

Wild *Lactuca* germplasm for lettuce breeding: current status, gaps and challenges

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Received: 22 November 2008 / Accepted: 2 March 2009 / Published online: 17 March 2009
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Abstract In this review, we present a critical analysis of the current status of wild *Lactuca* L. germplasm in relation to its utility for lettuce breeding. We discuss wild *Lactuca* germplasm in ex situ collections from the perspectives of taxonomy, biogeography, biology and ecology, gene pools, field exploration and acquisition, descriptor development, characterization and evaluation, and enhancement. Future research and other activities related to wild *Lactuca* germplasm and their continued exploitation in lettuce breeding are considered.

Keywords Taxonomy · Biogeography · Ecology · Gene pools · Collecting · Gene banks · Duplicates · Descriptors · Genetic diversity · Phenology · DNA content · Disease resistance · Biochemical features · Molecular polymorphism

Introduction

Genetic resources of wild *Lactuca* species as conserved in the world's genebanks are an integral part of our global plant heritage, and they play important

role in modern lettuce breeding (Lebeda et al. 2007c; Mikel 2007; Maggioni et al. 2008; Mou 2008). Considerable progress in both fundamental research on *Lactuca* germplasm and its practical applications has been achieved during last 25 years (Lebeda et al. 2007c). The most important remaining gaps, problems and sources of confusion related to the effective use of these key resources are highlighted in this paper along with a recent progress report.

Taxonomy of *Lactuca* L.

Taxonomic and phylogenetic studies clearly place the genus *Lactuca* L. in the tribe Lactuceae, subfamily Cichorioideae, of the Compositae (Asteraceae) (Funk et al. 2005), one of the largest plant families. A careful review of published literature confirmed the existence of about 100 wild *Lactuca* spp., with the highest number of autochthonous species and species richness in Asia (51 species) and Africa (43 species) (Lebeda et al. 2004b). The most recent molecular data on phylogenetic relationships among *Lactuca* species (Koopman et al. 1998) confirmed, with some modifications, a previously elaborated broader generic concept (summarized by Lebeda et al. 2007c). However, formal classification, including subgeneric divisions (Lebeda et al. 2007c), need critical reconsideration and further elaboration.

In addition, serious taxonomic discrepancies can be found in the main world collections of *Lactuca* L.

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germplasm. Doležalová et al. (2004) studied 49 accessions of 24 *Lactuca* species received from the main world genebanks. It was found, after taxonomic review, that 35% of accessions were wrongly taxonomically described and were redetermined (on the genus, species and subspecific level). Therefore, good knowledge of classical taxonomy combined with the comparative study of original herbarium specimens must be considered as a most important step for the efficient management and utilization of *Lactuca* genetic resources (Lebeda et al. 1999), and correct interpretation of experimental data (Lebeda et al. 2002).

Geographic distribution and hot-spots of diversity

There is increasing interest in the potential value of genes from wild species in crop improvement (Gass and Frese 1999). For lettuce, there are two crucial issues related to the utilization of genes from wild species: loss of genetic diversity in situ and limited access to wild *Lactuca* in current ex-situ germplasm collections (Lebeda et al. 2004a, 2007c). To overcome these challenges, genebanks should focus on

rapidly acquiring lettuce progenitors and wild relatives from the probable center of origin of lettuce and from those areas with the highest genetic diversity of *Lactuca* species (Lebeda et al. 2004c). High levels of diversity of *Lactuca* species found in the Mediterranean basin and southwestern Asia indicate that those regions should be seriously considered as hot-spots for lettuce conservation (Beharav et al. 2008a, b; Kitner et al. 2008; Lebeda et al. 2001b, c, 2008d). Future ecogeographic studies should also focus on central and southern Africa, central Asia, and North America to determine if other hot-spots exist and to develop collecting strategies accordingly (Lebeda et al. 2007c) (Fig. 1).

Biology and ecology

The genus *Lactuca* includes annual, biennial and perennial herbs, and rarely shrubs, with abundant latex. Sections *Phoenixopus*, *Mulgedium*, *Lactucopsis*, *Tuberosae*, *Micranthae* and *Sororiae* (see Table 1) are mostly biennial or perennial (Lebeda and Astley 1999). The division of section *Lactuca* into two subsections, *Lactuca* and *Cyanicae*, is based on



Fig. 1 Geographical distribution of diversity hot-spots of wild *Lactuca* species

Table 1 Sections, subsections and geographical groups of *Lactuca* genetic resources (modified following Lebeda et al. 2004b, 2007c)

| Sections/subsections |
|---|
| <i>Lactuca</i> |
| subsect. <i>Lactuca</i> (<i>L. aculeata</i> , <i>L. altaica</i> , <i>L. azerbaijanica</i> , <i>L. dregeana</i> , <i>L. georgica</i> , <i>L. livida</i> , <i>L. saligna</i> , <i>L. sativa</i> , <i>L. scarioloides</i> , <i>L. serriola</i> , <i>L. virosa</i>) |
| subsect. <i>Cyanicae</i> DC. (<i>L. perennis</i> , <i>L. tenerrima</i>) |
| <i>Phaenixopus</i> (Cass.) Bentham (<i>L. viminea</i>) |
| <i>Mulgedium</i> (Cass.) C.B. Clarke (<i>L. tatarica</i> , <i>L. sibirica</i> , <i>L. taraxacifolia</i>) |
| <i>Lactucopsis</i> (Schultz Bip. ex Vis. et Pančić) Rouy (<i>L. quercina</i>) |
| <i>Tuberosae</i> Boiss. (<i>L. indica</i>) |
| <i>Micranthae</i> Boiss. (<i>L. undulata</i>) |
| <i>Sororiae</i> Franchet (<i>L. sororia</i>) |
| Groups (geographical view) |
| North American (e.g. <i>L. biennis</i> , <i>L. canadensis</i> , <i>L. floridana</i> , <i>L. graminifolia</i>) |
| African (e.g. <i>L. capensis</i> , <i>L. dregeana</i> , <i>L. homblei</i>) |

the life cycle of their members (Feráková 1977). Subsection *Lactuca* comprises annual, winter annual or biennial herbs; perennial species belong to subsection *Cyanicae*. The autochthonous North American species are mostly biennial; however, at least one perennial species, *L. tatarica* subsp. *pulchella* (syn. *L. oblongifolia*), is also reported (McGregor et al. 1986). The African species are annual or perennial herbs or sub-shrubs, rarely scandent (Lebeda et al. 2004b).

