

Resistance of wild *Lactuca* germplasm to diseases and pests, and their exploitation in lettuce breeding



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Genus *Lactuca* (98 species, one species cultivated)

(Lebeda et al. 2007, CRC Press)

Sections/subsections

Lactuca L.

subsect. *Lactuca* L.

L. aculeata, *L. altaica*, *L. dregeana*,
L. livida, *L. saligna*,
L. sativa, *L. serriola*, ***L. virosa***
L. perennis, *L. tenerrima*

subsect. *Cyanicae* DC.

L. viminea
L. tatarica, *L. sibirica*, *L. taraxacifolia*
L. quercina
L. indica
L. undulata
L. sororia

Phaenixopus (Cass.) Bentham

Mulgedium (Cass.) C.B. Clarke

Lactucopsis (Schultz Bip. ex Vis. et Pančić) Rouy

Tuberosae Boiss.

Micranthae Boiss.

Sororiae Franchet

Groups (geographical view)

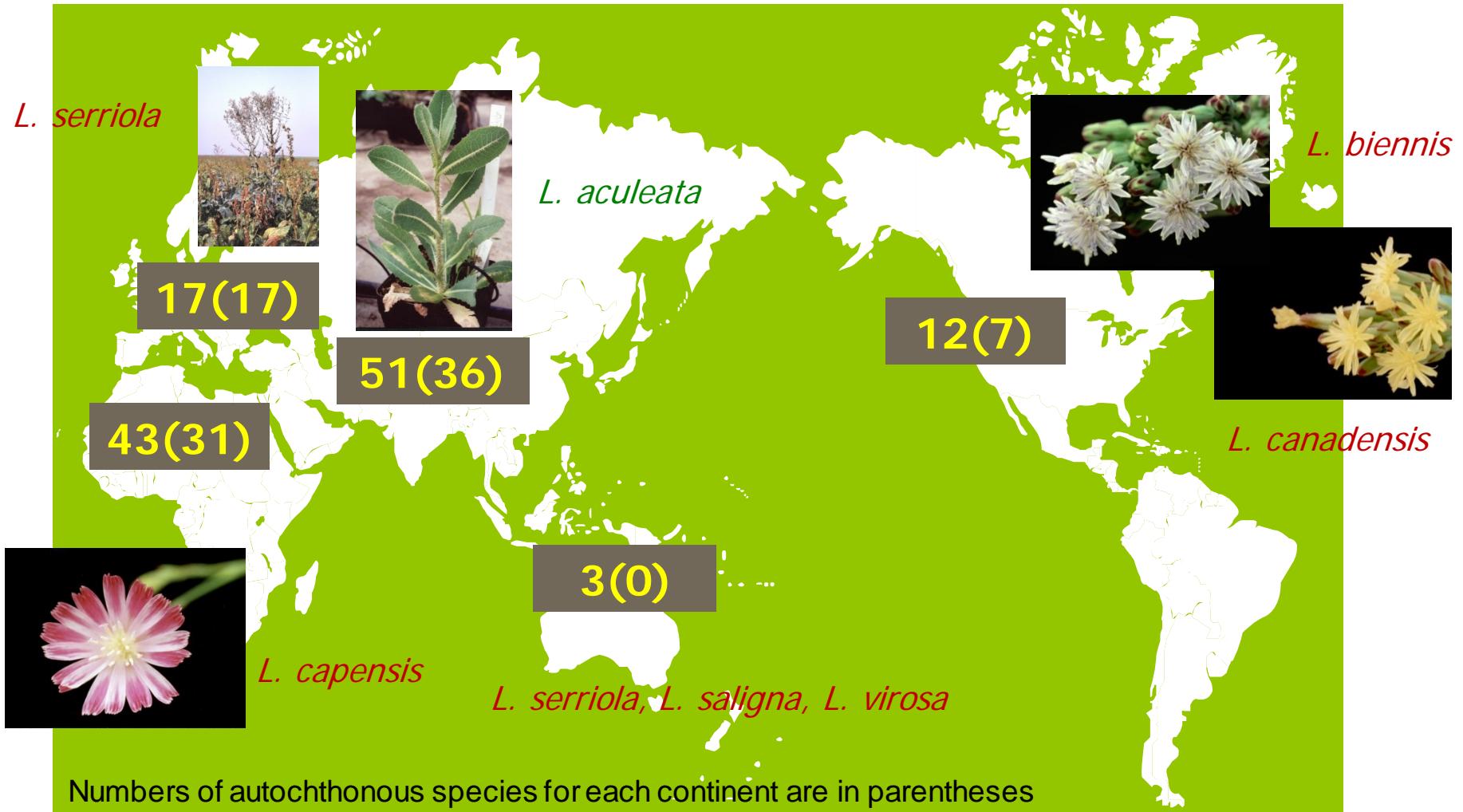
North American

L. biennis, *L. canadensis*, *L. floridana*,
L. graminifolia
L. capensis, *L. dregeana*, *L. homblei*

African

Geographical distribution of wild *Lactuca* spp.

(Lebeda et al. 2004, *The Bot. Rev.*)



Numbers of autochthonous species for each continent are in parentheses

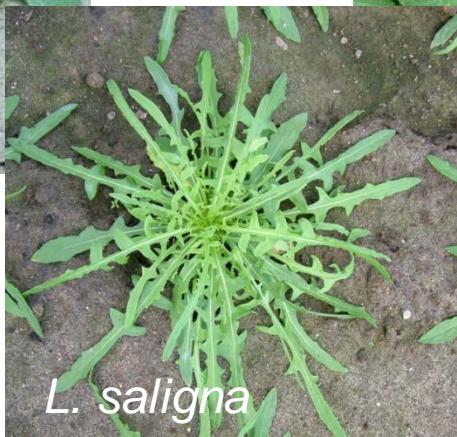
Various ecological requirements, very often on ruderal habitats.

Resistance to diseases and pests

Species of the main breeder's interest - sources of resistance genes against *B. lactucae*, root and leaf aphids, LMV, LBV



L. serriola



L. saligna

L. serriola

USA – utilization from the 30th of 20 century
Europe – from the 50th of 20 century



L. virosa



L. aculeata

L. saligna,
L. virosa

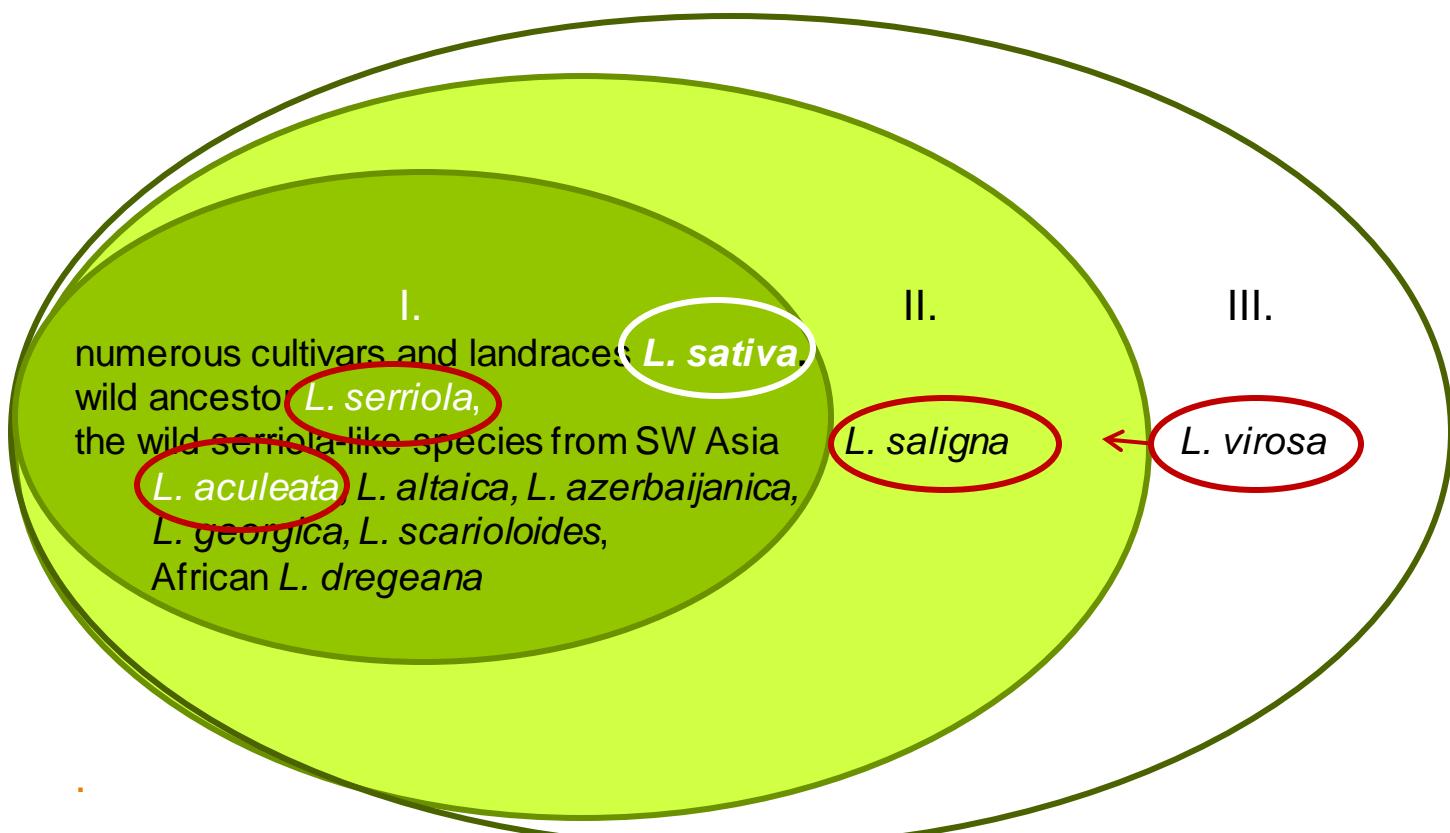
80th of 20 cent.

L. aculeata

end of 20 cent.

