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RYE GENETIC RESOURCES IN EUROPE

ABSTRACT

The European Secale Database contains passport data of 9,901 accessions. Twenty one European institutions contributed to ESDB. The biggest Secale collections are maintained in Poland, Russia and Germany. Thirty three per cent of accessions maintained in Secale collections throughout Europe can be preliminary identified as duplicates. The ESDB is available on the Internet www.ihar.edu.pl/gene_bank/ secale/secale.html.

Key words: central crop database, identification of duplicates, plant genetic resources, rye

INTRODUCTION

From its initiation in 1980, ECP/GR has focused on three principal objectives: the conservation of plant genetic resources, promoting the use of this germplasm and facilitating the international collaboration at the regional level. Documentation systems for crop genetic resources, and in particular central crop databases, play an essential role in reaching all three of these objectives. They provide a comprehensive overview of the collections maintained in Europe (Gass et al., 1998).

The usefulness of a database depends strongly on the quality of the data recorded. This quality is related to factors such as data comprehensiveness, date of last update and accuracy of data.

The first ECP/GR Secale Working Group meeting was held in Jokioinen, Finland, in August 1982. The Working Group designated the Polish Gene Bank as a crop germplasm centre for rye and recommended collation of passport data from other European rye collections. The first edition of the rye catalogue comprised passport data of rye accessions maintained in 11 genetic resources centres. The pioneer work carried out at the Plant Breeding and Acclimatization Institute was edited under auspices of ECP/GR Secretariat in 1984 (Serwiński and Konopka 1984).

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As the first of its kind, the rye catalogue was used as a reference as well as a model for other European databases.

The second edition has been initiated in 1995. Results of the work were presented during ECP/GR *Secale* Genetic Resources Workshop, which was held in Warsaw, Poland from 5–6 July 1996 (Gass, *et al.* 1998).

MATERIALS AND METHODS

Since eleven years passed from the first data gathering, the updated European *Secale* Database contains only newly requested data. Forty eight institutions in twenty five European countries were informed about the updating initiative. Until now 21 institutions provided data to PBAI Radzików (Table 1).

Secale collections contributing to European Secale Database

Table 1

INSTITUTION	Country	No of accessions
Bundesamt für Agrarbiologie	Austria	62
Landesanstalt für Pflanzenzucht und Samenprüfung Rinn	Austria	
Institute of Plant Introduction and Genetic Resources	Bulgaria	337
Station Fédérale de Recherches Agronomiques de Changins	Switzerland	63
Cereal Research Institute and Breeding Institute	Czech Rep.	659
Research Institute of Crop Producion	Czech Rep.	
Institut of Plant Genetics and Crop Plant Research-IPK	Germany	878
Institut für Pflanzebau–FAL	Germany	329
Instituto Nacional de Investigacion y Tecnologia Agraria y Alimentaria	Spain	428
Station d'amelioration des Plantes Clermont-Ferrand	France	41
Greek Genebank, Agricultural Research Center of Macedonia–Thrace, P.O.Box 312 570 01 Thermi –Thessaloniki	Grecce	11
C.N.R. Instituto del Germoplasma	Italy	382
Prekuli State Plant Breeding Station Selekeijas	Latvia	100
Plant Breeding and Acclimatization Institute	Poland	1354
Botanical Garden of the Polish Academy of Sciences	Poland	1630
Departamento de Genética Estaçao Agronómica Nacional	Portugal	33
Banca De Resurse Genetice Vegetale	Romania	45
N.I.Vavilov Institute of Plant Industry	Russia	2685
Research Institute of Plant Production	Slovakia	118
Nordic Gene Bank		63
Aegean Agricultural Research Institute	Turkey	512
Ukrainian Centre for Plant Genetic Resources	Ukraine	171
Total		9901

Total number of records containing passport data (9901) were provided to European *Secale* Database. Passport databases contained 71

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different descriptors. Three descriptors were common for all databases (accession number, name of cultivar and country of origin). Other frequent descriptors were: donor, donor number, geographical site.

The database structures and data formats were different. The files received were verified with regard to the content of columns and their completeness. A smaller list of descriptors was created, which contains all other descriptors. Descriptors close in meaning were joined together.