The genus *Lactuca* comprises species with various ecological requirements occupying diverse habitats. The species of lettuce's genepool (those of the breeders' main interest), *L. serriola*, *L. saligna* and *L. virosa*, are weedy and occur on waste places and ruderal habitats—mainly along roads, highways and ditches (Lebeda et al. 2001b, c, 2004b, 2007a) (Fig. 2). Most species, i.e. *L. perennis*, *L. viminea*, *L. graeca*, and *L. tenerrima*, are calciphilous plants found in limestone and dolomite areas, often on rocky slopes. Endemic, lianlike species are found in rain forests of East Africa. Comprehensive surveys regarding the biology and ecology of European *Lactuca* species were conducted by Feráková (1977) and Lebeda et al. (2004b), who summarized available information on about 100 species from current world literature. However, basic data about

the biology and ecology of most species, especially those of African and Asian origin, are still unavailable.

Gene pools and genetic diversity

Human effort in the process of domestication probably involved selection of wild relatives for leaves that had a reduction in leaf spines, latex content and bitter flavor, and for plants with delayed bolting. Domestication has also led to a shortening of internodes, bunching of leaves, increased seed size and non-shattering (Fig. 3), and changes in photoperiodism (enabling cultivation under various daylengths). These processes have been accompanied by bottlenecks that restricted the genetic diversity available in the primary gene pool.

In general, the primary gene pool of cultivated lettuce comprises the numerous cultivars and landraces of *L. sativa* and its wild ancestor, *L. serriola*. The wild *serriola*-like species from southwestern Asia (i.e., *L. aculeata*, *L. altaica*, *L. azerbaijanica*, *L. georgica*, and *L. scarioloides*) and the African species, *L. dregeana*, all display similar levels of interfertility with the crop and belong to the primary gene pool as well (Lebeda et al. 2007c). Although *L. saligna* and *L. virosa* have been intensively studied by both evolutionary biologists and plant breeders, their categorization to the secondary or tertiary gene pools has remained an open question (Fig. 4). A view rather different from that outlined above was proposed by Koopman et al. (1998), who suggested that section *Lactuca* subsection *Lactuca* comprises the primary and secondary gene pools, while sections *Phaenixopus*, *Mulgedium* and *Lactucopsis* make up the tertiary gene pool. However, the categorization of many *Lactuca* species into gene pools is still unclear and needs additional attention.

Germplasm collections—recent status and problems

Collections, their structure and gaps

Data describing wild *Lactuca* germplasm collections in Europe and around the world were summarized by Lebeda and Boukema (2001) and Lebeda et al.

Fig. 2 Examples of *L. serriola* habitats: agricultural areas (**a, d**), piles of debris (**b**), urban areas—sterile substrate (**c**), pavement (**e**), along transport corridors—roadside (**f**), fallow lands—“*Lactuca* fields” (**g**)



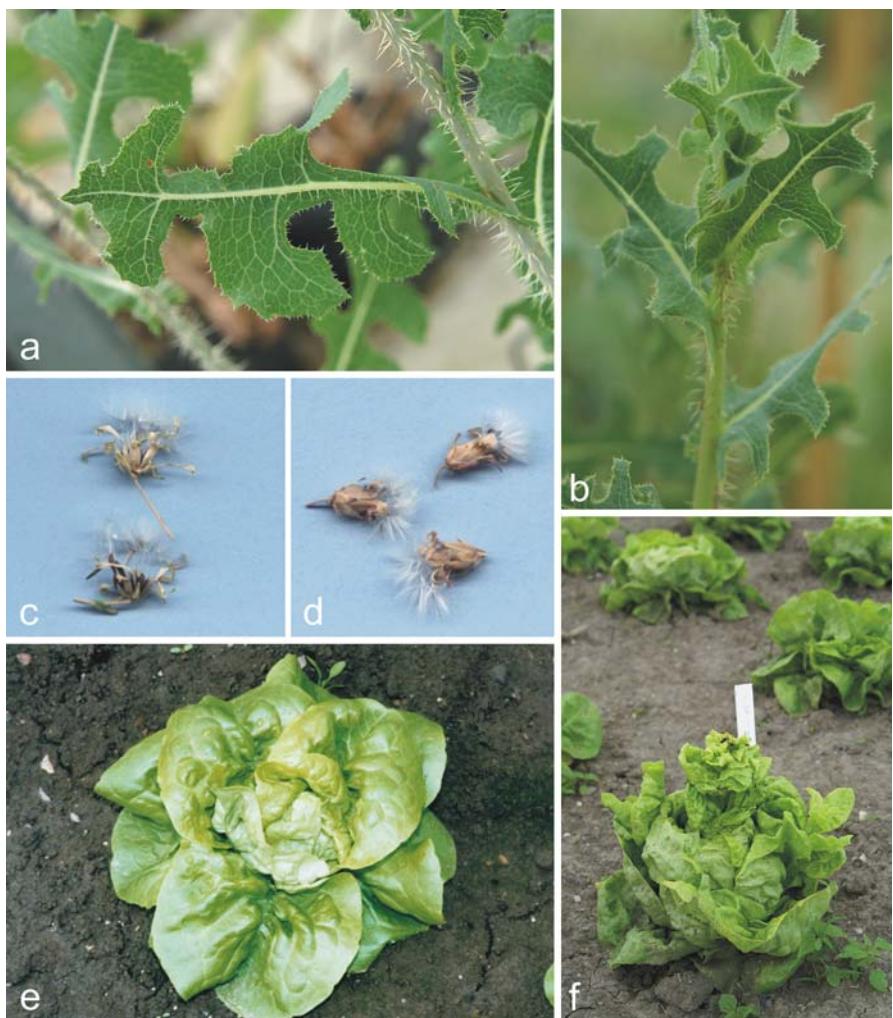
(2007c), and information concerning the exploitation of these wild relatives in commercial lettuce breeding has been summarized by Lebeda et al. (2007c) and Mou (2008). From these reports, it is clear that there are only few important collections in Europe (ca. 5) and the USA (ca. 3). In geographic centres of high species richness and diversity there are no significant germplasm collections with local accessions. Analysis of the International *Lactuca* Database (ILDB) showed that over 90% of wild collections are represented by only three species, *L. serriola*, *L. saligna*, and *L. virosa*, mostly of European origin. The autochthonous species from other continents (Asia, Africa, and the Americas), which form ca. 83% of known *Lactuca* species richness (Lebeda et al. 2004b), are represented in collections by only about

