters the genebank and is a record of seed movement as well as a biological record. The record is updated continually and all aspects of the regeneration history noted.

Relevant data include:

- accession into genebank
    - date, donor, species, number of seed or plants or seed weight
    - packet number, location in genebank
- regeneration required

- how many seed germinated for regeneration
- how many plants used for regeneration

- regeneration location, date, pot size, compost type
- date of peak anthesis, harvest, threshing, germination test and results, etc.

All data should be entered in the genebank documentation system: seed quantity, seed quality, identity verification, control of genetic integrity.

Information technology-based preparation of labels, bags, etc. is recommended as part of quality assurance and the prevention of misidentification.

4. References

FAO. 1996. The State of the World's Plant Genetic Resources for Food and Agriculture: Background Documentation prepared for the International Technical Conference on Plant Genetic Resources, 17-23 June 1996. Food and Agriculture Organization of the United Nations, Rome, Italy.

FAO/IPGRI. 1994. Genebank Standards. Food and Agriculture Organization of the United Nations, Rome/International Plant Genetic Resources Institute, Rome, Italy.

Sackville Hamilton, N.R. and K.H. Chorlton. 1997. Regeneration of Accessions in Seed Collections: A Decision Guide. Handbooks for Genebanks No. 5. International Plant Genetic Resources Institute, Rome, Italy.

Appendix IV. Summary of germplasm holdings

Petter Marum [1], Ian D. Thomas [2] and Merja Veteläinen [3]

[1] The Norwegian Crop Research Institute, Løken Research Station, Norway
[2] IGER, Aberystwyth, United Kingdom
[3] Nordic Gene Bank, Alnarp, Sweden

On the basis of information supplied in advance from the participants, we prepared the following summaries. For some countries we used information from the 'Directory of European Institutions Holding Crop Genetic Resources Collections' (Frison and Serwinski 1995) and from the 'Report of a working group on forages. Fifth meeting' (Gass *et al.* 1995) as indicated in Table 1.

Not all countries had filled out the forms completely. Except for the number of accessions, about 70% of the information was supplied.

Table 1 gives the number of accessions for the eight genera: *Trifolium*, *Medicago, Vicia*, *Lolium*, *Festuca, Phleum*, *Poa* and *Dactylis*. The genus *Trifolium* has the largest number of accessions of the forage legumes, and the genus *Lolium* has the largest number of accessions among the grasses. In total there are 96 975 accessions in these eight genera. Poland has the largest number of accessions with 18 314.

Table 2 gives the percentage of accessions in long- and medium-term storage. Information is available for 89% of the accessions. At some locations accessions are stored under both long- and medium-term conditions. In these cases the number of accessions under medium-term storage has been set to zero. Overall, 36% of the accessions are stored under long-term conditions and 58% under medium-term conditions. The remaining 6% are stored under other conditions.

Regeneration status is summarized in Table 3. Information on the need for regeneration was supplied for 67% of the accessions. Of these, 22% or 14 367 accessions were described as being in urgent need of regeneration. Extrapolating to the whole collection, it is estimated that 21 335 accessions are in urgent need of regeneration. Each year 4670 accessions are regenerated, of which about 51% are regenerated in Russia.

The number of accessions available for distribution is given in Table 4. Information was supplied for 73% of the accessions. A total of 51 638 accessions are available. There are large differences between countries.

Table 5 gives the distribution of accessions to different 'Status of Sample': 46% are classified as wild and 16% as advanced cultivars. The wild category also includes 'semi-natural' populations, which although not sown have been subjected to agricultural management, such as cutting or grazing on a regular basis. 'Botanic Garden samples' have been obtained from a known donor, usually a Botanic Garden or University collection, but no further details of origin are known.

References

Frison, E. and J. Serwinski, editors. 1995. Directory of European Institutions Holding Crop Genetic Resources Collections, fourth edition. Vols. 1 and 2. International Plant Genetic Resources Institute, Rome, Italy.

Gass, T., R. Sackville Hamilton, K. Kolshus and E. Frison, editors. 1995. Report of a working group on forages. Fifth meeting, 31 March-2 April 1995, Hissar, Bulgaria. European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR). International Plant Genetic Resources Institute, Rome, Italy.