As the first step, an unified structure of the database was designed. From the data provided, the most common descriptors were chosen and data files from all collections were transformed using the unified structure. Less frequent descriptors, often specific for a single database, were included into 'wide' descriptors containing related data. The adopted database structure contains 29 descriptors (Podyma, 1998) which base on the multicrop passport descriptors (Hazekamp *et al.* 1997).

The botanical names were verified using *Secale* monographs (Hammer *et al.* 1987; Kobylyanskyi, 1989) and obvious misspellings were corrected whenever possible. Different codes used for information such as countries, population types, donors, collectors are used in documentation systems. An attempt to standardization of donor institutions names was made. Different types of notation were unified according acronyms of institutions (Serwiński *et al.*, 1987) and were used with some exceptions, when provided information was not complete enough to recognize the donor exactly. In ESDB the country of origin is abbreviated as recommended by ISO 3166 codes (Hintum *et al.*, 1995).

The main objective of a CCDB and also ESDB are to increase accessibility of information about accessions. This increased accessibility can benefit many applications (Hintum, 1997):

Improve accessibility of germplasm for users and curators,

Identify omissions in the combined collections

Identify probable duplications between collections

RESULTS

Database content

A preliminary survey of the assembled data shows that 69 per cent of material has identified species names. The database contains 1208 accessions for collected materials (wild, landraces) and 1966 for breeding materials (cultivars, breeding lines). Based on differences in growth habit, 5176 winter, 465 spring, and 75 intermediate *Secale* accessions were identified.

Majority of maintained accessions is European origin. ESDB consists of 84% of germplasm originated form Europe (including Turkey). Should be stressed key position of Russia and Turkey as sources of germplasm. Russia probably with all former states provide 19% of European genetic resources, Turkey 16% of total number of accessions (Fig.1). Non-European accessions are mainly originated from middle Asia, North Wiesław Podyma

America and South America (Argentina and Brazil). Species composition in European collections is unbalanced, 97% of accessions belong to *Secale cereale*, other species classified according to Kobylyanskyi (1989) are represented by not numerous entries (Table2).



Fig. 1 European countries of origin of the *Secale* genetic resources maintained in European collections

Table 2

Species composition of the European Secale collections			
Species	Number of accessions		
S. silvestre	59		
S. iranicum	2		
S. montanum	175		
S. cereale	9665		

The bigest *Secale* collections are maintained in Poland (37% of European *Secale* genetic resources), Russia (25%) and Germany (11%) (Table1). Each country tends to store large collections of germplasm for those crops which its breeders are working with (Frison and Serwiński 1995), whereby the motivation for assembling comprehensive national collections is frequently related to lack of information about material available from another country rather than fear of losing access to the germplasm. Under such circumstances, the level of duplication of effort is potentially very high.

Identification of probable duplicates

To improve the efficiency of plant genetic resources conservation the rationalization of the content of collections is urgently needed. Identifying and minimizing unnecessary duplication within and between collections is the first part of this effort. The problem of identifying duplicates and its principles was discussed by van Hintum and Knüpffer (1995). Passport data are useful for identification of probable duplicates between and within collections but this can be rarely done automatically. The procedure requires detailed knowledge of breeding process, collecting history of particular crop, and of the procedures used at the genebanks for data management.

GENE BANK	ACC. NUMBER	NAME
BGRIIPR	89104052	NISKOSTIEBIELNAJA
CSKKROM	C0300224	VIR K
POLIHAR	PL030106	К
POLIHAR	PL030332	LOCAL/VIR
POLIHAR	PL030126	C0300224
POLPAN	8837	К
POLPAN	7915	NISKOSTEBIELNAJA
RUSVIR		NIZKOSTEBEL'NAJA

Fig. 2 Example of duplication in European Secale collections

The variety name is convenient data type for identification probable duplicates. Preliminary analysis of accession names showed that 20 per cent of records are duplicates of other accession. The identification of probable duplicates using variety names or other designation encounters many problems (Podyma, 1998) and use of the more sophisticated methods is necessary. To assist in the identification of probable duplicates, the KWIC (key word in context) index, commonly known from bibliographic databases, was used (Knüpffer, 1988, 1989). Based on accession number, donor number, collection number, other number and variety name a common descriptor describing all accessions has been built. This method makes possible to detect accessions with 'matching' of similar elements of information, even if these elements are not stored in the database in an unique way. All errors in passport data mentioned by Hintum and Knüpffer (1995) were detected in the database. The efficiency of searching for duplicates increased significantly: 33% of accessions maintained in Secale collections throughout Europe can be preliminary identified as duplicates. An example of results of KWIC

index application are presented at Fig. 2 where cultivar NIZKOSTEBEL'NAJA is maintained in genebanks with different designations.