3% of the accessions (Lebeda et al. 2004a). Recently, Pandey et al. (2008) collected 373 species of wild crop relatives representing 120 genera and 48 families in the Indian gene centre; however, they made no mention of lettuce nor of its wild relatives. This example illustrates the underrepresentation of wild *Lactuca* species in recent collecting activities, which is a crucial feature needing attention for the future development of these collections (Lebeda et al. 2007c; Beharav et al. 2008b).

Taxonomic status of accessions and duplicates

The correct use of botanical nomenclature and, more importantly, the accurate taxonomic identification of genebank accessions are core tasks for the effective

Fig. 3 Domestication of lettuce involved selection against latex content (**a**), leaf and stem spines (**a, b**), increase in seed size and non-shattering seeds (**c, d**), shortening of internodes, bunching of leaves (**e**), and selection for late bolting (**f**); **a,b,c** *L. serriola*; **d,e,f** *L. sativa*



management and utilization of plant genetic resources. Insufficient or incorrect passport data, including taxonomic identification, complicate the evaluation of accessions (van Hintum and Boukema 1999; Lebeda et al. 2007c; Rajcic and Dehmer 2008), and make it more difficult to preserve genetic integrity, reduce collection redundancy, and interpret research findings.

Basic errors in the taxonomic status of accessions as reported by genebanks have been found repeatedly. When evaluating a set of 49 accessions of 24 wild *Lactuca* species for morphological characters, chromosome number, relative DNA content and isozyme polymorphisms, 17 accessions were reclassified and/or their taxonomic status criticized (Doležalová et al. 2004). Within a set of 95 accessions provided by gene banks in the Czech Republic,

Germany, Netherlands, UK and the USA, nominally representing 12 species (*L. aculeata*, *L. altaica*, *L. dentata*, *L. dregeana*, *L. indica*, *L. livida*, *L. perennis*, *L. quercina*, *L. saligna*, *L. serriola*, *L. tatarica* and *L. virosa*), a morphological assessment confirmed the taxonomic identities of only 50 accessions; 31 accessions were re-determined (Lebeda et al. 2007d). Examples are given in Fig. 5. The remaining 14 accessions represented mixtures of *L. serriola* forms, mixtures of different *Lactuca* species, and interspecific hybrids (Doležalová et al. 2007a) (Fig. 6).

An understanding of accession redundancy/duplication within and among genebanks is another important aspect of efficient plant genetic resource management (Spooner et al. 2005). Comparison of passport data from four large *Lactuca* collections

Fig. 4 Wild *Lactuca* species involved in lettuce improvement: **a** cultivated *L. sativa*; wild species, **b** *L. serriola* f. *serriola*, **c** *L. serriola* f. *integrifolia*, **d** *L. saligna*, **e** *L. aculeata*, **f** *L. virosa*



(CGN, WRPIS, IPK and HRI) showed that 60% of 95 accessions are duplicated at least once among these collections (van Hintum and Boukema 1999). A morphological assessment of the abovementioned set of 95 *Lactuca* species accessions identified 34 duplicate groups on the basis of passport data, and showed that 69 accessions can be considered as morphological duplicates (Doležalová et al. 2007a; Lebeda et al. 2007d).

Field studies and collection activities

An increasing interest in determining the geographic distribution of wild *Lactuca* populations and sampling those populations in natural habitats resulted in the initiation of collection expeditions coordinated by the Department of Botany, Palacký University in Olomouc (Czech Republic) beginning in the early

1990s. From 1995 to 2008, expeditions were conducted in 14 European countries (Austria, Croatia, the Czech Republic, France, Hungary, Germany, Greece, Italy, Lithuania, The Netherlands, Slovakia, Slovenia, Spain, Sweden, Switzerland, the United Kingdom), 15 states of the USA (Arizona, California, Colorado, Idaho, Iowa, Nevada, North Carolina, Minnesota, Montana, Oregon, South Dakota, Utah, Washington, Wisconsin, Wyoming), and Canada. Field studies and germplasm collections were also made in Turkey, Israel, Jordan, Kazakhstan, South Korea, New Zealand and South Africa (Fig. 7). Collectively, these efforts have resulted in the collection of nearly 1,300 seed samples of 12 wild *Lactuca* species (Kríštková and Lebeda 1999; Doležalová et al. 2001; Kríštková et al. 2001; Lebeda et al. 2001b, c, 2007e; Beharav et al. 2008b; Doležalová et al. 2008).