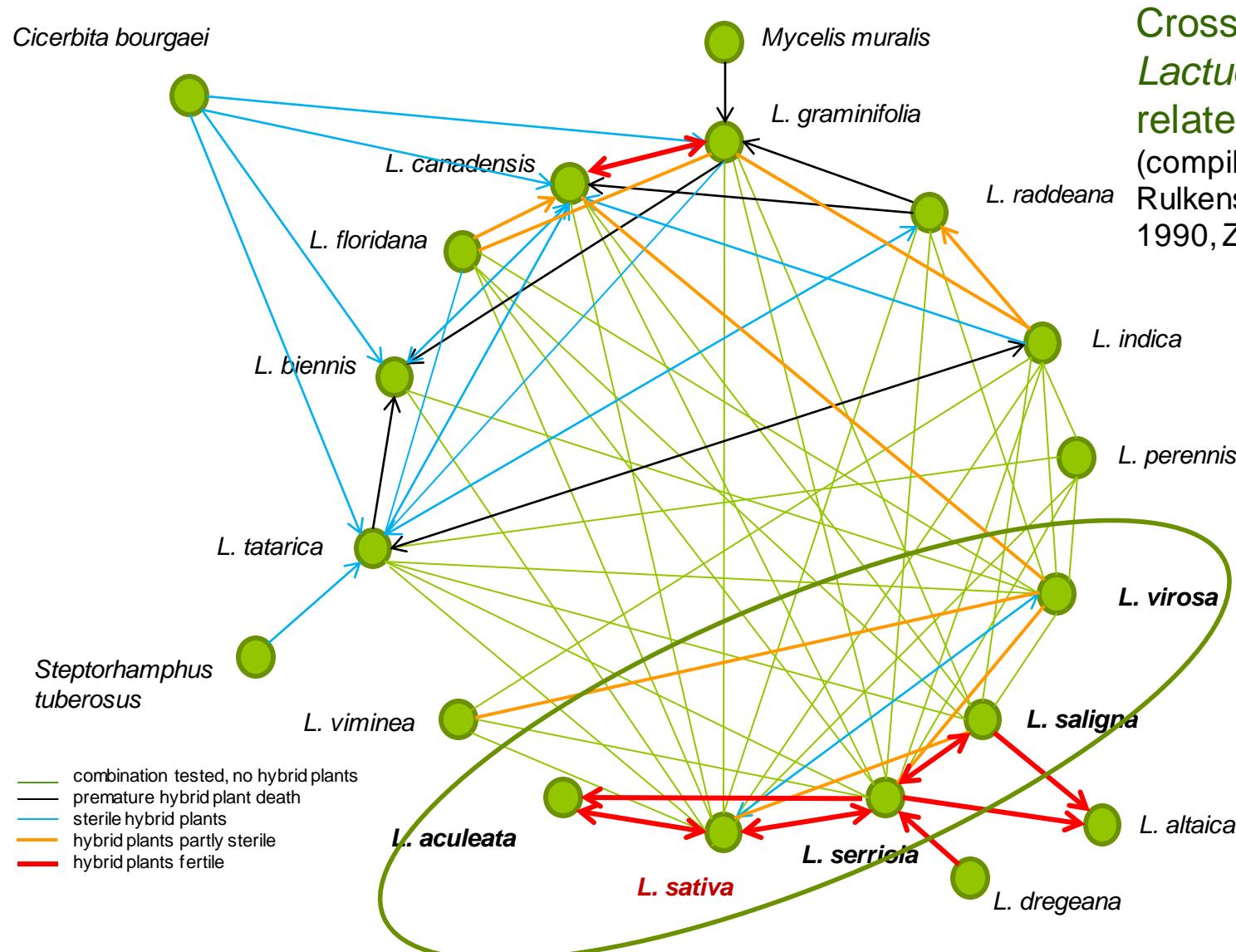
Gene pools of *Lactuca* spp.

Categorization of *Lactuca* spp. into gene pools following to recent concept
(Lebeda et al. 2007, CRC Press)



Categorization of *L. saligna* and *L. virosa* to secondary and tertiary gene pools has remained open to question (compare to Koopman et al. 1998, Amer. J. Bot.)

Interspecific crossing of *L. serriola*, *L. saligna*, *L. virosa* and *L. aculeata* with cultivated lettuce *L. sativa*

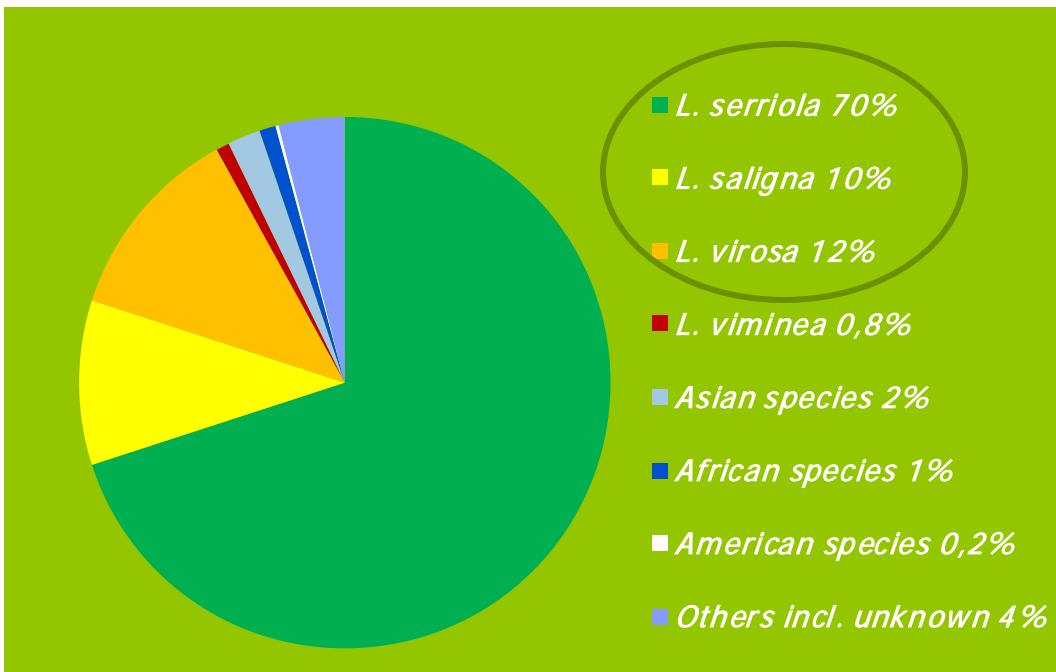


Lactuca saligna is known to produce hybrids with *L. sativa* and *L. serriola* when used as the female parent (Pink and Keane 1993)

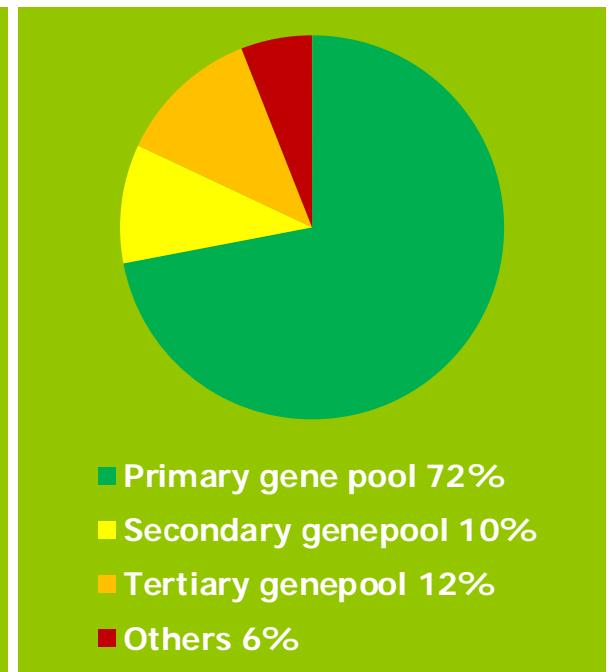
Representation of wild *Lactuca* spp. in genebank collections according to number of accessions

(Lebeda et al. 2004, *Genet Res. Crop Evol.*)

Species



Gene pools



Source of primary data: International Lactuca database (www.plant.wageningen-ur.nl/cgn/ildb)

The genetic variability of the genus *Lactuca* L. maintained in gene bank collections is represented by only about 20 wild species and cultivated *L. sativa* (Doležalová et al. 2004, *Acta Hort.*)

Field studies and collecting missions (since end of 1970th)

Palacký University in Olomouc (CR):