Indigenous materials and duplicates in Secale collections (Podyma 1997)					
INSTITUTION	Country ^{****}	% of accessions originated from the country	% of accessions originated from the country duplicated in other collections	% duplicated accession in collection (excluded accessions from the country)	
Bundesamt für Agrarbiologie	AUT	79	29	8	
Landesanstalt für Pflanzenzucht und Samenprüfung Rinn	AUT				
Institute of Plant Introduction and Genetic Resources	BGR	5	1	72	
Station Fédérale de Recherches Agronomiques de Changins	CHE	21	3	44	
Cereal Research Institute and Breeding Institute	CZE	7	5	63	
Research Institute of Crop Producion	CZE				
Institut of Plant Genetics and Crop Plant Research–IPK	DEU	8	1	12	
Institut für Pflanzebau–FAL	DEU	11	2	31	
Instituto Nacional de Investigacion y Tecnologia Agraria y Alimentaria	ESP	63 [*] (427)	0	0	
Station d'Amelioration des Plantes Clermont–Ferrand	FRA	70	0	2	
Greek Genebank, Agricultural Research Center of Macedonia–Thrace	GRC	100	0	0	
C.N.R. Instituto del Germoplasma	ITA	23**(96)	13	3	
Prekuli State Plant Breeding Station Selekeijas	LVA	8	25	64	
Plant Breeding and Acclimatization Institute	POL	12	3	65	
Botanical Garden of the Polish Academy of Sciences	POL	7	6	55	
Departamento de Genética Estaçao Agronómica Nacional	PRT	100	0	0	
Banca De Resurse Genetice Vegetale	ROM	96	0	0	
N.I.Vavilov Institute of Plant Industry	RUS	32	43	7	
Nordic Gene Bank	SWE	100	24	0	
Aegean Agricultural Research Institute	TUR	100	30	0	

	Table 3
Indigenous materials and duplicates in <i>Secale</i> collections (Podyma 1997)	

 * – accessions from Spain and Portugal; ** – accessions from Mediterranean region; *** – country codes according to ISO 3166

UKR

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Ukrainian Centre for Plant Genetic Resources

The number of duplicated accessions depends on type of collection. Some big collections as Polish and the Czech Republic collections gather worldwide *Secale* materials. The number of duplicates in these collections is high. There are collections focused on indigenous materials, where maintained materials are unique (Portuguese, Romanian, Swedish or Turkish collections). The value of a collection for conservation purposes is ,to a large extent, determined by that part of the collection that is unique. Even if this part is small, the collection value can be extremely high. Table 3 contains estimation of the per cent of duplicates in all studied *Secale* collections.

During the analysis the problem of homonyms and synonyms which is common for commercial varieties, was not considered. The establishment of list of homonyms and synonyms needs engagement of rye curators in this work.

The rapid development of technology in the areas of communication and electronic data storage and processing allows for direct access to databases. The ESDB is available and searchable on line on the Internet at the following URL: <u>www.ihar.edu.pl/gene_bank/ secale/secale.html</u>.

REMARKS

The apparent poor quality of passport data makes identification of probable duplication difficult. In some databases only a little information is stored. A more complete spectrum of information is necessary not only for studies on relations among accessions (e.g. studies on duplicates) but also for the evaluation of data in a single database.

Relying on perfect matches of information contained in corresponding data fields results in a low percentage of the identifiable probable dupli– cation being found. KWIC index method significantly increases efficiency of searching probable duplicates.

The free availability of the European *Secale* Database will facilitate rationalization of the content of contributing collections and exchange of germplasm. The central crop database is an important factor determining the chance of finding probable duplication. It is also a very useful tool for filing up gaps in collections.

CONCLUSIONS

- There are maintained in European gene banks 9901 accessions of Secale
- There can be 33 % of accessions in *Secale* collections preliminary identified as duplicates
- Central Crop databases facilitate access to plant genetic resources, identification of gaps, and improvement of data quality.

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