Expeditions to collect *L. serriola* germplasm in four European countries were conducted within the



Fig. 5 Redetermination of accessions received from main world gene banks (RICP, IPK, GNG, HRI, WG, LET), on the genus level **a** *L. dentata* (acc. PI 234204 LET) re-determined as *Sonchus oleraceus*; and on species level, **b** *L. livida* (acc. RICP09H5801127) re-determined as *L. dregeana*

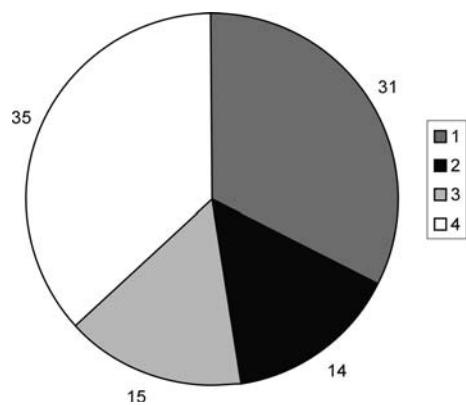


Fig. 6 Taxonomic status of a set of 95 *Lactuca* species accessions representing 12 species received from main world gene banks (RICP, IPK, GNG, HRI, WG, LET). 1) plants of 31 morphologically uniform accessions, their taxonomic status re-determined; 2) 14 accessions represented by mixtures of *L. serriola* forms, different *Lactuca* species or interspecific hybrids; 3) taxonomic status of 15 accessions of *L. serriola* completed by determination of a lower taxonomic unit (f. *serriola*, f. *integrifolia*); 4) plants of 35 morphologically uniform accessions, their declared taxonomic status confirmed

framework of the EU-funded project “GENE-MINE” in 2001 (Lebeda et al. 2007a). The seed material (800 accessions from 50 locations) was used for regeneration, inclusion in national genebanks in the respective countries, and research purposes in follow-up studies (e.g., Lebeda and Petrželová 2004a; Lebeda et al. 2008a).

In cooperation with the Institute of Evolution (University of Haifa, Israel), expeditions focusing on the wild species, *L. saligna*, were conducted in 2004–2007 in Israel (Beharav et al. 2008a, b), following international standards for germplasm acquisition (Guarino et al. 1995) designed in a manner to avoid the collection of duplicates (van Hintum and Boukema 1999; Lebeda et al. 2004a).

Descriptor development

Precise descriptions of genetic resources serve as tool for their correct taxonomic determination and help define both interspecific and intraspecific variation (Lebeda et al. 2007b). A basic international descriptor list has been described for the genetic resources of *L. sativa* and of *L. serriola* and related species from the primary gene pool by a representatives of European genebanks within the activities of the European Cooperative Programme (ECP/GR), Working Group of Leafy Vegetables (Lebeda and Boukema 2005; Maggioni et al. 2008). In addition, an international list of the most important morphological characters of wild *Lactuca* species was created through the EU-funded project “GENE-MINE” (Doležalová et al. 2003a).

There have also been national descriptor lists published for the characterization of major *Lactuca* collections, including those from the Centre for Genetic Resources (CGN, Wageningen, The Netherlands) (Boukema et al. 1990), the Western Regional Plant Introduction Station (Pullman, Washington, USA) (McGuire et al. 1993), and the National Programme of Conservation and Utilization of Plant Genetic Resources of the Czech Republic for both cultivated lettuce (*Lactuca sativa* L.) (Kříšťková et al. 2008) and wild species (Doležalová et al. 2002a).

As descriptor lists for cultivated lettuce are developed or revised, serious consideration should be given to the inclusion of phenotypic traits of the wild *Lactuca* species being used to breed new lettuce



Fig. 7 Field studies and collecting activities coordinated by the Department of Botany, PU Olomouc, Czech Republic

cultivars. Because of these breeding efforts, during last decade new lettuce cultivars have been released with characteristics that do not conform to earlier groups of morphotypes.