Table 1. Number of accessions in national collections

Country	*Dactylis*	*Festuca*	*Lolium*	*Medicago*	*Phleum*	*Poa*	*Trifolium*	Vicieae	Total
Austria	47	80	80	0	50	60	103	0	420
Belgium	0	0	60	0	1	0	0	0	61
Bulgaria	234	136	291	542	37	53	357	1669	3319
Cyprus	0	0	14	29	0	0	0	82	125
Czech Rep.	139	333	709	487	118	224	363	32	2405
France [†]	653	325	1740	2793	34	27	686	3629	9887
Germany [‡]	1268	1522	2135	1259	886	651	1549	2279	11549
Greece	252	183	182	573	12	0	553	578	2333
Hungary	250	589	194	825	65	172	1142	504	3741
Ireland	55	20	605	0	31	0	246	0	957
Italy [§]	444	343	716	2383	65	62	2275	2211	8499
Lithuania	16	17	10	3	3	7	15	4	75
Netherlands	28	0	194	0	102	0	142	0	466
Nordic Gene Bank	239	542	154	23	355	342	388	4	2047
Poland	6092	4606	2374	20	2568	2408	246	0	18314
Portugal	331	99	138	503	0	0	445	591	2107
Russia	1088	1856	732	2950	1267	626	3692	0	12211
Slovakia	208	709	276	252	105	232	307	256	2345
Spain	338	18	213	564	0	0	2800	0	3933
Switzerland	142	98	4	0	0	114	55	0	413
Turkey	178	27	0	889	24	13	763	1621	3515
United Kingdom [¶]	947	1236	2484	109	129	103	920	2173	8101
F.R. Yugoslavia	5	0	10	63	0	0	74	0	152
Total	**12954**	**14739**	**13315**	**14267**	**5652**	**5094**	**17121**	**15633**	**96975**

[†] Data mainly from the *Directory of European Institutions Holding Crop Genetic Resources Collections* (Frison and Serwinski 1995)

[‡] Data for Braunschweig from the *Directory of European Institutions Holding Crop Genetic Resources Collections* (Frison and Serwinski 1995).

[§] Data for Bari from the *Directory of European Institutions Holding Crop Genetic Resources Collections* (Frison and Serwinski 1995).

[¶] Includes data for Southampton from the *Report of a working group on forages. Fifth meeting* (Gass *et al.* 1995).

Table 2. Accessions in long- or medium-term storage calculated from accessions with available information (information is available for 89% of accessions in Table 1)

Country	No. of accessions with available information	In long-term storage (%)	In medium-term storage† (%)
Austria	420	0	100
Belgium	61	0	100
Bulgaria	3275	75	25
Cyprus	125	0	100
Czech Rep.	2405	63	37
France	9887	7	93
Germany	7176	100	0
Greece	2333	0	37
Hungary	3741	15	85
Ireland	957	85	15
Italy	4961	59	39
Lithuania	75	100	0
Netherlands	466	100	0
Nordic Gene Bank	2047	100	0
Poland	18314	0	100
Portugal	2107	30	70
Russia	12211	47	24
Slovakia	2345	0	100
Spain	3933	50	50
Switzerland	413	24	76
Turkey	3515	58	42
United Kingdom	5836	34	66
F.R. Yugoslavia	152	100	0
Total	**86755**	**36**	**58**

† Percentage of accessions that are stored only in medium-term storage (accessions that are stored under both long-term and medium-term conditions are not included in this column).

Table 3. Accessions in urgent need of regeneration and number of accessions regenerated/year calculated from accessions with available information (information is available on 67% of the accessions in Table 1)

	Accessions in urgent need of regeneration:		No. of accessions
Country	**Number**	**%**	**regenerated/year**
Austria	242	58	11
Belgium	0	0	
Bulgaria	9	3	94
Cyprus	23	53	3
Czech Rep.	85	4	16
France	120	10	
Germany	674	25	145
Greece	521	22	0
Hungary	249	7	367
Ireland	65	30	0
Italy	1041	21	326
Lithuania	0	0	0
Netherlands	0	0	88
Nordic Gene Bank	253	12	76
Poland	2023	12	0
Portugal	941	45	110
Russia	3975	33	2398
Slovakia	1318	57	210
Spain	228	6	387
Switzerland	113	27	9
Turkey	1175	46	280
United Kingdom	1311	22	150
F.R. Yugoslavia			
Total	**14367**	**22**	**4670**

Table 4. Number of accessions available for distribution, based on the accessions with available information (information on 73% of the accessions is in Table 1)

	Available accessions:	
Country	**Number**	**%**
Austria	13	3
Belgium	61	100
Bulgaria	533	18
Cyprus		
Czech Rep.	2130	89
France		
Germany	4803	88
Greece	116	5
Hungary	3741	100
Ireland		
Italy	3372	68
Lithuania	64	85
Netherlands	455	100
Nordic Gene Bank	2047	100
Poland	18314	100
Portugal		
Russia	5531	45
Slovakia	927	40
Spain	2598	66
Switzerland	100	24
Turkey	743	24
United Kingdom	5934	100
F.R. Yugoslavia	152	100
Total	**51638**	**74**

Table 5. Percentage by 'Status of sample' by country

Country	No. accessions	% Advanced cultivars	% Landraces	% Breeding material	% Wild and ecotypes	% Botanic garden sample	% Unknown or info. not available
Austria	420	5			95		
Belgium	61				100		
Bulgaria	3319	33	13		43		11
Cyprus	125		89		11		
Czech Rep.	2405	71	1	8	19		1
France	9887	16	9	1	11		63
Germany	11549	17	26	5	2		50
Greece	2333	12	3	26	35		24
Hungary	3741	32					68
Ireland	957	15			84		1
Italy	8499	3	2	24	41		29
Lithuania	75	39		61			
Netherlands	466	31	19	2	49		
Nordic Gene Bank	2047	18	8	1	74		
Poland	18314	4	0		96		
Portugal	2107	0			87		13
Russia	12211	39	22		40		
Slovakia	2345	41	6	5	48		1
Spain	3993	1	1	3	93		1
Switzerland	413		13		87		
Turkey	3515		27		73		
United Kingdom	8101	11	2	3	43	5	36
F.R. Yugoslavia	152				100		
Total	**96975**	**16**	**9**	**4**	**46**	**0**	**24**

Appendix V. Survey on safety-duplication capacities

As a result of a survey completed after the meeting, the following institutes have declared their availability to host safety-duplicates of forages under 'black box' arrangements.

