

Genetic resources conservation of wild relatives with a users' perspective

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Abstract

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Wild relatives of our cultivated crops are an important source for the genetic improvement of these crops. This paper describes the presence of wild relatives in the collections of Centre for Genetic Resources, the Netherlands (CGN). It shows that the collections differ substantially in the presence of wild relatives. It is demonstrated that former working collections of breeders are often dominated by cultivated material.

This paper briefly reviews the utilization of wild relatives of *Solanum* and *Lactuca* in breeding. It is emphasized that the evaluation of wild relatives for certain properties is a prerequisite for the utilization of this material. Evaluation of wild relatives will also reveal the geographical distribution of specific characters in the original collecting sites. Examples of the geographical distribution of wild potato species with resistance to economic pests and diseases are presented.

Introduction

Genepools of our cultivated crops are often divided in: primary, secondary and tertiary genepools (Harlan & de Wet 1971, Bothmer & al. 1991). The primary genepool includes mainly the cultivated species of the crop and sometimes some very related primitive cultivars and wild species with no crossing barriers. The tertiary group mainly consists of wild relatives with crossing barriers, whereas the secondary pool consists of primitive cultivars and wild relatives which can be crossed with the cultivated species but usually not without difficulties.

During the last decades breeders have been increasingly utilizing the secondary and tertiary genepools of our cultivated crops which very often include wild relatives. The need to broaden the genetic bases of our crop species is required because the primary genepools do not provide sufficient genes for important properties such as resistance to diseases and pests, physiological and quality characters.

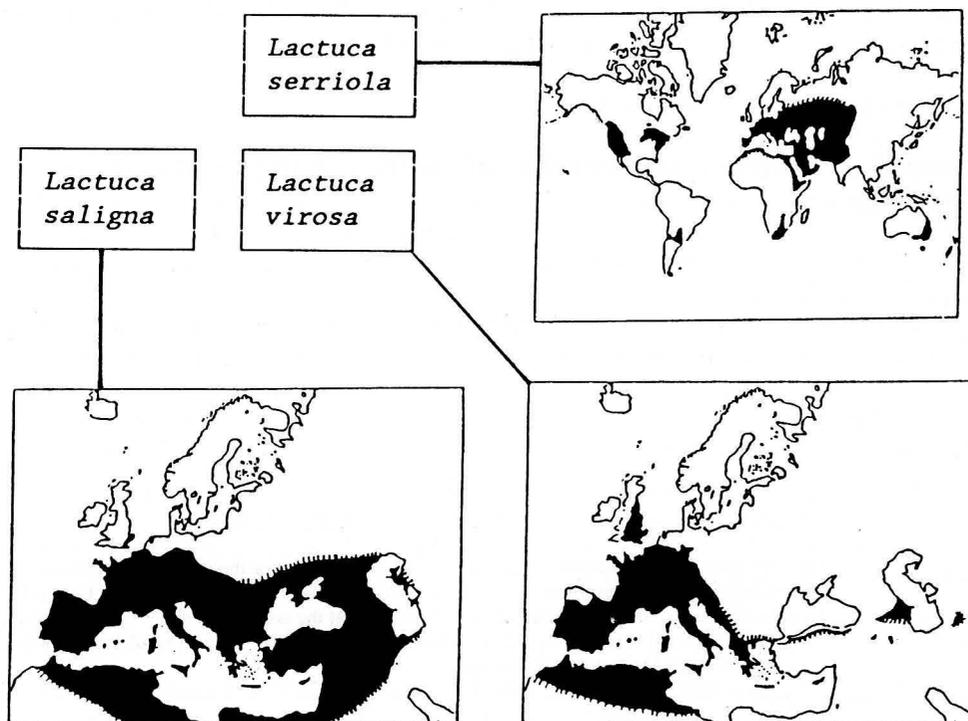


Fig. 1. Geographical distribution of four wild *Lactuca* species.