Characterization and evaluation of wild *Lactuca* germplasm

Morphology

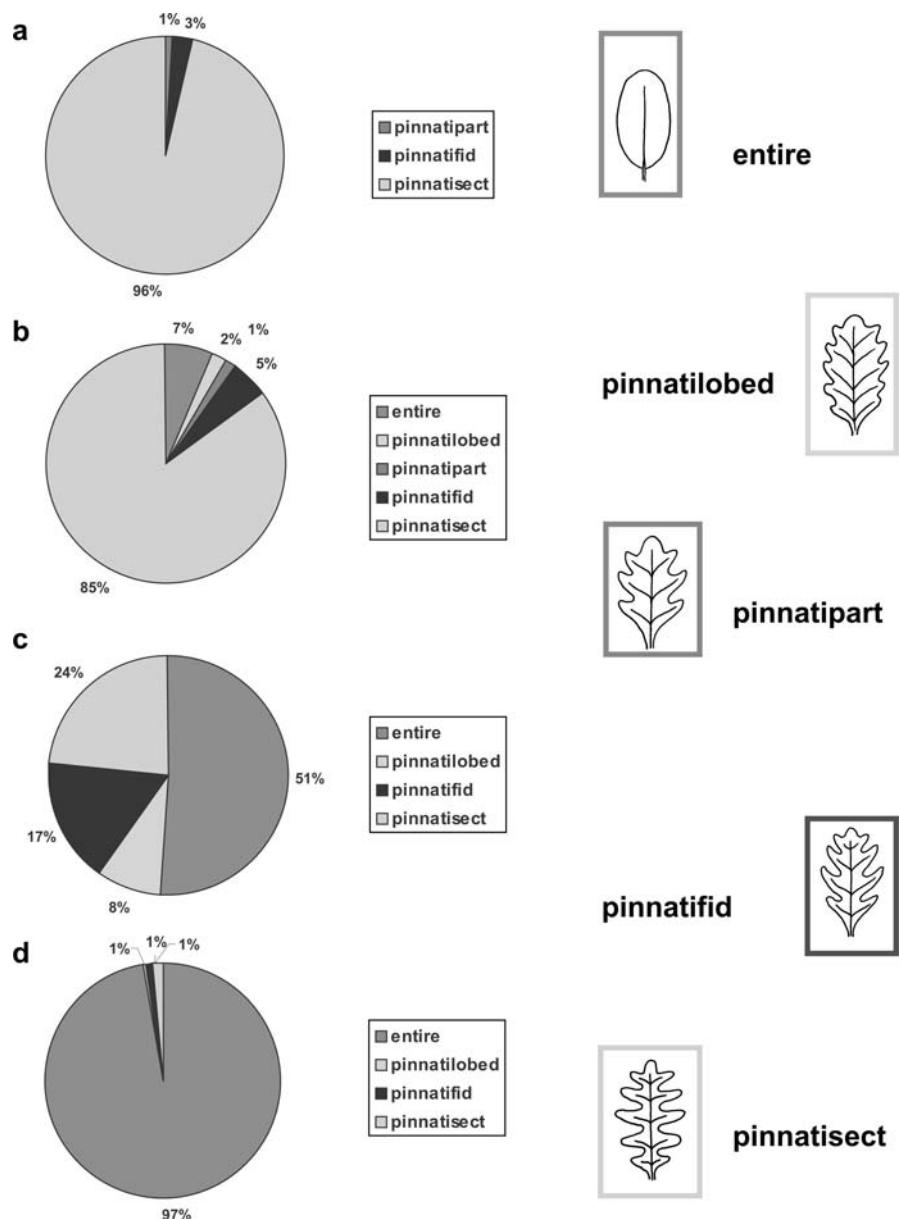
Morphological assessment of accessions can be performed during their regeneration by genebanks (Doležalová et al. 2002a, 2003a; Kříšková et al. 2008), but this can have serious limitations, as the expression of morphological traits under controlled, regeneration conditions may differ significantly from expression under typical field conditions. Detailed studies of morphological variation have been performed for collections of *L. serriola* and *L. saligna*. Fifty *L. serriola* populations collected in four European countries (Czech Republic, Germany, The Netherlands, United Kingdom) (Lebeda et al. 2007a) were cultivated in a greenhouse under controlled conditions. Assessment included 26 quantitative and

qualitative characters of stems (e.g., stem length), rosette and cauline leaves (e.g., depth of incisions) (Fig. 8), inflorescences and flowers (e.g., anthocyanin coloration on bracts) (summarized in Lebeda et al. 2007b), and fruits (e.g., length and width of achene body, length of achene beak and number of ribs) (Doležalová et al. 2007b) (Fig. 9). A similar morphological assessment was performed for about 70 populations of *L. saligna* from Czech Republic, France, Italy, Portugal, Israel, Jordan and Turkey (Kříšková et al. 2007a; Beharav et al. 2008a, b). These studies revealed considerable (and previously unremarked) phenotypic variation, which must be seriously considered in future research and characterization activities with wild *Lactuca* germplasm, especially in relation to genotyping.

Phenology

The genus *Lactuca* is extremely variable in terms of phenology and plant development. Among developmental characteristics, substantial differences in time of anthesis were recorded among a geographically diverse set of accessions of *L. serriola* (Doležalová et al. 2005; Lebeda et al. 2007b, c). Substantial

Fig. 8 Example of variability in a qualitative character. Descriptor number 1.3.7.—Divided caulin leaf—depth of incisions, fully developed leaf from the middle part of stem at a stage of full flowering of *Lactuca serriola* accessions from **a** Czech Republic, **b** Germany, **c** The Netherlands, **d** United Kingdom



differences in developmental stages (beginning of bolting and flowering) were recorded among 89 *L. serriola* samples from different ecogeographic regions in Europe when grown under common conditions in a greenhouse. Developmental stages of plants, as influenced through selective processes under the original eco-geographic conditions where they evolved (Lebeda et al. 2001b, c), can persist when plants are cultivated under common environmental conditions and may be fixed genetically (Kříštková et al. 2007b).

Karyology and DNA content

Wild *Lactuca* species can be divided into three main groups, according to their base chromosome number (Feráková 1977). The first group is relatively small and contains perennial species of Europe and the Himalayas with haploid chromosome number, $n = 8$. The haploid chromosome number, $n = 9$, characterizes the majority of European and Mediterranean species, as well as species from the Middle East, Africa and India. The third group, containing of

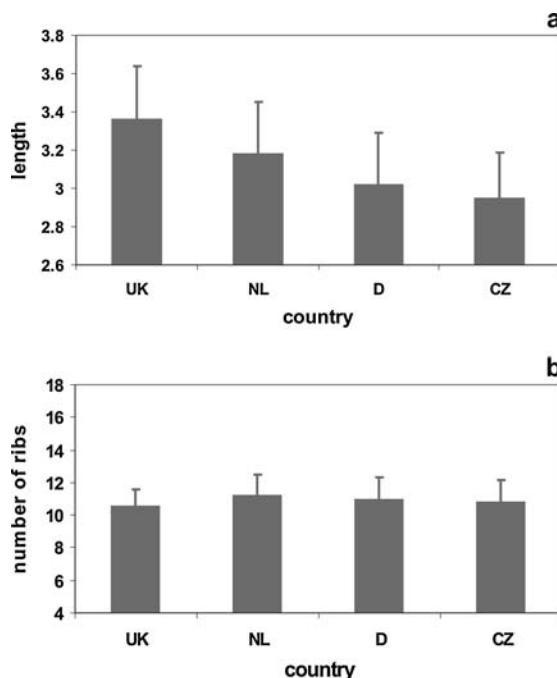


Fig. 9 Example of variability in two quantitative characters. Means of achene length (a) and number of ribs (b) of *Lactuca serriola* collected in four European countries (CZ Czech Republic, D Germany, NL The Netherlands, UK United Kingdom)

North American species distributed from Canada to Florida, is marked by a haploid chromosome number of $n = 17$. It is of amphidiploid origin and is somewhat geographically and genetically isolated. Our understanding of genus remains incomplete, because the chromosome numbers of numerous *Lactuca* species are not known (Lebeda and Astley 1999) or may differ from reported data, as was reported by Doležalová et al. (2002b) for certain North American species.