since 1995 collected over 2500 wild *Lactuca* samples



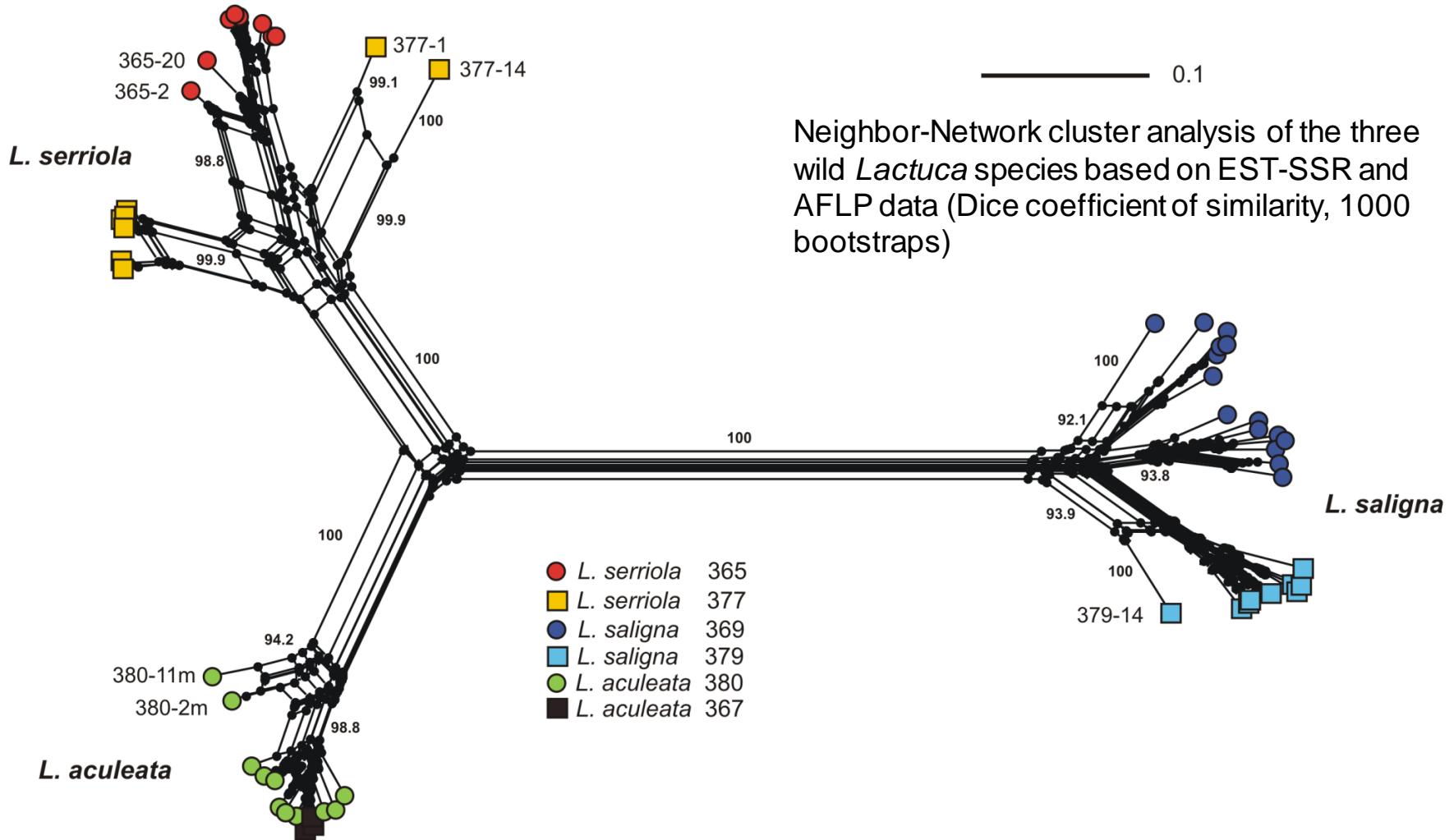
Tréport, France, 2012

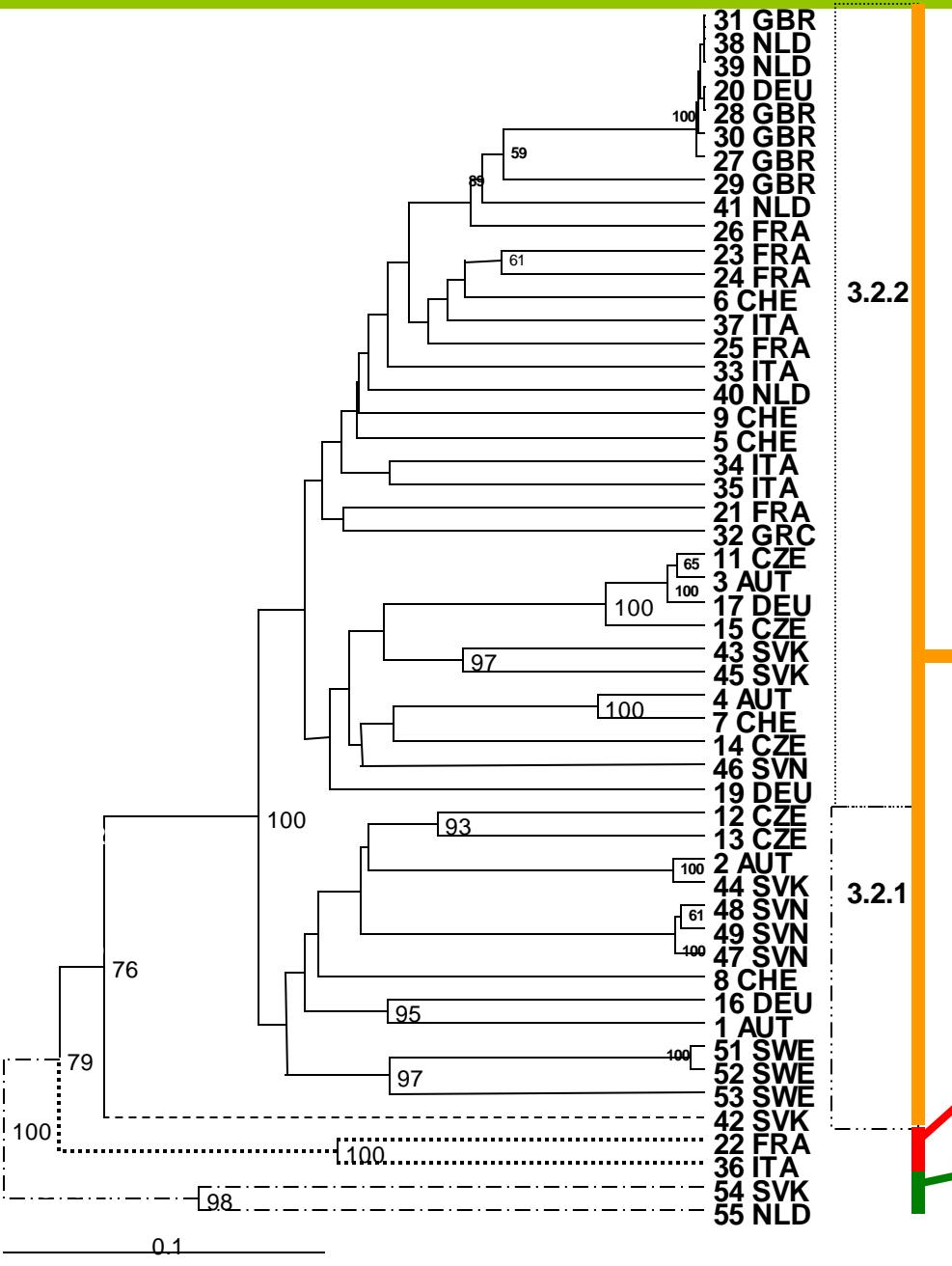
Regeneration, phenotyping, verification of taxonomic status



DNA profiles

Genetic structure and diversity in natural populations of three predominantly self-pollinating wild *Lactuca* species in Israel





AFLP polymorphism

50 accessions of *L. serriola* European populations and

2 accessions of *L. sativa* (no. 54, 55)

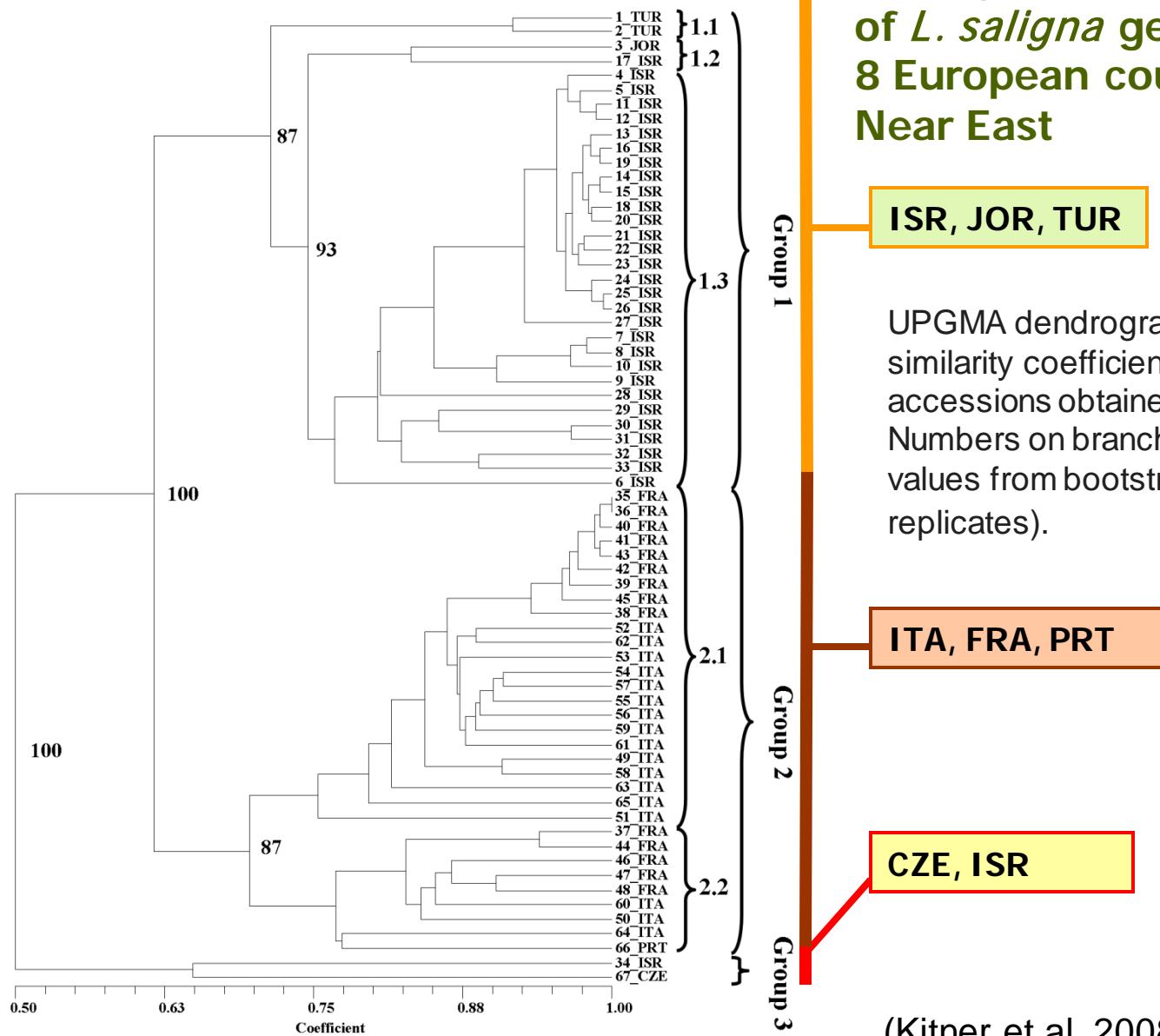
based on six primer combinations

Group 3 = *L. serriola*
 (f. *serriola* + f. *integrifolia*)
 3.2.2 – FRA, ITA, CHE
 3.2.1 – NLD, GBR, DEU

Group 2 = *L. serriola*
 2.1. – *L. serriola* f. *integrifolia*
 2.2. – a mixture of *L. serriola*

Group 1 = *L. sativa*
 (controls)

AFLP genetic polymorphism of *L. saligna* germplasm from 8 European countries and Near East



(Kitner et al. 2008, Israel J. Plant Sci.)

Variation of wild *Lactuca* spp. in reaction to pathogens and pests

Viral pathogens

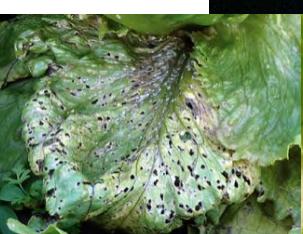
Bacterial pathogens

Fungal pathogens

Nematodes

Insects and Mites

(reviewed by Lebeda et al.,
2014, EJPP, 138:597–640)



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Wild *Lactuca* species, their genetic diversity, resistance to diseases and pests, and exploitation in lettuce breeding

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Abstract Current knowledge of wild *Lactuca* L. species, their taxonomy, biogeography, gene-pools, germplasm collection quality and quantity, and accession availability is reviewed in this paper. Genetic diversity of *Lactuca* spp. is characterized at the level of phenotypic and phenological variation, variation in karyology and DNA content, biochemical traits, and protein and molecular polymorphism. The reported variation in reaction to pathogens and pests of wild *Lactuca* spp. is summarized, including the viral pathogens (Lettuce mosaic virus-*LMV*, Mirafiori lettuce virus/Lettuce big vein virus-*LBV*, Beet western yellows virus-*BWYV*, Tomato spotted wilt virus-*TSWV*, Cucumber mosaic virus-*CMV*, Lettuce necrotic stunt virus-*LNSV*), bacterial pathogens (corky root-*Rhizomonas suberifaciens*, bacterial leaf spot-*Xanthomonas campestris* pv. *vitiensis*), fungal pathogens (downy mildew-*Bremia lactucae*, powdery mildew-*Golovinomyces cichoracearum*, anthracnose-*Microdochium panattoniana*, stemphylium leaf spot-*Stemphylium* spp., sclerotinia drop-*Sclerotinia* spp., verticillium wilt-*Verticillium dahliae*, fusarium wilt-*Fusarium* spp., pythium wilt-*Pythium tracheiphylum*, *P. uncinulatum*), nematodes (potato cyst nematode-

Globodera rostochiensis, root-knot nematode-*Meloidogyne* spp., *incognita*, *hapla*, *javanica*, *enterolobii*), insects and mites (the green lettuce aphid-*Nasonovia ribisnigri*, the green peach aphid-*Myzus persicae*, the potato aphid-*Macrosiphum euphorbiae*, leafminer-*Liriomyza* spp., *L. langei*). The approaches used to exploit wild *Lactuca* spp. in lettuce breeding (interspecific hybridization, cell and tissue culture, transformation) are discussed, and known examples of lettuce cultivars with traits derived from wild *Lactuca* spp. are described.