In barley, breeders have been using the wild progenitor *H. vulgare* subsp. *spontaneum* (C. Koch) Thell., considered by Bothmer & al. (1991) as part of the primary genepool of *Hordeum*, as source for mildew resistance (Fischbeck 1981). The wild emmer wheat (*Triticum turgidum* (L.) Thell. subsp. *dicoccoides* (Korn) Thell.) has been used over the last 15 years in several breeding programmes, particularly for resistance breeding and improvement of wheat quality (Groenewegen 1988, Lange & Balkema-Boomstra 1988, Williams & al. 1990, Cox 1991). More recently wheat breeders are also utilizing different wild progenitors of wheat such as *T. speltoides* (Tausch) Gren. ex K. Richt., *T. squarrosium* L. and other wild species (Miller & al. 1988, Gorham & Wyn Jones 1990) for the same purposes.

The utilization of wild relatives for the improvement of lettuce and potato will be discussed later in this paper. Wild relatives of lettuce are found in Europe and other continents (Fig. 1), whereas for potato they are only located in the Americas (Fig. 3).

The centres of origin of our cultivated crops are situated in a relatively confined geographical area around the Tropic of Cancer (23.5 °N.) and the Tropic of Capricorn (23.5°S.). In general the wild relatives of our crops are also found in these confined geographic regions. As a consequence not many wild relatives of important cultivated crops are of European origin. In the Mediterranean region only wild relatives of beet, cabbage, lettuce, oats and wheat can be found. Consequently breeders in Europe are very

much dependent of wild germplasm from other parts in the world and there is a need to increase this type of genetic resources in European collections.

Survey of wild relatives in CGN holdings

The Centre for Genetic Resources The Netherlands (CGN) is the national genebank of The Netherlands and was officially established in 1985. Presently, it maintains over 20000 accessions divided over some 20 groups of agricultural and horticultural crops (van Soest & al. 1995). It is expected that the collections will increase in the next few years to approximately 25 000 accessions.

The collections maintained by CGN were mainly received from former plant breeding institutes and private breeding companies in The Netherlands. These former working collections are dominated by cultivated material, including research material from former breeding programmes (van Soest & al. 1995). Therefore most CGN collections, including the cereals, pulses and some vegetables, consist predominately of cultivated material (Table 1).

Table 1. Survey of wild relatives in CGN holdings, including cooperative German-Netherlands collections (status 1 May 1995).

Genus	Crop	Total accessions	Wild relatives (number of species)		% wild relatives
Agricultural crops					
<i>Triticum</i>	(wheat)	5259	234	(16)	4.4
<i>Hordeum</i>	(barley)	3382	79	(15)	2.3
<i>Avena</i>	(oats)	532	18	(8)	3.4
<i>Zea</i>	(maize)	482	0	(0)	0.0
<i>Pisum</i>	(peas)	986	21	(3)	2.1
<i>Vicia</i>	(faba bean)	607	0	(0)	0.0
<i>Solanum*</i>	(potato)	2700	1950	(113)	72.2
<i>Beta</i> (CGN)	(beet)	205	168	(7)	81.9
<i>Beta**</i>	(beet)	1606	1122	(12)	69.9
Horticultural crops					
<i>Lactuca</i>	(lettuce)	1950	666	(19)	34.2
<i>Allium</i>	(onion/leek)	198	14	(6)	7.0
<i>Lycopersicon</i>	(tomato)	830	82	(9)	9.9
<i>Spinacia</i>	(spinach)	363	3	(1)	0.8
<i>Cruciferae*</i>	(crucifers)	1374	22	(7)	1.6

* German-Netherlands Potato Collection

** German-Netherlands Beet Collection

*** both agricultural and horticultural *Cruciferae*

However, some collections including the cooperative German-Dutch collections of *Beta* and of tuber-bearing *Solanum* species, as well as the *Lactuca* collection include a substantial amount of related wild species. The 72 % of wild relatives included in the German-Netherlands Potato Collection is rather high because of the large number of wild species (113) and the fact that the collection does not include European cultivars. The 28% of cultivated material is mainly of cultivars and cultivated primitive forms from the American centres of origin. The lettuce collection with 34 % of wild relatives is an exception under the group of horticultural crops.