To date, analyses of variation in nuclear DNA content have been performed on only a limited number of *Lactuca* species (i.e., *L. sativa*, *L. serriola*, *L. saligna*, and *L. virosa*) (Bennett and Leitch 1995; Koopman and De Jong 1996; Koopman 1999, 2000). Flow cytometry was tested for its reliability as a tool to distinguish among *Lactuca* species (Koopman 1999, 2000). Doležalová et al. (2002b) analyzed 50 accessions of 25 *Lactuca* species, along with *Mycelis muralis*, for chromosome number and relative DNA-content variation. Later, Koopman (2002) showed that five *Lactuca* species (*L. viminea*, *L. virosa*, *L. serriola*, *L. sativa* and *L. sibirica*) have significant

intraspecific variation in DNA content, but concluded that only the variation within *L. virosa* seemed to have evolutionary significance. More recent studies have focused on intraspecific differences in DNA content in *L. serriola* germplasm originating from 12 European countries (Lebeda et al. 2004c, 2007c).

Karyotype analysis and relative DNA content were used to help characterize *L. sativa*, *L. serriola*, *L. saligna* and *L. virosa* and describe their evolutionary relationships (Koopman and De Jong 1996). Matoba et al. (2007) described detailed karyotype analyses of lettuce and allied species. These analyses revealed a dissimilarity between *L. virosa* and the remaining species. The simultaneous FISH (Fluorescence in situ hybridization) of 5S and 18S rDNAs revealed that both rDNA loci of *L. sativa*, *L. serriola* and *L. saligna* were identical; however, those of *L. virosa* differed from the other species, supporting a closer relationship between *L. sativa/L. serriola* and *L. saligna* than with *L. virosa*.

Protein and molecular diversity

The status of characterization of *Lactuca* species germplasm by protein and molecular markers has been recently summarized by Dziechciarková et al. (2004a) and Lebeda et al. (2007c). Various methods and approaches have been applied for this purpose; however, only a relatively limited number of wild *Lactuca* species and accessions have been analysed (Table 2) (e.g., Jansen et al. 2006). More extensive studies covering a broader geographic range and a larger number of populations are needed to describe relationships between ecogeographical conditions and corresponding genetic polymorphisms. Studies of this sort for *L. saligna* and *L. serriola* are now underway (Dziechciarková et al. 2004b; Kitner et al. 2008; Kuang et al. 2006, 2008; Lebeda et al. 2008c).

Biochemical diversity

The body of research on the evaluation of *Lactuca* germplasm also includes work on the detection and characterization of secondary phytochemicals, such as sesquiterpene lactones, phenolics, glucosides, and flavonoids, of pharmacological importance (Rees and Harborne 1984; Kisiel and Barszcz 1998; Kisiel and Zielińska 2000) (Fig. 10). This aspect has probably been underestimated, but we see increasing potential

Table 2 Survey of wild *Lactuca* species characterized by isozyme analysis and molecular markers

| Taxon | Method | References |
|--|-----------------|---|
| <i>L. serriola</i> | Isozymes | Kesseli and Michelmore (1986), Cole et al. (1991), Lebeda et al. (1999, 2001a), Doležalová et al. (2003b), Mizutani and Tanaka (2003) and Dziechciarková et al. (2004b) |
| | RFLP | Kesseli et al. (1991) and Vermeulen et al. (1994) |
| | AFLP | Hill et al. (1996), Koopman et al. (2001) and Kuang et al. (2008) |
| | TRAP | Hu et al. (2005) |
| | Microsatellites | Witsenboer et al. (1997) and van de Wiel et al. (1998, 1999) |
| | ITS-1 DNA | Koopman et al. (1998) |
| | seq. | |
| | SSAP | van de Wiel et al. (2004) |
| | NBS-profiling | van de Wiel et al. (2004) and Sicard et al. (1999) |
| | | |
| <i>L. saligna</i> | Isozymes | Kesseli and Michelmore (1986), Cole et al. (1991), Lebeda et al. (1999, 2001a), Doležalová et al. (2003b) and Mizutani and Tanaka (2003) |
| | RFLP | Kesseli et al. (1991) and Vermeulen et al. (1994) |
| | AFLP | Hill et al. (1996), Jeukens et al. (2001) and Koopman et al. (2001) |
| | TRAP | Hu et al. (2005) |
| | Microsatellites | Witsenboer et al. (1997) and van de Wiel et al. (1998, 1999) |
| | ITS-1 DNA | Koopman et al. (1998) |
| | seq. | |
| | NBS-profiling | Sicard et al. (1999) |
| | | |
| | | |
| <i>L. virosa</i> | Isozymes | Kesseli and Michelmore (1986), Cole et al. (1991), Lebeda et al. (1999, 2001a), Doležalová et al. (2003b) and Mizutani and Tanaka (2003) |
| | RFLP | Kesseli et al. (1991) and Vermeulen et al. (1994) |
| | AFLP | Hill et al. (1996) and Koopman et al. (2001) |
| | Microsatellites | Witsenboer et al. (1997) and van de Wiel et al. (1998, 1999) |
| | ITS-1 DNA | Koopman et al. (1998) |
| | seq. | |
| | NBS-profiling | Sicard et al. (1999) |
| | | |
| | | |
| | | |
| <i>L. indica</i> | Isozymes | Lebeda et al. (1999, 2001a), Doležalová et al. (2003b) and Mizutani and Tanaka (2003) |
| | RFLP | Kesseli et al. (1991) |
| | AFLP | Hill et al. (1996) and Koopman et al. (2001) |
| | Microsatellites | Witsenboer et al. (1997) |
| | ITS-1 DNA | Koopman et al. (1998) |
| | seq. | |
| | NBS-profiling | Sicard et al. (1999) |
| | | |
| | | |
| | | |
| <i>L. perennis</i> | Isozymes | Lebeda et al. (1999, 2001a) and Doležalová et al. (2003b) |
| | RFLP | Kesseli et al. (1991) and Vermeulen et al. (1994) |
| | AFLP | Hill et al. (1996) and Koopman et al. (2001) |
| | Microsatellites | Witsenboer et al. (1997) |
| | ITS-1 DNA | Koopman et al. (1998) |
| | seq. | |
| | NBS-profiling | Sicard et al. (1999) |
| | | |
| | | |
| | | |
| <i>L. canadensis</i> and <i>L. taraxacifolia</i> | Isozymes | Lebeda et al. (1999, 2001a) and Doležalová et al. (2003b) |
| | AFLP | Koopman et al. (2001) |
| | ITS-1 DNA | Koopman et al. (1998) |
| <i>L. quercina</i> and <i>L. sibirica</i> | seq. | |
| | | |
| | | |