Institute	Country	Storage conditions	Comments
RvP, Merelbeke (now DvP, Melle)	Belgium	–10°C	
IPK-Gatersleben	Germany	–15°C	in Malchow or Gatersleben
Inst. of Agrobotany, Tápiószele	Hungary	–20°C /–4°C	
IMGV-UNIPG, Perugia	Italy	–18°C	
Research Institute of Plant Production, Piestany	Slovakia	–18°C/0°C	
NGB, Alnarp	Sweden	–20°C (limited amount)/-4°C	negotiate about costs and packing
RAC, Changins	Switzerland	–21°C	
CGN, Wageningen	the Netherlands	–20°C	– reciprocal duplication – to be delivered/packed in aluminium foil bags
IGER, Aberystwyth	United Kingdom	–25°C/~1°C (depends on amount)	

Additional information:

- Other country representatives in the meeting also indicated that they would investigate possibilities to host safety-duplicates under 'black box' arrangements (Cyprus, Czech Republic, France, Greece, Hungary, Portugal, Russia, Spain and F.R. Yugoslavia).
- Lithuania cannot host safety-duplicates.

Appendix VI. Acronyms and abbreviations

AARI	Aegean Agricultural Research Institute, Menemen, Izmir, Turkey
ARI	Agricultural Research Institute, Nicosia, Cyprus
ARO	Agricultural Research Organization, Bet Dagan, Israel
ASSINSEL	Association Internationale des Sélectionneurs
BAL	Federal Research Institute for Agriculture in Alpine Regions, Austria
BAZ	Bundesanstalt für Züchtungsforschung an Kulturpflanzen (Federal Centre for Breeding Research on Cultivated Plants), Quedlinburg, Germany
CCDB	Central Crop Database
CGN	Centre for Genetic Resources The Netherlands, Wageningen, The Netherlands
CLIMA	Cooperative Research Center for Legumes in Mediterranean Agriculture
CNR	Consiglio Nazionale delle Ricerche (National Research Council), Bari, Italy
CRF	Centro de Recursos Fitogenéticos, Madrid, Spain
EC	European Commission
ECP/GR	European Cooperative Programme for Crop Genetic Resources Networks
EGDS	Eastern European Germplasm Documentation Systems Project
ENMP	Estação Nacional de Melhoramento de Plantas, Elvas, Portugal
EU	European Union
CGARC/FCPI	Central Greece Agricultural Research Center, Fodder Crops and Pastures Institute
CYPARI	Agricultural Research Institute, Nicosia, Cyprus
GEVES	Groupe d'étude et de contrôle des variétés et des semences, France
HRI	Horticulture Research International, Wellesbourne, UK
ICARDA	International Center for Agricultural Research in the Dry Areas, Syria
IGER	Institute for Grassland and Environmental Research, Aberystwyth, UK
IHAR	Plant Breeding and Acclimatization Institute, Radzikow, Poland
INIA	Instituto Nacional de Investigaciones Agrarias, Badajoz, Spain
INRA	Institut National de la Recherche Agronomique, France
IPGR	Institute of Introduction and Plant Genetic Resources, Sadovo, Bulgaria
IPK	Institut für Pflanzengenetik und Kulturpflanzenforschung, Gatersleben, Germany
ISA	Instituto Superior de Agronomia, Lisbon, Portugal
MAFF	Ministry of Agriculture Fisheries and Food, UK
MBG	Mision Biologíca de Galicia, Pontevedra, Spain
MTARC/GGB	Macedonia-Thraki Agricultural Research Center, Greek Gene Bank
NAGREF	National Agricultural Research Foundation, Greece
NGB	Nordic Gene Bank, Alnarp, Sweden
NGO	Non-governmental organization
PGR	Plant genetic resources
RAC	Institute for Agrobotany, Tápiószele, Hungary
RAPD	Random Amplified Polymorphic DNA
RICP	Research Institute of Crop Production, Prague, Czech Republic
RIPP	Research Institute of Plant Production, Piestany, Slovakia
SIA	Servicio de Investigaciónes Agrarias, Spain
UPM	Universidad Politécnica de Madrid, Spain
UPV	Universidad Politécnica de Valencia, Spain
VIR	N.I. Vavilov Research Institute of Plant Industry, St. Petersburg
WADA	Western Australia Department of Agriculture
WANA	West Asia North Africa Region
WIEWS	World Information and Early Warning System on plant genetic resources (FAO)
ZADI/IGR	Zentralsstelle für Agrardokumentation und -information / Informationszenttrum für Genetische Ressourcen, Bonn, Germany (Centre for Agricultural Documentation and Information/Information Centre for Genetic Resources)

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