In general collections of multi-crop genebanks include limited numbers of accessions of wild relatives and the majority of the accessions maintained is of cultivated origin. There are however a number of genebanks which specialize on the maintenance of wild relatives of some cultivated crops.

Wild relatives of lettuce (*Lactuca sativa* L.)

Origin and collections

The genus *Lactuca* includes over 100 species distributed over Europe, North America, East Africa and Asia (Boukema & al. 1990). However, there is no general agreement among taxonomist about the classification and limits of the genus. CGN largely adopted the concepts of Ferakova (1977). According to Ferakova the species closely related to the cultivated lettuce (*L. sativa* L.) belong to the section *Lactuca* subsection *Lactuca*. This section includes the wild species like *L. serriola* L., *L. saligna* L., *L. altaica* Fisch. & Mey. and *L. virosa* L. The species *L. aculeata* Boiss. and *L. dregeana* DC. can also be included in this subsection, because they are fully sexually compatible with *L. sativa* and *L. serriola* (Zohary 1991). The number of accessions of these wild *Lactuca* species in the CGN collection and their region of origin is presented in Table 2. The distribution of the most important wild species is shown in Fig. 1. It demonstrates that a large part of these species originate from Europe. The above mentioned species can be regarded as belonging to the secondary genepool of the cultivated lettuce. *L. serriola* which has no crossing barriers at all with cultivated lettuce, can even be regarded as belonging to the primary genepool. Recently, Frietema de Vries & al. (1994) suggested, that cultivated lettuce *L. sativa* and the wild *L. serriola* can be regarded as the same species, only differing in characters influenced by domestication. Because *L. virosa* has more severe crossing barriers than the other species mentioned, this species was regarded by Zohary (1991) as belonging to the tertiary genepool.

The other wild *Lactuca* species and the species of genera closely related to *Lactuca* of the CGN collection (Table 2), can be regarded as belonging to the tertiary genepool or not belonging to the genepool at all. The number of these accessions, and region of origin are also presented in Table 2. Only a few accessions of these other *Lactuca* species are of European origin.

From the 1950 accessions of the CGN lettuce collection more than 30% are wild relatives (Table 1). 50% of the wild species are of European origin, and most likely a substantial number of the 161 accessions of which the origin is not known (Table 2) are also from Europe.

Table 2. The wild lettuce collection of CGN. Number of accessions per region of origin.

Species	Region of origin						Total
	AF	AM	EU	ME	FE	?	
<i>L. serriola</i>	1		255	125	4	92	477
<i>L. dregeana</i>						2	2
<i>L. aculeata</i>			1	1			2
<i>L. altaica</i>			1			1	2
<i>L. saligna</i>			19	28		9	56
<i>L. virosa</i>			47	2		29	78
<i>L. indica</i>					2	2	4
Other wild <i>Lactuca</i> species ¹	2	1	12		1	13	29
<i>Lactuca</i> species not known						4	4
Genera related to <i>Lactuca</i> ²			2	1		9	12
Total	3	1	337	157	7	161	666

¹ *L. biennis*, *L. canadensis*, *L. dentata*, *L. homblei*, *L. perennis*, *L. quercina*, *L. tatarica*, *L. tenerrima* and *L. viminea*.

² *Chondrilla juncea*, *Mycelis muralis* and *Steptorrhampus tuberosus*.

AF = Africa; AM = America; EU = Europe; ME = Middle East; FE = East and Far East

The lettuce collection of CGN is together with the collections from the USA (McGuire & al. 1993) one of the largest of the world and the largest in Europe. Other important collections are those from HRI, Wellesbourne, UK; VIR, St. Petersburg, Russia and from Olomouc, Czech Republic.