Table 2 continued

| Taxon | Method | References |
|--|----------------|---|
| <i>L. aculeata</i> , <i>L. altaica</i> , <i>L. dregeana</i> , <i>L. tatarica</i> , <i>L. tenerrima</i> and <i>L. viminea</i> | Isozymes | Lebeda et al. (1999, 2001a) and Doležalová et al. (2003b) |
| | AFLP | Koopman et al. (2001) |
| | ITS-1 DNA seq. | Koopman et al. (1998) |

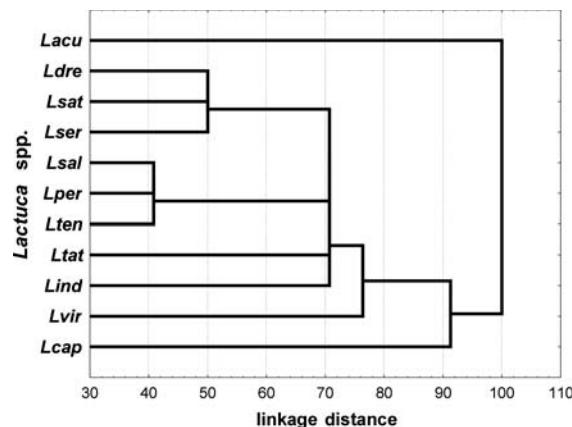


Fig. 10 A dendrogram showing clustering (Tree clustering method) of *Lactuca* species in relationship to the content of different sesquiterpene lactones in leaves [elaborated by authors on the basis of data in Michalska et al. (2008)]

for the exploitation of at least some wild *Lactuca* germplasm in medicinal and pharmacological applications (Chen et al. 2007; Kim et al. 2007). Recently, phytochemical analyses have also been applied to the clarification of taxonomical relationships among various Asteraceae (Bohm and Stuessy 2001) including *Lactuca* species (Michalska et al. 2008).

Resistance to diseases and pests

Recent advancement in research and breeding of lettuce for resistance to diseases and pests has been summarized elsewhere (Lebeda et al. 2007c; Mou 2008). Many sources of resistance to pathogens and pests have been found and described in wild *Lactuca* species (Table 3). Traditionally, *Bremia lactucae* has been considered the most important pathogen causing disease in cultivated lettuce. Limited availability of durable sources of resistance to *Bremia* has stimulated interest among breeders in new sources from wild *Lactuca* species (Lebeda et al. 2002, 2007c).

Numerous reports (Lebeda and Zinkernagel 2003b; Beharav et al. 2006; Petrželová et al. 2007; Lebeda et al. 2008a) have demonstrated that wild *Lactuca* germplasm, especially of *L. saligna* and *L. serriola*, has enormous potential. More intensive exploitation of these new sources of resistance is primarily based on the increasing number of wild, characterized *Lactuca* accessions from various ecogeographical areas (Lebeda et al. 2004a, b, 2007c, 2008a, b, c). *Lactuca saligna* is currently considered to be the most important source of highly efficient resistance, which is expected to be nonhost specific (Lebeda et al. 2002; Lebeda and Zinkernagel 2003b; Petrželová et al. 2007). However, our understanding of both the mechanism (Lebeda and Reinink 1994; Lebeda and Pink 1998; Lebeda et al. 2001b, c, 2002, 2006, 2008b; Sedlářová et al. 2007a) and genetics (Jeuken and Lindhout 2002, 2004; Jeuken et al. 2001, 2008; Zhang 2008) of this resistance is still incomplete.

Conclusions and future prospects

Despite enormous progress in research on wild *Lactuca* germplasm, this review has demonstrated many important gaps in our understanding. The following list of topics can be considered as key challenges for future research and exploitation in lettuce breeding:

1. Complex taxonomic and phylogenetic relationships within the genus;
2. Detailed floristic, biogeographic and ecologic delimitation of the distributions of known *Lactuca* spp.;
3. Clarification of the structure of *Lactuca* gene pools;
4. Reconsideration of germplasm collection structure from the viewpoint of diversity, quality, and quantity;