Keywords Taxonomy · Biodiversity · Gene-pools · Gene banks · Disease resistance · Molecular polymorphism · *L. serriola* · *L. saligna* · *L. virosa* · Pest resistance · Breeding strategies · Transfer of resistance · Wild lettuce · Germplasm

Introduction

The potential of wild *Lactuca* species to be used in lettuce breeding is being demonstrated by means of classical biology and modern approaches and the study of their diversity has been a subject of theoretical research and practical application during the last 25 years (Ryder 1999; Lebeda et al. 2007c; Mou 2008). The currently available knowledge of wild *Lactuca* species as donors (sources) of traits important in lettuce breeding was thoroughly analyzed in our previous paper focused on wild *Lactuca* germplasm (Lebeda et al. 2009a, b). The main aim of this paper is to critically summarize the available information

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Viral pathogens

Lettuce mosaic virus (LMV)

Mirafiori lettuce virus (MLV) (Lettuce big vein virus, LBV)

Beet western yellows virus (BWYV)

Tomato spotted wilt virus (TSWV)

Cucumber mosaic virus (CMV)

Lettuce necrotic stunt virus (LNSV)

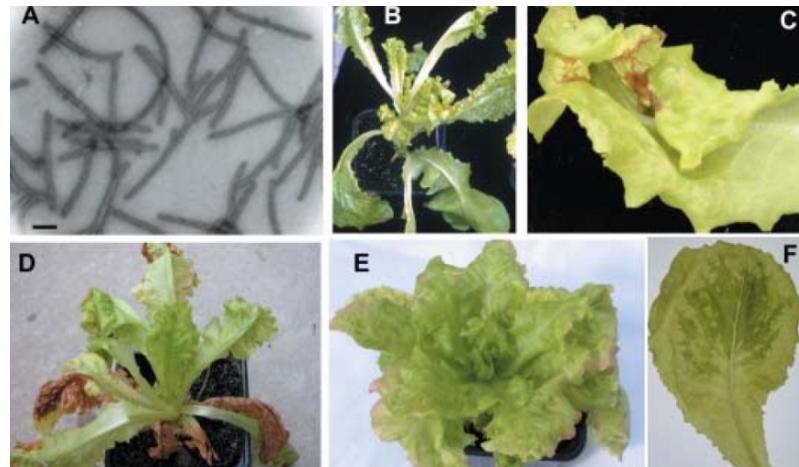
Lettuce necrotic yellow virus (LNYV)

Lettuce chlorotic virus (LCV)

(reviewed by Lebeda et al. 2014, EJPP)



Lettuce mosaic virus (LMV)



- worldwide distribution
- genus Potyvirus, family Potyviridae
- transmission by aphids – *Myzus persicae*, *Macrosiphum euphorbiae*, *Aphis gossipii*
- resistance or tolerance depends on the presence or absence of genes – mo (mo¹, mo²) and Mo2
- **Sources of strain-specific resistance to LMV are confirmed in accessions of *Lactuca virosa* and *Lactuca serriola***

(German-Retana et al. 2008, Mol. Plant. Pathol.)

Lettuce mosaic virus (LMV)

Name of pathogen (strain)	Source of resistance				
	Lactuca spp.	No. of accession/sample	Type of resistance	Remark	References
LMV 0	<i>L. virosa</i>	PIVT 1398 (CGN 9365)	complete resistance	LMV resistance gene Mo3 effective against all known isolates	Maisonneuve et al. (1999) Maisonneuve (2003) Mazier et al. (2003)
		PIVT 280 (CGN 4683)	complete resistance		Maisonneuve. (2003)
LMV-1	<i>L. virosa</i>	PIVT 1398 (CGN 9365)	resistance	LMV resistance gene Mo3 effective against all known isolates	Maisonneuve et al. (1999) Mazier et al. (2003)
		PIVT 1398 (CGN 9365)	complete resistance	in vitro experiment, DAS ELISA test	Mazier et al. (2003) Maisonneuve (2003)
LMV-9	<i>L. virosa</i>	PIVT 280 (CGN 4683)	complete resistance		Maisonneuve (2003)
		PIVT 1398 (CGN 9365)	resistance	LMV resistance gene Mo3 effective against all known isolates	Maisonneuve et al. (1999) Maisonneuve (2003)
LMV-13	<i>L. virosa</i>	PIVT 280 (CGN 4683)	complete resistance		Maisonneuve (2003)
		PIVT 1398 (CGN 9365)	resistance	LMV resistance gene Mo3 effective against all known isolates	Maisonneuve et al. (1999) Maisonneuve (2003)
LMV-E	<i>L. virosa</i>	PIVT 1398 (CGN 9365)	complete resistance	LMV resistance gene Mo3 effective against all known isolates	Maisonneuve et al. (1999) Maisonneuve (2003)
		PIVT 280 (CGN 4683)	complete resistance		Maisonneuve (2003)
LMV_Ls-252	<i>L. perennis</i>	n.s.	resistance		Bos et al. (1994)
	<i>L. tatarica</i>	n.s.	resistance?	plants symptomless, but positive in ELISA	Bos et al. (1994)
LMV (strain not specif.)	<i>L. serriola</i>	PI 251245	resistance	original source of resistance used in breeding program	Ryder (2002)

Mirafiori lettuce virus MLV (Lettuce big vein virus, LBV)

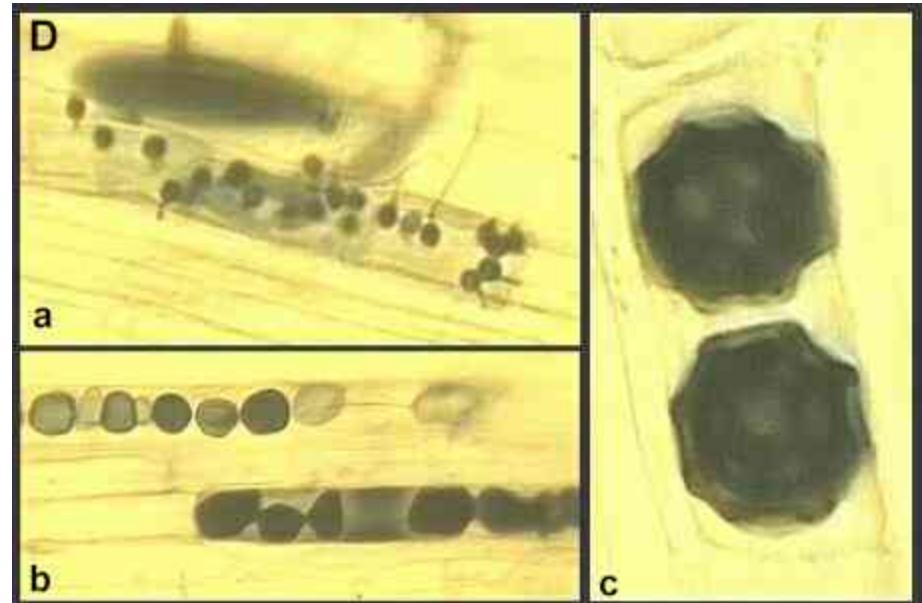
Lettuce big-vein associated virus (LBVV) – genus Varicosavirus

Mirafiori lettuce big-vein virus (MLBVV) – genus Ophiovirus

- transmission by *Olpidium brassicae*

- **only *Lactuca virosa* (IVT 280) was identified as resistant**

(Hayes et al. 2006, *Plant Disease*)



Mirafiori lettuce virus (Lettuce big vein virus, LBV)

Name of pathogen	Source of resistance				
	Lactuca spp.	No. of accession/sample	Type of resistance	Remark	References
LBVV	<i>L. virosa</i>	IVT 280	no symptoms, resistance; high level of resistance		Bos and Huijborts (1990) Ryder et al. (2003)
		IVT 280	asymptomatic	14/14 plants remained asymptomatic by testing RT-PCR	Hayes et al. (2006)
		n.s.	no symptoms, resistance; high level of resistance		Bos and Huijborts (1990) Ryder et al. (2003)
		n.s.	n.s.	greenhouse reaction – 62 asymptomatic <i>L. virosa</i> ; 7 <i>L. virosa</i> with leaf crinkling and 1 <i>L. virosa</i> with typical vein banding symptoms	Hayes et al. (2008)
LBVV (big-vein)	<i>L. virosa</i>	IVT 280, PI 271938, SAL 012	n.s.	asymptomatic	Hayes et al. (2008)
		CGN 16272	n.s.	34 tested plants - 9% symptomatic	Hayes et al. (2008)
		CGN 16273	n.s.	35 tested plants - 17% symptomatic	Hayes et al. (2008)
		CGN 16274	n.s.	32 tested plants - 13% symptomatic	Hayes et al. (2008)
		CGN 16275	n.s.	34 tested plants - 15% symptomatic	Hayes et al. (2008)
		CGN 16276	n.s.	34 tested plants - 6% symptomatic	Hayes et al. (2008)
		CGN 16277	n.s.	35 tested plants - 3% symptomatic	Hayes et al. (2008)
		SAL 177	n.s.	34 tested plants - 3% symptomatic	Hayes et al. (2008)
MLBVV	<i>L. virosa</i>	CGN 16272	n.s.	9 plants tested - 89% symptomatic	Hayes et al. (2008)
		CGN 16273	n.s.	12 plants tested - 92% symptomatic	Hayes et al. (2008)
		CGN 16274	n.s.	10 plants tested - 100% symptomatic	Hayes et al. (2008)
		SAL 177	positive MLBVV	12 plants tested – 33% symptomatic (by the help NASH test – 92% positive)	Hayes et al. (2008)
		SAL 012	n.s.	12 plants tested – 0 % symptomatic (by the help NASH test- 17% positive)	Hayes et al. (2008)
		IVT 280	n.s.	12 plants tested – 17% symptomatic (by the help NASH test- 75% positive)	Hayes et al. (2008)
		IVT 280	asymptomatic	14/14 plants remained asymptomatic – by testing RT-PCR	Hayes et al. (2006)

Bacterial pathogens

Corky root

(caused by *Sphingomonas suberifaciens*, formerly
Rhizomonas suberifaciens)

Corky root (*Sphingomonas suberifaciens*, formerly *Rhizomonas suberifaciens*)

- first resistant lettuce cvs. **Marquette, Montello and Green Lake** developed by Sequiera (1970, 1978), **released from crosses with a resistant line *L. serriola* (PI 171669)**, identified by Dickson (1963) as a local lettuce landrace from Turkey;
- resistance conferred by a recessive allele (*cor*) at a single locus (Brown & Michelmore 1988), present in many modern crisphead lettuce cvs. (Mou et al. 2007), but only few leaf lettuce cvs. with this resistance (Mou 2011a).



A head of healthy lettuce (left) next to one with corky root disease.

Wild *Lactuca* spp. with resistance to corky root

<i>Lactuca</i> spp.	No. of accession/sample	Type of resistance	Remark	References
<i>L. dentata</i>	PI 234204	not known	<i>Sonchus oleraceus</i>	Brown and Michelmore (1988)
<i>L. saligna</i>	PI 261653, PI 490999, PI 491204, PI 491206, UC83UK2, UC83US1	not known		Brown and Michelmore (1988)
<i>L. serriola</i>	PI 2556665, PI 289064-1, PI 289064-2	not known		Brown and Michelmore (1988)
	PI 491096, PI 491110, PI 491239	not known	resistant in grow chamber, greenhouse and field experiments	Mou and Bull (2004)
	PI 491249, PI 491250, PI 491251	not known		Brown and Michelmore (1988)
<i>L. virosa</i>	PI 273597c	not known	resistant in grow chamber, greenhouse and field experiments	Mou and Bull (2004)
	UC83UK1	not known		Brown and Michelmore (1988)
<i>Lactuca</i> spp.	PI 274376	not known		Brown and Michelmore (1988)

Fungal pathogens

Downy mildew (*Bremia lactucae*)

Powdery mildew (*Golovinomyces cichoracearum*)

Anthracnose (*Microdochium panattoniana*)

Sclerotinia drop (*Sclerotinia* spp.)

Stemphylium leaf spot (*Stemphylium* spp.)