Evaluation and utilization

The CGN lettuce collection has been widely used. In the last ten years over 4200 seed samples were requested for evaluation and utilized in breeding programmes. About 70 % were used in the Netherlands and the rest in Europe and the USA. A large part of the collection, including several wild species were screened for resistance to a number of downy mildew (*Bremia lactucea*) isolates (Bonnier & al. 1992, Lebeda & Boukema 1991). The species *L. saligna* seems completely resistant to all isolates tested. In most of the other species race specific resistance is found, but in *L. perennis* L. the 7 accessions tested were all resistant. A part of the wild species were screened for natural infection to powdery mildew (*Erysiphe cichoracearum*). There was a large variation in attack for powdery mildew in most species (Lebeda 1994). Substantial parts of the wild species belonging to the subsection *Lactuca* are tested now for the aphid *Macrosiphum euphorbiae* and 'Tomato Spotted Wilt Virus' (WSTV).

Besides lettuce breeding in Europe, extensive work on lettuce was carried out in the USA. McCuire & al. (1993) present overviews of known qualitative genes for lettuce and related species. They also mentioned that the wild species *L. serriola*, *L. saligna* and *L. virosa* have been or are being used in lettuce breeding to introduce genes for resistance to downy mildew, aphids, and corky root into lettuce cultivars.

Wild relatives of potato (*Solanum tuberosum* L.)

Origin and collections

The tuber-bearing *Solanum* species are widely distributed in the Americas from the south-western states of the USA to southern Argentina and Chile. Hawkes (1990) classified the genus *Solanum* L., subgenus *Potatoe* (G. Don) A'Arcy in 19 series, including 7 cultivated potato species and 218 wild relatives. There are 8 important potato collections in the world conserving approximately 13 500 accessions of some 200 wild relatives and over 10 000 accessions of 7 cultivated primitive cultivars from the centres of origin, excluding material of the European cultivated potato *S. tuberosum* L. subsp. *tuberosum* (Hoekstra, pers. commun. 1996).

The German-Netherlands Potato Genebank, established in 1974 in the FAL, Braunschweig (Germany) and since 1995 situated at CGN, Wageningen (The Netherlands) presently maintains 750 accessions of primitive cultivars and 1950 accessions of 113 wild relatives.

Evaluation and utilization

The wild potato gene pool has been intensively screened for important properties (Ross 1986, Hoekstra & Seidewitz 1987, Hawkes 1990, Bamberg & al. 1994).

A programme to evaluate the German-Netherlands Potato Collection started in 1976 (van Soest 1983). Evaluation data of important properties, particularly information on resistances to pest and diseases have been published in several papers (van Soest & Seidewitz 1981, van Soest & al. 1983, van Soest & Hondelmann 1984, van Soest & al. 1984, Hoekstra 1986, Dellaert & Hoekstra 1987, Hoekstra & Seidewitz 1987, Hoekstra 1988, Langerfeld & Hoekstra 1992, Colon 1994, Langerfeld & Hoekstra 1994).

Ross (1986) concludes that genes of only six wild species have been incorporated into European cultivars.

Some various important pest and diseases of potato in Europe are presented in Table 3. The table lists five wild potato relatives of which resistance genes are now frequently incorporated in European cultivars.

S. stoloniferum Schlecht. & Bché has been widely used as source of resistance to late blight and potato virus Y. In Germany 10 cultivars were produced with resistance to potato virus Y from *S. stoloniferum* (Ross 1979).

S. demissum Lindl. is a well known source for resistance to late blight and was already used in breeding programmes before the last world war (Hawkes 1979). Many varieties have been developed with genes of this Mexican potato species (Ross 1986).

Table 3. Utilization of wild potato species in breeding.