Table 3 Survey of wild *Lactuca* species described as a sources of resistance to the most important pathogens and pests of lettuce

| Taxon | Pathogens and pests | References |
|--------------------|---|---|
| <i>L. serriola</i> | <i>Lettuce Mosaic Virus</i> (LMV) | Maisonneuve et al. (1999) |
| | <i>Corky Root</i> | Mou and Bull (2004) |
| | <i>Bremia lactucae</i> | Welch et al. (1965), Norwood et al. (1981), Lebeda (1986, 1989, 1990, 2002), Gustafsson (1989), Lebeda and Jendrůlek (1989), Crute (1990, 1992a, b, c), Lebeda and Boukema (1991), Reuveni et al. (1991), Bonnier et al. (1992), Lebeda and Pink (1998), Doležalová et al. (2001), Lebeda and Petrželová (2001, 2004a, b, 2005, 2007), Lebeda et al. (2001a, b, c, 2002, 2004b, 2007a, b, c, 2008a, b), Jeuken and Lindhout (2002), Michelmore (2002), Lebeda and Zinkernagel (2003b), Maisonneuve (2003), Petrželová and Lebeda (2003, 2004a, b, c), Michelmore and Ochoa (2005), Beharav et al. (2006), Hooftman et al. (2007), Kuang et al. (2006), Mieslerová et al. (2007) and Sedlářová et al. (2007a, b) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, b, 1994, 1999) and Lebeda and Buczkowski (1986) |
| | (Lettuce Powdery Mildew) | Lebeda and Mieslerová (2003) |
| | <i>Verticillium Wilt</i> | Grube et al. (2005a, b) |
| | <i>Lettuce Mosaic Virus</i> (LMV) | Maisonneuve et al. (1999) |
| | <i>Other Yellowing Virus Diseases</i> | McCreight (1987) |
| | <i>Tomato Spotted Wilt Virus</i> (TSWV) | Wang et al. (1992) |
| | <i>Cucumber Mosaic Virus</i> (CMV) | Provvidenti et al. (1980) |
| | <i>Bremia lactucae</i> | Netzer et al. (1976), Provvidenti et al. (1980), Lebeda (1986, 1990), Gustafsson (1989), Lebeda and Pink (1998), Bonnier et al. (1992), Lebeda and Reinink (1994), Lebeda et al. (2001b, c, 2002, 2006, 2007c), Sedlářová and Lebeda (2001), Sedlářová et al. (2001, 2007a, b), Jeuken and Lindhout (2002), Michelmore (2002), Lebeda and Zinkernagel (2003a, b), Maisonneuve (2003), Michelmore and Ochoa (2005), Beharav et al. (2006), Petrželová et al. (2007), Kitner et al. (2008) and Zhang (2008) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, b, 1994, 1999), Lebeda and Buczkowski (1986) and Lebeda and Mieslerová (2003) |
| <i>L. virosa</i> | <i>Stemphylium Leaf Spot</i> | Netzer et al. (1985) |
| | <i>Lettuce Mosaic Virus</i> (LMV) | Maisonneuve et al. (1999) and Ryder (2002) |
| | <i>Mirafiori Lettuce Big-Vein Virus</i> (MLBVV) | Bos and Huijberts (1990), Hayes et al. (2004, 2008) and Hayes and Ryder (2007) |
| | <i>Beet Western Yellows Virus</i> (BWYV) | Maisonneuve et al. (1991) |
| | <i>Corky Root</i> | Mou and Bull (2004) |
| | <i>Bremia lactucae</i> | Norwood et al. (1981), Bonnier et al. (1992), Lebeda and Reinink (1994), Lebeda and Pink (1998), Maisonneuve et al. (1999), Sedlářová et al. (2001, 2007a), Lebeda et al. (2002, 2006, 2007c), Michelmore (2002), Lebeda and Zinkernagel (2003b), Maisonneuve (2003), Michelmore and Ochoa (2005) and Beharav et al. (2006) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, b, 1994, 1999) and Michelmore and Ochoa (2005) |
| | <i>Verticillium Wilt</i> | Grube et al. (2005a, b) |
| <i>L. indica</i> | <i>Bremia lactucae</i> | Lebeda (1990) and Lebeda and Petrželová (2001) |

Table 3 continued

| Taxon | Pathogens and pests | References |
|---|--|--|
| <i>L. perennis</i> | <i>Lettuce Mosaic Virus</i> (LMV) | Maisonneuve et al. (1995) |
| | <i>Beet Western Yellows Virus</i> (BWYV) | Walkey and Pink (1990) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, b, 1994, 1999) and Lebeda and Buczkowski (1986) |
| <i>L. quercina</i> | <i>Bremia lactucae</i> | Lebeda and Petrželová (2001) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, 1999) |
| <i>L. sibirica</i> | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, 1999) |
| <i>L. aculeata</i> | <i>Bremia lactucae</i> | Lebeda (1990) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985b, 1994) and Lebeda and Buczkowski (1986) |
| <i>L. biennis</i> | <i>Bremia lactucae</i> | Lebeda and Petrželová (2001) |
| <i>L. tatarica</i> | <i>Bremia lactucae</i> | Lebeda and Petrželová (2001) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985b, 1994) and Lebeda and Buczkowski (1986) |
| <i>L. tenerrima</i> | <i>Golovinomyces cichoracearum</i> | Lebeda (1985b, 1994) |
| <i>L. viminea</i> | <i>Bremia lactucae</i> | Lebeda and Petrželová (2001) |
| | <i>Golovinomyces cichoracearum</i> | Lebeda (1985a, b, 1994, 1999) |
| <i>L. viminea</i> subsp. <i>chondrilliflora</i> | <i>Golovinomyces cichoracearum</i> | Lebeda et al. (2002) |

5. Collecting and exploration missions, especially to areas of high species richness and diversity (e.g., South Africa and Asia);
6. Enlargement of activities focused on complex characterization and evaluation with importance for the management of wild *Lactuca* genebank collections and their efficient utilization in lettuce breeding;
7. Broad international cooperation among diverse institutions, including Bioversity International.

Acknowledgments Critical reading and valuable remarks by Dr. M. P. Widrlechner (USDA-ARS, Iowa State University, North Central Regional Plant Introduction Station, Ames, Iowa, USA) are gratefully acknowledged. The research was supported by grant MSM 6198959215 (Ministry of Education, Youth and Sports of the Czech Republic).

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