Verticillium wilt (*Verticillium dahliae*)

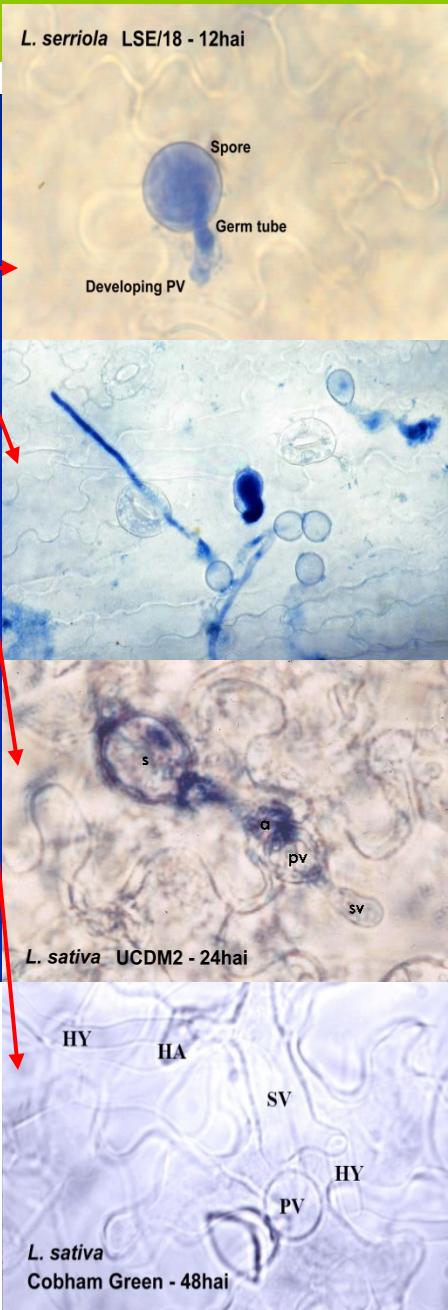
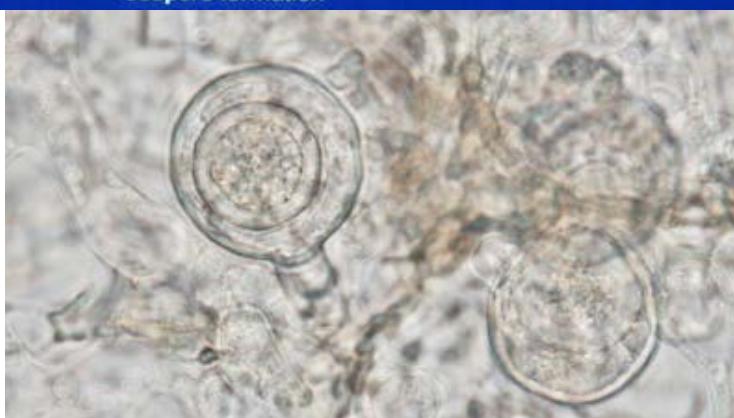
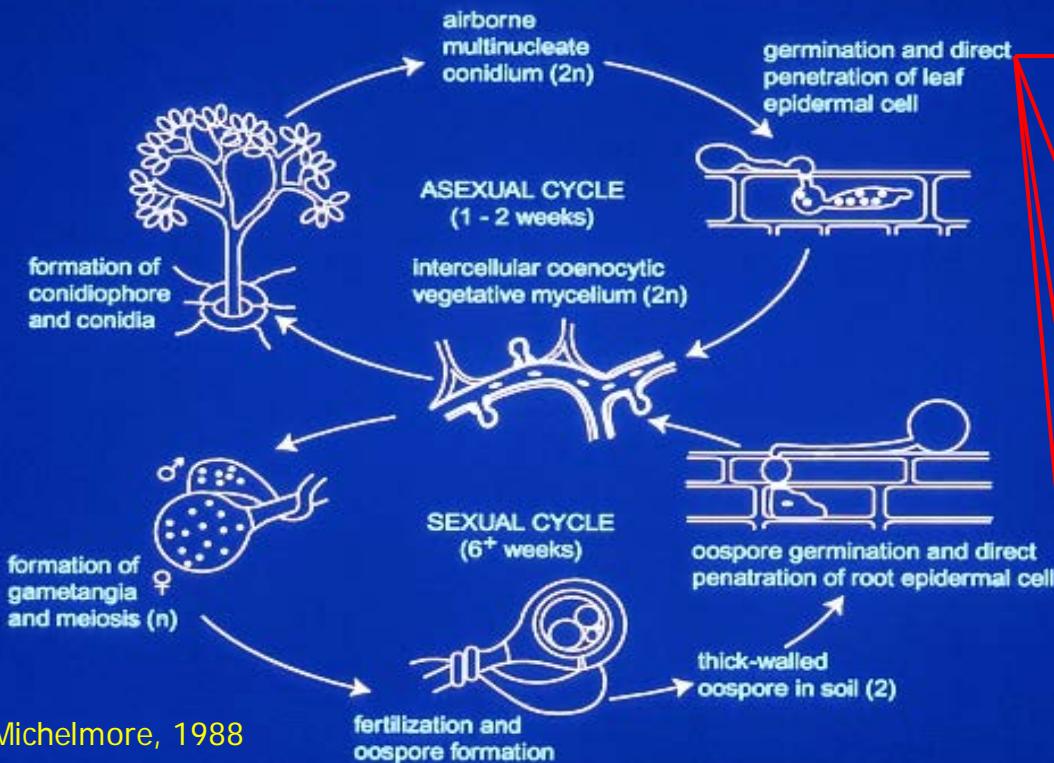
Fusarium wilt (*Fusarium* spp.)

Pythium wilt (*Pythium* spp.)

Lettuce downy mildew (*Bremia lactucae*)



Lifecycle of *Bremia lactucae*



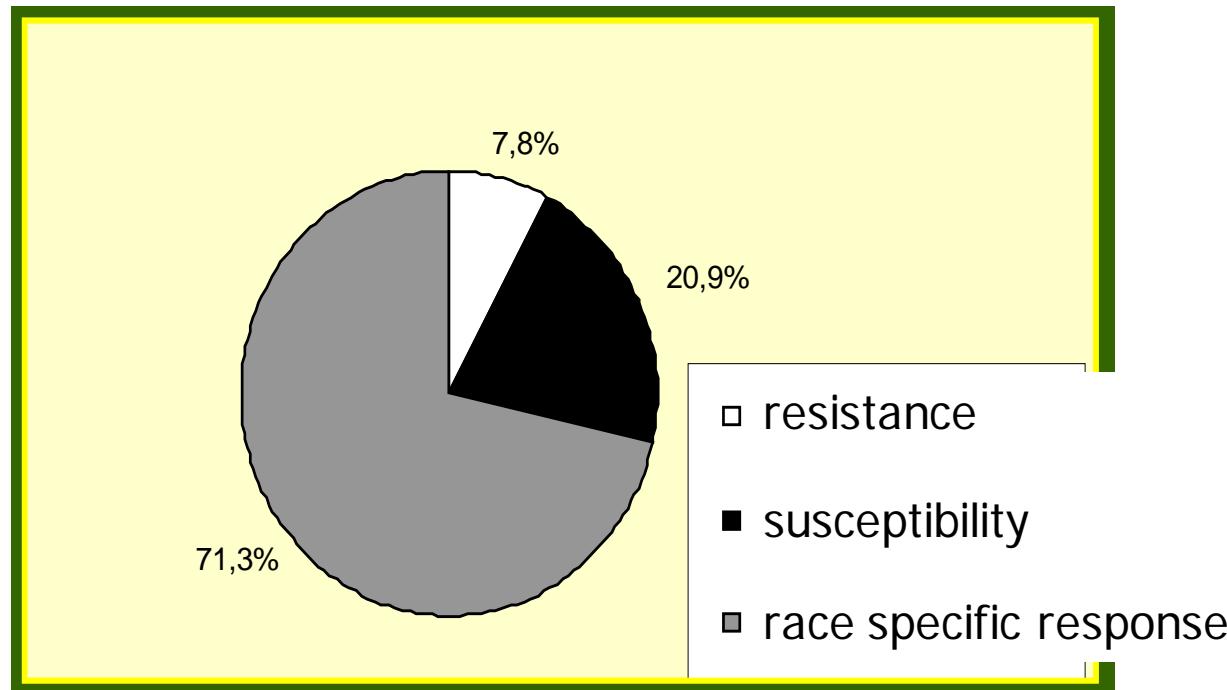
Mechanisms of resistance of *Lactuca sativa* and wild *Lactuca* spp. against *Bremia lactucae*

(Lebeda et al. 2002, Advances in Downy Mildew Research, Kluwer Academic Publishers, the Netherlands)

Section/subsection <i>Lactuca</i> spp.	Response to <i>B. lactucae</i> from <i>L. sativa</i>	Response to <i>B. lactucae</i> from <i>L. serriola</i>	Possible resistance mechanisms
Lactuca			
Lactuca			
<i>L. aculeata</i>	+/-	+/-	RS
<i>L. altaica</i>	+/-	+/-	RS
<i>L. dregeana</i>	+/-	+/-	RS
<i>L. livida</i>	+	+	RS?
<i>L. saligna</i>	+/-	(-)	RS, NR?
<i>L. sativa</i>	+/-	+/-	RS, FR
<i>L. serriola</i>	+/-	+/-	RS, RNS, FR
<i>L. virosa</i>	+/-	+/-	RS, FR
Cyanicae			
<i>L. perennis</i>	+/-	-	RS
<i>L. tenerrima</i>	+/-	+/-	RS
			FR – field resistance
			NR - non-host resistance
			RS – race specific
			RNS – race non-specific

Distribution* of resistance to *B. lactucae* among *L. serriola* samples (individual plants) (n=752) within the European metapopulation of *L. serriola*

(adapted according to data published by Lebeda and Petrželová, 2004, Genetic Variation for Plant Breeding, EUCARPIA & BOKU; Lebeda et al., 2008, EJPP)