Property	Genes incorporated in potato cultivars	Potential sources*
Fungus resistance		
late blight	<i>S. demissum</i> <i>S. stoloniferum</i>	<i>S. berthaultii</i> <i>S. microdontum</i> <i>S. verrucosum</i>
Virus resistance		
Potato Virus Y	<i>S. stoloniferum</i>	<i>S. acaule</i> <i>S. gourlayi</i>
Potato Virus X	<i>S. acaule</i>	<i>S. chacoense</i> <i>S. tarijense</i>
Nematode resistance (cyst nematodes)		
<i>G. rostochiensis</i>	<i>S. spegazzinii</i>	<i>S. gourlayi</i> <i>S. sparsipilum</i> <i>S. vernei</i>
<i>G. pallida</i>	<i>S. vernei</i>	<i>S. circaeifolium</i> <i>S. oplocense</i> <i>S. sparsipilum</i>

* some species are or have been used in interspecific hybridization programmes.

S. vernei Bitt. et Wittm. and somewhat later *S. spegazzinii* Bitt. were used in breeding for resistance to the potato cyst eelworm and more than 60 cultivars have been produced using genes of these two species (Ross 1986). New pathotypes of the common nematode (*Globodera rostochiensis*) developed and another species which several pathotypes (*G. pallida*) was detected. Resistance to this new species was found in *S. vernei* and was incorporated into many European cultivars, particularly those for starch production.

S. acaule Bitt. was used as source for extreme resistance to potato virus X and incorporated in several German cultivars (Ross 1979).

Hawkes (1990) presents a summary of evaluation results on the major potato diseases and pests, and adaptation to environmental extremes. This list includes more than 50 important species and in some species resistance to different diseases and pests and physiological extremes have been detected. Many of these wild species have been used or are presently included in interspecific hybridization programmes (Hermsen 1979, van Soest 1986, Ross 1986, Hawkes 1990, Colon 1994). Some of the genes for resistance of these wild species may be transferred in the near future into new cultivars. Other genes of some species however may never reach this stage.

Geographical distribution of *Solanum* species with resistance to late blight and cyst nematodes

Evaluation of accessions of the German-Netherlands Potato Collection resulted in the detection of species or accessions which have particular properties but also identify geographical areas where a concentration of specific properties can be found.

Figs. 2 and 3 show respectively the geographical distribution of wild potato species with resistance to *G. pallida* (pathotype Pa3) and high levels of race non-specific resistance to late blight (*P. infestans*).