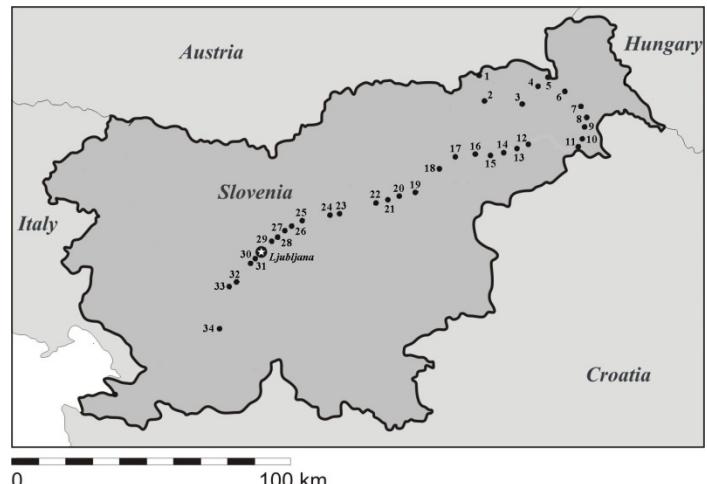
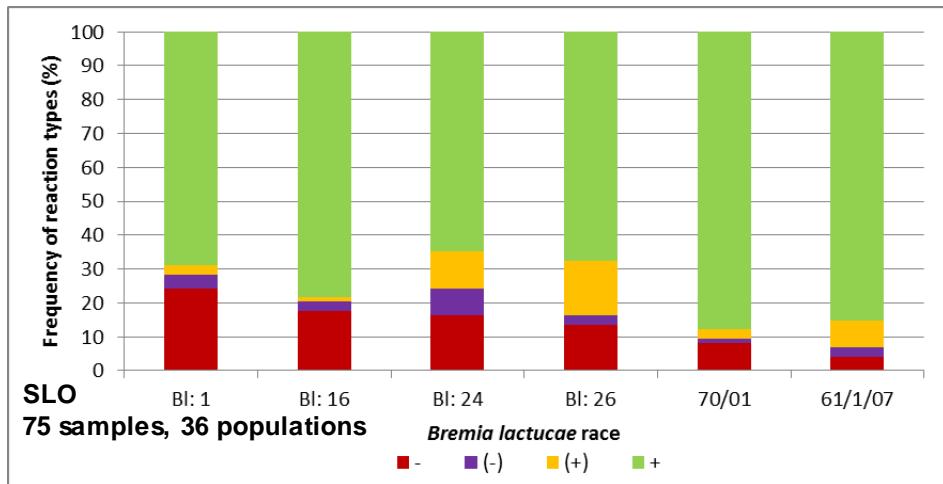
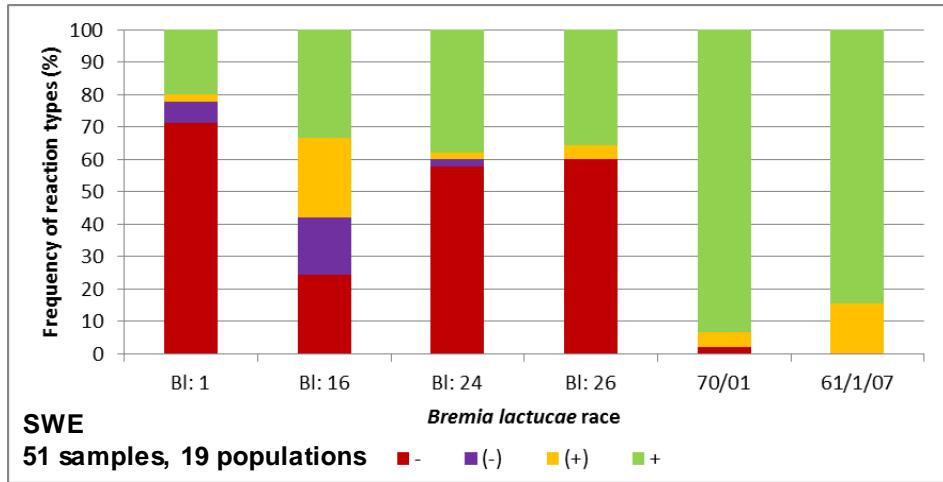
*Proportion of *L. serriola* samples which were completely resistant, completely susceptible or expressed race-specific **response to the set of 10 used races of *B. lactucae***

Assessment of resistance of European *L. serriola* samples (individual plants) to ten races of *B. lactucae*

(Lebeda and Petrželová (2004): Genetic Variation for Plant Breeding, EUCARPIA & BOKU, pp. 113-116;
Petrželová and Lebeda, 2011, EJPP)

Populations	Number (%) of <i>L. serriola</i> samples			
	Completely resistant	Completely susceptible	Race-specific response	Totally
CZ	24 (9.6)	76 (30.4)	150 (60.0)	250
D	35 (14.5)	66 (27.4)	140 (58.1)	241
NL	0 (0)	15 (12.5)	105 (87.5)	120
UK	0 (0)	0 (0)	141 (100)	141
Totally	59 (7.8)	157 (20.9)	536 (71.3)	752

Variation of resistance to *B. lactucae* among Swedish and Slovenian populations of *L. serriola* (Jemelková et al., 2015 prepared for press)



Diversity of race-specific *B. lactucae* resistance

- About fifty *Dm* race-specific resistance genes identified in lettuce
- (Michelmore and Wong 2008, Eur. J. Plant Pathol.)
- Twenty of them located to four major resistance clusters
- (Christopoulou et al. 2015, Mol. Plant-Microbe Interact.)

Most of the mapped *Dm* genes are clustered at three linkage groups (LGs):

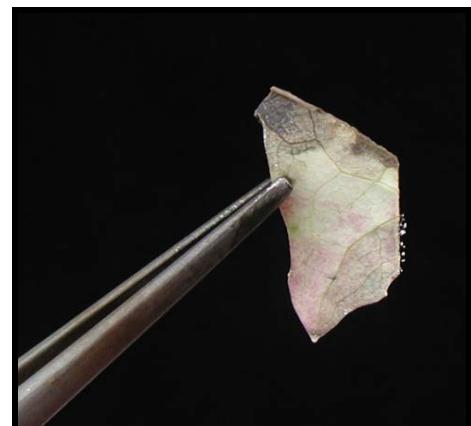
- *Dm5/8, Dm10, Dm17, Dm43, and Dm45* at **LG 1**;
- *Dm1, Dm2, Dm3, Dm6, Dm14, Dm15, Dm16, m18* at **LG 2**;
- *Dm4, Dm7, Dm11, Dm44, Dm48, and Dm49* at **LG 4**
- A single *Dm* gene, *Dm13*, is located at **LG 3**

(Simko, I., 2013 – on line. Marker-Assisted Selection for Disease Resistance in Lettuce; In Varshney, R.V. and Tuberosa, R. (eds.) Translational Genomics for Crop Breeding, vol. I. Biotic Stress, Wiley Blackwell)

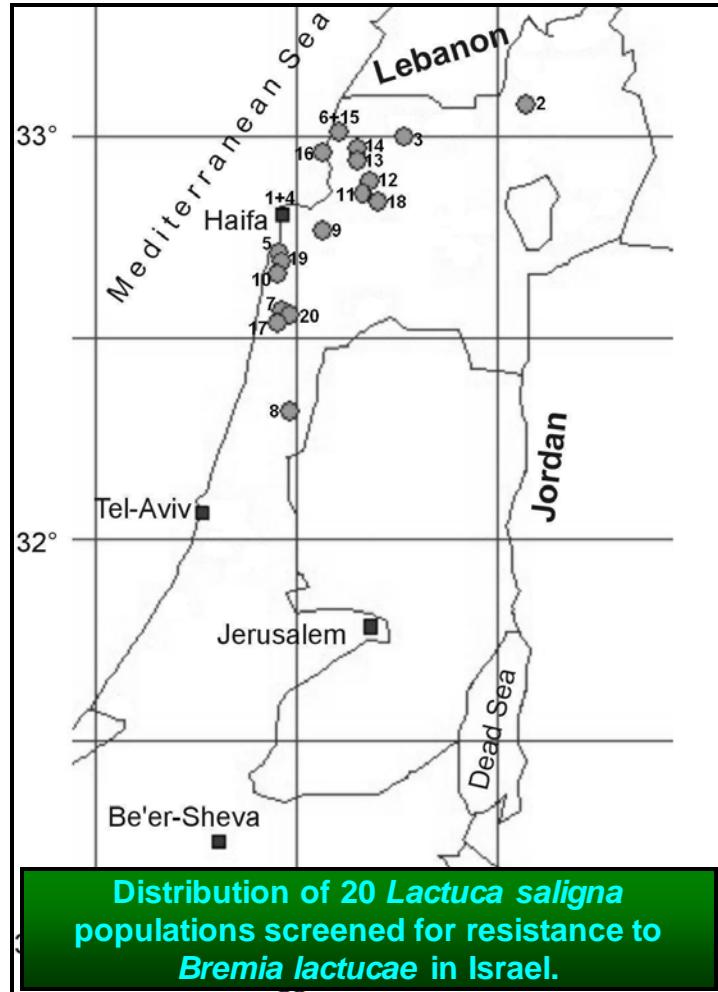
L. saligna – *B. lactucae* interaction

Research of non-host resistance in *Lactuca saligna* populations

(Petrželová et al. 2011, Ann. Appl. Biol.)



Materials for screening of resistance to *Bremia lactucae* in populations of *Lactuca saligna* naturally growing in three Middle Eastern countries and France

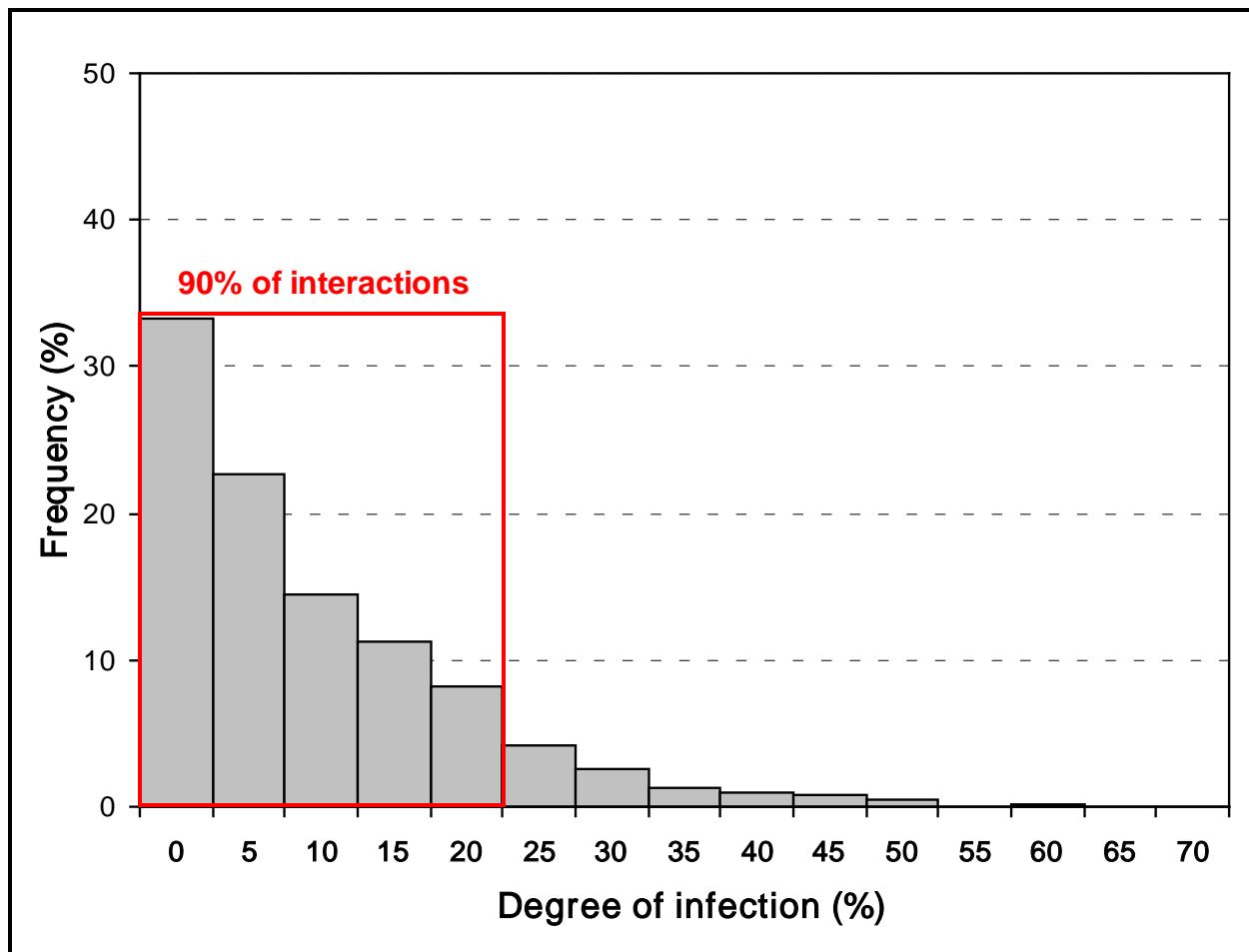


Origin of <i>L. saligna</i> seed samples	Number of populations	Number of individuals
Israel	20	136
France	3	8
Jordan	1	1
Turkey	1	1
Totally	25	146



L. saligna individuals were tested at a seedling stage for their resistance to 10 highly virulent isolates (races) of *B. lactucae* from *L. sativa* (DEG2, Bl:5, Bl:15, Bl:16, Bl:17, Bl:18, Bl:21, Bl:22, Bl:24 and Bl:25) with known virulence patterns.

Frequency of different degrees of infection
(in percentages of *Bremia lactucae* sporulation intensity)
among *Lactuca saligna*-*Bremia lactucae* interactions (N=146×10)





Response of *Lactuca aculeata* accessions to *Bremia lactucae* races (from *L. sativa*), with records of different reaction patterns

(Jemelková et al. 2013, Wild Plant Pathosystems)

Pattern no.	Response to race of <i>Bremia lactucae</i>								
	BL 17	BL 18	BL 24	BL 27	BL 28	TUR	JOR	ISR	
1	+	+	+	+	+	5	2	6	
2	-	+	+	+	+		10	9	
3	-	-	+	+	+			1	
4	-	+	+	+	-		1	1	
5	-	-	-	+	-			4	
6	-	-	-	-	-			2	

+ ... susceptibility; - ... resistance **N = 41**

A subset of 41 *L. aculeata* accessions originating from Turkey (TUR), Jordan (JOR) and Israel (ISR) was tested for the resistance against *Bremia lactucae*. Altogether 5 isolates (BI races – BI 17, BI 18, BI 24, BI 27 and BI 28) were used for seedling test (Lebeda and Petrželová, 2010).

Lettuce powdery mildew
(Golovinomyces cichoracearum s. str.)
on *Lactuca serriola* and *L. sativa*



Sources of resistance to lettuce powdery mildew in wild *Lactuca* spp.

Source of resistance			
<i>Lactuca</i> spp.	No. of accession, sample	Type of resistance	References
<i>L. aculeata</i>	LAC/92/2	?	Lebeda (1985)
<i>L. perennis</i>	09318, 09319, 09323	?	Lebeda (1994)
<i>L. saligna</i>	LSA/92/1 and LSA/92/2	?	Lebeda (1985)
<i>L. saligna</i>	05282, 05304, 05306, 05308, 05309, 05311, 05313, 05314, 05315, 05318, 05319, 05320, 05322, 05323, 05326, 05330, 05895, 09311, 09313	?	Lebeda (1994)
<i>L. saligna</i>	09-H58-1013	Race-specific	Lebeda et al. (2012)
<i>L. serriola</i>	PI 255665	?	Lebeda (1985)
<i>L. serriola</i>	PI 273617	Race-specific	Lebeda et al. (2012)
<i>L. tatarica</i>	09389, 09390	?	Lebeda (1994)
<i>L. tenerrima</i>	09386, 09387, 09388	?	Lebeda (1994)
<i>L. viminea</i>	09326	?	Lebeda (1994)
<i>L. virosa</i>	LVIR/26 and LVIR/57/1	?	Lebeda (1985)
<i>L. virosa</i>	04678, 04679, 04680, 04681, 04682, 04683, 04954, 04955, 04956, 04963, 04964, 04970, 04972, 05020, 05077, 05145, 05148, 05266, 05268, 05270, 05283, 05331, 05332, 05333, 05793, 05794, 05816, 05869, 05941, 05978, 09315, 09316, 09364, 09365, PI 271938	?	Lebeda (1994)
<i>L. virosa</i>	LVIR/50	Race-specific	Lebeda et al. (2012)

Survey of race-specific reaction patterns of *G. cichoracearum* isolates from *L. serriola* on a set of *Lactuca* spp. accessions (Lebeda et al., 2012, Fungal Ecology)

<i>Lactuca</i> spp.	<i>G. cichoracearum</i> isolates/reaction patterns												
	14/ 08*	20/ 07	7/ 08	18/ 08	15/ 08	2/ 08	7/ 07	11/ 08	9/ 08	3/ 08	19/ 08	4/ 08	21/ 07
<i>L. serriola</i> (LSE/57/15) – control	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>L. serriola</i> (PI 273617)	+	(-)	(-)	(-)	(-)	(-)	+	(-)	(-)	-	-	-	-
<i>L. sativa</i> (Sabine)	+	+	+	+	+	+	+	+	+	+	(-)	+	-
<i>L. sativa</i> (Colorado)	+	(-)	+	(-)	-	+	-	-	(-)	(-)	-	-	-
<i>L. sativa</i> (UCDM2)	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>L. sativa</i> (Capitan)	+	+	+	+	+	+	+	+	(-)	x	+	+	+
<i>L. saligna</i> (09–H58–1013)	+	+	(-)	-	+	-	-	-	-	-	-	-	-
<i>L. virosa</i> (LVIR/50)	+	+	-	(-)	(-)	-	(-)	+	-	-	(-)	-	-
<i>L. virosa</i> (09–H58–0998)	+	+	+	+	(-)	+	+	(-)	(-)	(-)	+	(-)	+

*

code of isolate (number of isolate/year of collection)

+

susceptible (% max ID > 60)

-

resistant (% max ID < 30)

(-)

moderately resistant (% max ID 30–60)

x

reaction not known

For assessment of infection degree (ID), a 0–3 scale was used (Mieslerová et al., 2007a).

For each accession percentage of maximum infection degree (% max ID) was calculated.

Anthracnose (*Microdochium panattoniana*)

- Serious damage of lettuce crops in the southern states of Australia, in California and throughout Europe;
- Especially under cool wet conditions when application of fungicides is difficult (Galea and Price 1988);
- **Sources of resistance identified in wild *Lactuca* species *L. angustana*, *L. livida*, *L. perennis*, *L. serriola*, *L. saligna*, *L. virosa*.**

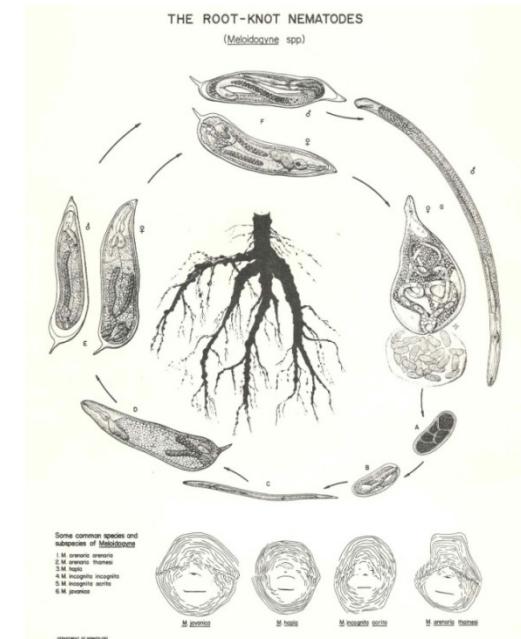
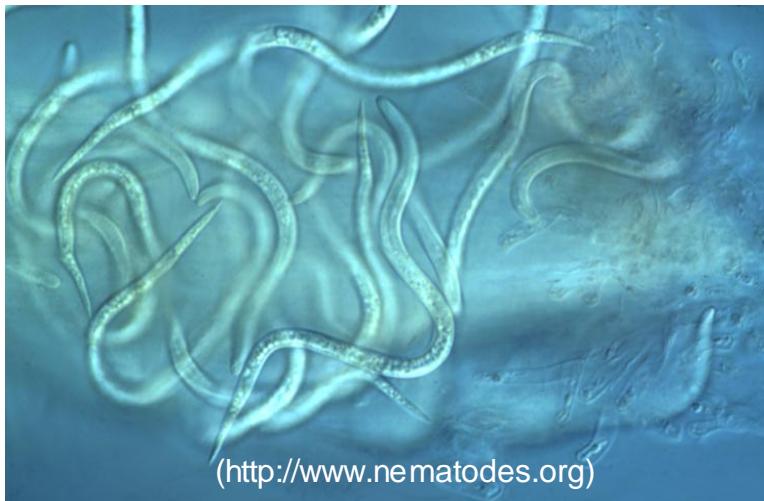


Wild *Lactuca* spp. with resistance to anthracnose

<i>Lactuca</i> spp.	No. of accession, sample	Type of resistance	Remark	References
<i>L. angustana</i>	PI 190906			Ochoa et al. (1987)
<i>L. livida</i>	PI 273585		re-determined as <i>Lactuca</i> sp. (Doležalová et al., 2004; Lebeda et al. 2007c)	Ochoa et al. (1987)
<i>L. perennis</i>	PI 273594			Ochoa et al. (1987)
	PI 274415			Ochoa et al. (1987)
	PI 274378			Ochoa et al. (1987)
<i>L. saligna</i>	LAG1	immune	coll. in Hillston, NSW	Galea and Price (1988)
	UC83US1	resistant to races A, B, C, D, E		Ochoa et al. (1987)
	PI 273482			Ochoa et al. (1987)
	UC83UK2			Ochoa et al. (1987)
	PI 490999			Ochoa et al. (1987)
<i>L. serriola</i>	LAG2	highly resistant	coll. from Zoology Reserve, La Trobe University	Galea and Price (1988)
	PI 274372			Ochoa et al. (1987)
	PI 274457			Ochoa et al. (1987)
	PI 289064			Ochoa et al. (1987)
<i>L. virosa</i>	PI 271939			Ochoa et al. (1987)
	PI 273579			Ochoa et al. (1987)
	PI 274375			Ochoa et al. (1987)

Nematodes

- 23 genera (Davis et al. 1997, *Compendium of Lettuce Diseases*)
- documented impact to lettuce growth and yield:
 - the needle nematode (*Longidorus africanus*)
 - root-knot nematode (*Meloidogyne* spp.)
 - root lesion nematode (*Pratylenchus penetrans*)
 - the spiral nematode (*Rotylenchus robustus*)



(<http://plpnemweb.ucdavis.edu>)

- Limited number of studies dealing with nematodal infection/diseases on lettuce wild progenitors.
- Two reports related to identification of **resistant accessions to root-knot nematode (*Meloidogyne hapla*)** in a larger germplasm collections:

(Abawi & Robinson 1991, *J. of Nematol.*;
Kaur & Mitkowski 2010, *Inter. J. of Veg. Science*)

Moderate-highly resistant genotypes

- *L. serriola* (3738)
- *L. saligna* (PI 281876, PI 491000, PI 261653, PI 273582)
- *L. virosa* (PI 273579, PI 271938, PI 273597)



Insects and Mites

At least sixteen genera of aphids occur on *Lactuca* spp.