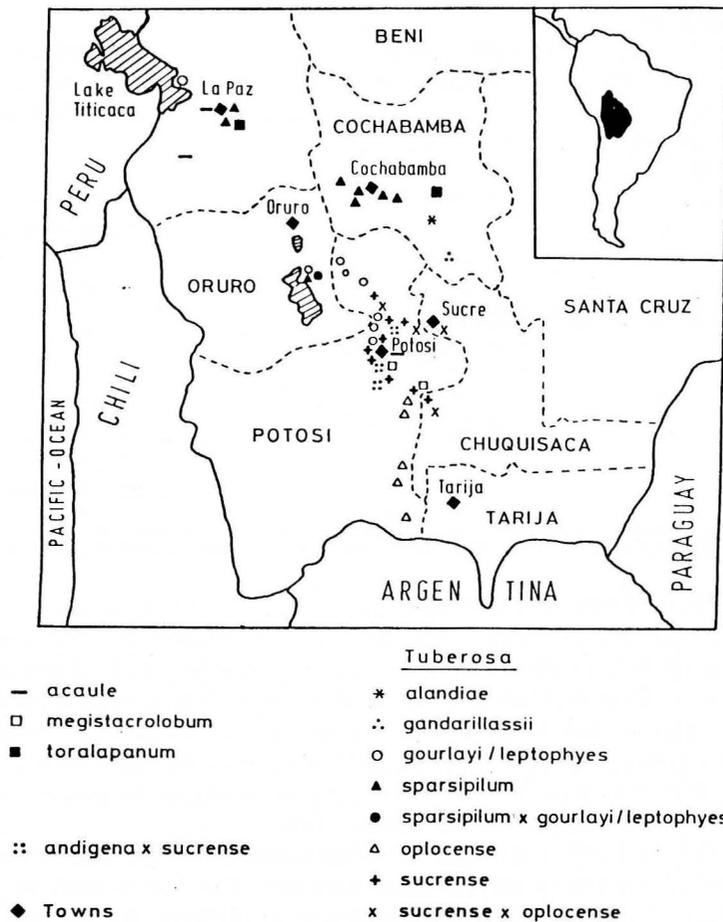


Fig. 2. Geographical distribution of tuber-bearing *Solanum* species with *G. pallida* pathotype Pa3 resistance in Bolivia.

This information is based on the evaluation of numerous accessions of the German-Netherlands Potato Collection (van Soest & al. 1983, van Soest & Hondelmann 1984, van Soest & al. 1984). From these geographical studies it could be concluded that:

- a remarkable concentration of species with resistance to the cyst nematode (*G. pallida* pathotype Pa3) is found around Potosi in central Bolivia, although the distribution extends northwards towards Cochabamba and Oruro, and southwards to the Argentine border;
- there are two important areas in the centre of origin with a concentration of species showing high levels of non-specific resistance to late blight. Nine wild species are from

Mexican origin and six from regions in Bolivia and Argentina (Fig. 3.). These studies revealed that several underexploited species such as *S. fendleri* Asa Gray, *S. hjertingii* Hawkes, *S. capsicibaccatum* Cárđ. and *S. circaeifolium* Bitt. have cyst nematode resistance and *S. alandiae* Cárđ., *S. leptophyes* Bitt., *S. gandarillassii* Cárđ. and *S. toralapanum* Cárđ. et Hawkes show non-specific resistance to late blight. These underexploited species are found in confined regions of the centres of origin of our cultivated potato and may be of value for future resistance breeding in this crop. Other species, some mentioned in Table 3., have already been included in interspecific hybridization programmes (Ross 1986, Hawkes 1990, Colon 1994).



Fig. 3. Geographical distribution of tuber-bearing *Solanum* species with high levels of non-specific late blight resistance.

Discussion

Few wild relatives of economically important crop plants are found in Europe. Exceptions are some wild species of a few crops mainly distributed in southern Europe. As a consequence genetic crop improvement in Europe depends to a large extent on wild relatives of crops from confined areas mostly in the tropics.

Most of the national genebanks are multi-crop genebanks. These genebanks, as is the situation in the Dutch genebank (CGN), conserve mainly cultivated material. The percentage of wild relatives in the collections is often limited. Only specialized genebanks,

several of them included in the 'Base collection of seed crops system' of IPGRI (IBPGR 1989) maintain large numbers of wild relatives. It is expected however that wild species will receive more attention, particularly to fill the need for special genes for the genetic improvement of cultivated crops. Broadening of the collections with wild relatives should be done in cooperation with other genebanks linked through International Crop Data Bases, after identifying gaps in existing collections and joint actions needed to fill such gaps.

Wild related species of crops are an important source for new characters. Evaluation of such materials is a prerequisite for better utilization of the germplasm. The screening of large collections of wild species may not only result in the detection of species and accessions which have economical important properties but also identify geographical areas where a concentration of specific characters can be found. This paper shows, that cyst nematode resistance is predominantly concentrated in the Andean *Solanum* species that have their distribution at altitudes between 2500 and 4250 m. Non-specific resistance to late blight is concentrated in two confined regions in Mexico and Bolivia/Argentina.

Classical interspecific hybridization programmes are becoming rare at public research organizations, as emphasis and funding opportunities has shifted to biotechnological gene transfer. The importance of such programmes is increasing as new developments in biotechnology are widening possibilities of transferring genetic characters across natural species barriers including genes from wild relatives of our cultivated crops.

It is concluded that the genes available in the genepools of the wild relatives of both lettuce and potato have been insufficiently used in breeding of these two crops.

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