Three most important species:

(Blackman & Eastop 2000, *Aphids on the World's Crops*)

Nasonovia ribisnigri Mosley

the „green lettuce aphid“ (GLA)

or „currant-lettuce aphid“ (CLA)

Pemphigus bursarius (L.)

the „lettuce root aphid“ (LRA)

Liriomyza langei Frick

„leafminer“



CLA colouration is dependent on the host plant

Nasonovia ribisnigri Mosley (Green lettuce aphid)

- 1982: *L. virosa* (IVT 280) - resistance to GLA biotype 0 (Nr:0) transferred to *L. sativa* by a bridge cross to *L. serriola* (Eenink et al. 1982, *Euphytica*) and many other commercially available cultivars
- 2007: occurrence of Nr:1 biotype feeding on resistant cultivars
(Sauer 2008, <http://www.agroscope.admin.ch>)
- Based on these results the resistance was successfully transferred to lettuce cultivars
- *Lactuca* spp. – sources of new resistance genes:
 - resistance to Nr:0 in *L. serriola* acc. PI 491093 (p.r.) and *L. virosa* PI 274378 (c.r.) (McCreight 2008, *HortScience*)
 - 64 *L. serriola* and *L. virosa* acces. resistant to Nr:1 in CGN germplasm collection
 - several acces. resistant to Nr:0 and Nr:1 (Anonymous 2008, <http://ip.com/IPCOM/000176078>)
 - *L. serriola* (10G.913571) with resistance to Nr:0 and Nr:1 (Thabuis et al. 2011, *World Intell. Prop. Org.*):



Examples of multiple disease resistance - *L. saligna*

Acc/sample	Pathogen	Type of resistance	References
LAG1	ANT	immune	Galea and Price (1988)
PI 261653	CMV-B	resistance	Edwards et al. (1983)
PI 261653	LNYV		Haley and McCreight (1990)
PI 261653	CR	not known	Brown, Michelmore (1988)
PI 261653	nematodes		
PI 271940	LNSV		Grube et al. (2005)
PI 273482	ANT		Ochoa et al. (1987)
PI 273582	nematodes		
PI 281876	nematodes		
PI 490999	LNSV		Grube et al. (2005)
PI 490999	CR	not known	Brown, Michelmore (1988)
PI 490999	ANT		Ochoa et al. (1987)
PI 491000	nematodes		
PI 491204	CR	not known	Brown, Michelmore (1988)
PI 491206	CR	not known	Brown, Michelmore (1988)
UC83UK2	CR	not known	Brown, Michelmore (1988)
UC83UK2	ANT		Ochoa et al. (1987)
UC83US1	CR	not known	Brown, Michelmore (1988)
UC83US1	ANT	res. races A, B, C, D, E	Ochoa et al. (1987)
unspecified line	STEM		Netzer et al. (1985)
	DM		
LSA/92/1,	PM	not known	Lebeda (1985)
LSA/92/2	PM	not known	Lebeda (1985)
05282, 05304, 05306, 05308, 05309, 05311,05313, 05314,05315, 05318,05319,05320, 05322,05323,05326, 05330, 05895,09311, 09313 09-H58-1013	PM	?	Lebeda (1994)
	PM	Race-specific	Lebeda et al. (2012)

Known examples of lettuce cultivars issued from exploitation of wild *Lactuca* spp.

- 1958 - the cultivar '**Vanguard**' developed from a cross between a *L. sativa* × *L. serriola* which was then crossed to *L. virosa* (Ryder 1999);
- crosses between *L. sativa* and *L. virosa* - low seed set, unviable seeds, stunted plants and/or sterile hybrids (Lindqvist 1960);
- viable hybrid plants were obtained only when *L. serriola* was used as a bridging species (Thompson and Ryder 1961; Eenink et al. 1982b);
- *L. saligna* crossed to a cultivated iceberg type by R.W. Robinson (Providenti et al. 1980) who developed a cultivar '**Salad Crisp**';
- report of downy mildew resistance in the hybrid of *L. sativa* × *L. serriola* (Lebeda 1982, Lebeda and Blok 1991), developed cv. '**Libusa**';
- from that cross. Jeuken and Lindhout (2004) developed backcross inbred lines in which chromosome segments from *L. saligna* were introgressed into cultivated lettuce;

Genealogy of Contemporary North American Lettuce (1970-2004)

328 proprietary and publicly developed cvs:

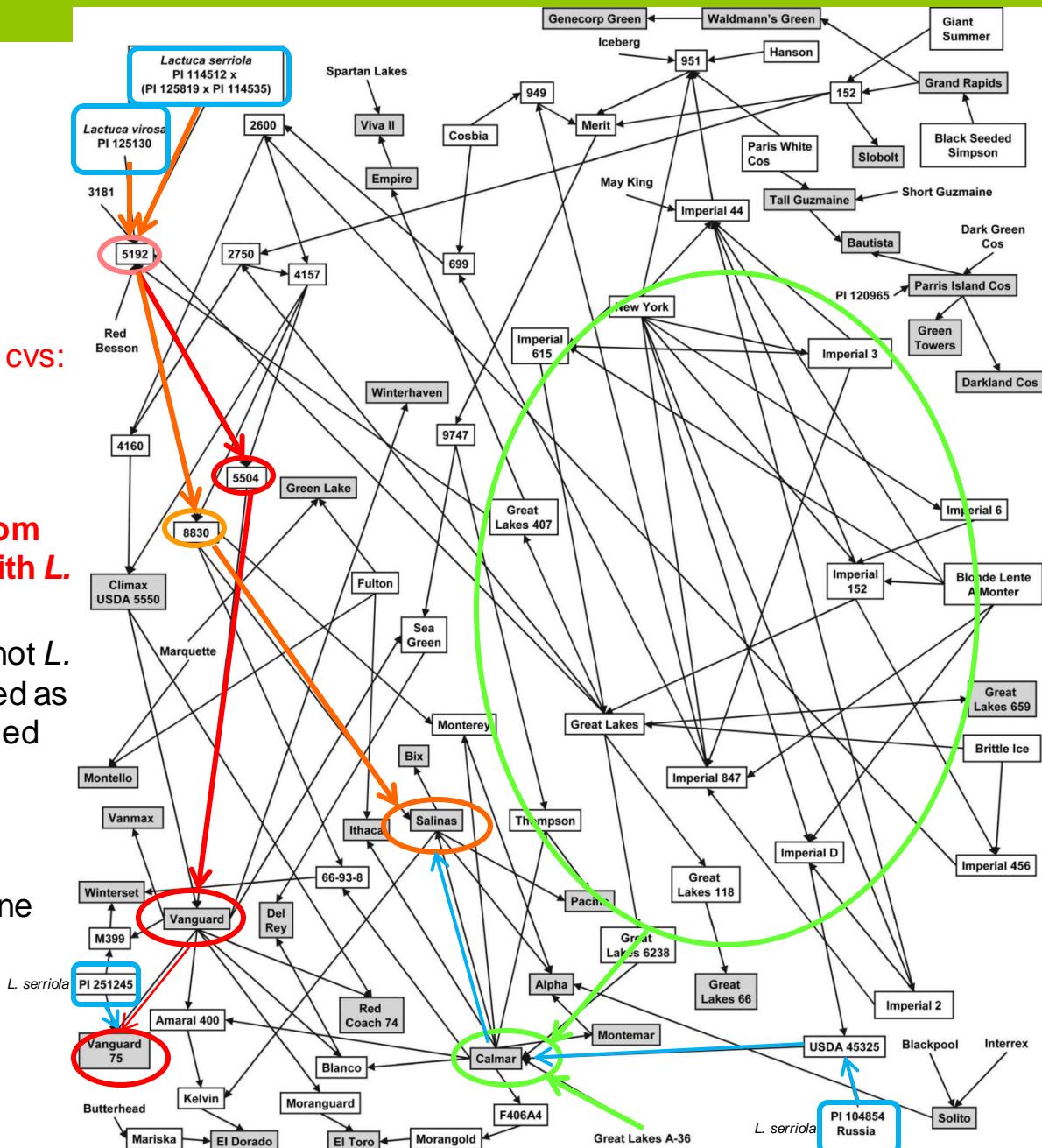
- 1% of these cvs. developed from interspecific crosses (*L. serriola*, *L. saligna*, *L. virosa*)

- 'Vanguard' and 'Salinas' descend from the interspecific cross of *L. sativa* with *L. virosa* and *L. serriola*

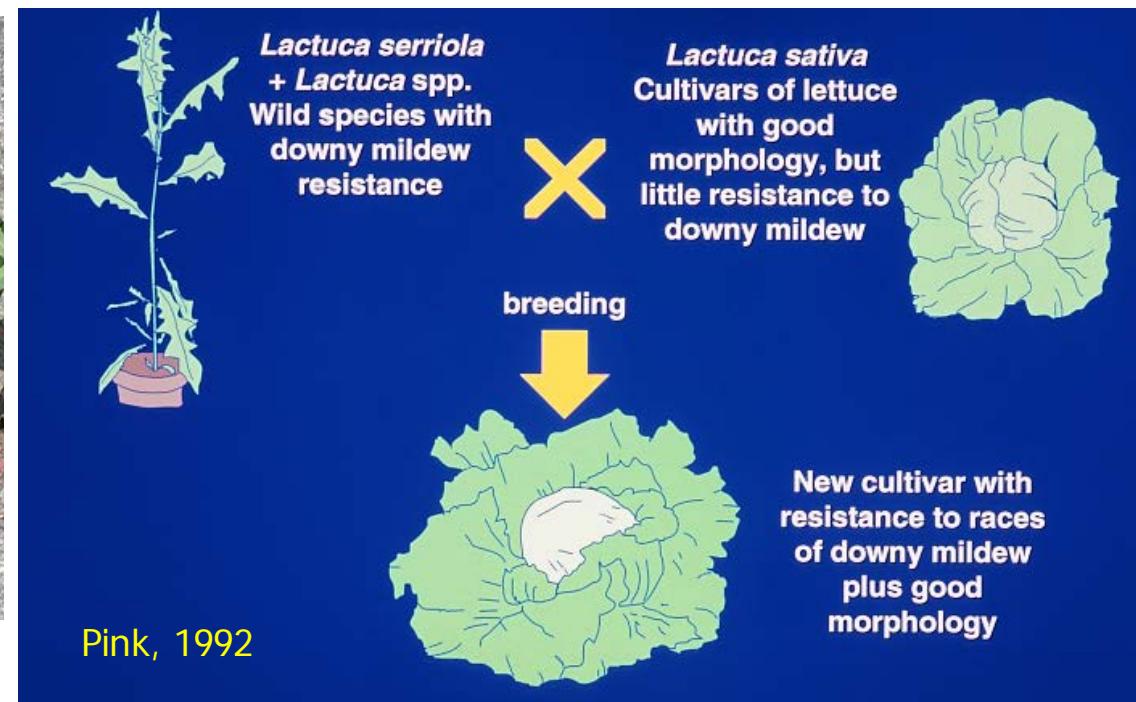
- 'Vanguard' and 'Salinas' followed by "not *L. virosa*" cultivar 'Calmar' were determined as elite programme cultivars, frequently used in lettuce breeding

- 'Vanguard' - contributed 23.8% of the genes to crisphead lettuce

- 'Salinas' frequently crossed with romaine lettuce types



Own practical result of lettuce breeding for resistance against *B. lactucae*



cv. LIBUSA

Conclusions and future prospects

- **Research of resistance of wild *Lactuca* germplasm** is still in the beginning in the relation to my many important diseases and pest of cultivated lettuce;
- **Genetics of interactions** is mostly not known;
- **Mechanisms of resistance** are very poorly known;
- **Multiple disease and pest resistance** was not studied in detail till now;
- **Pyramiding** of race-specific resistance genes;
- **Exploitation of nonhost resistance** need more theoretical research as well as practical exploitation in lettuce breeding;
- **Strategy of durable resistance** must be elaborated;
- **New technologies** (genetic mapping and resequencing) offer new ways to screen germplasm collections.

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