



Sunflower genetic resources: pre-breeding experience from Serbia

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The sunflower plant

- From the first varieties in Russia in 1880, in the relatively short period of time, sunflower reached the second place on the list of oilseeds, right after soybeans - in 1970
- Intensive work on breeding resulted with the first sunflower hybrids in the 70's, and sunflower was developed into a high-yielding plant with relatively low requirements



Revisiting the ancestors

1916: T. Sazyperow crosses *H. annuus* and *H. argophyllus* for rust resistance

1935: Pustovoit, disease resistance introduction through interspecific crosses

1945: Heiser, large scale interspecific crosses focused on taxonomy

1955: Georgieva-Todorova, crosses with *H. laetiflorus*

1957: Putt, *Puccinia helianthi* resistance from a wild *H. annuus* x Armavirsky 3497

1969: Leclercq, first source of cytoplasmic male sterility in a cross with *H. petiolaris*

1970: Vranceanu, Downy mildew pl 1 gene from material developed on the basis of wild sunflowers

1978: VNIIMK, varietal populations on the basis of *H. tuberosus*. Varieties Yubilejnaya 60, Progress, October, incorporated genes of resistance to *Puccinia helianthi*, *Plasmopara helianthi*, *Phoma* sp., and *Orobanche cumana*.

1978: Škorić, restorer lines resistant to downy mildew based on *H. tuberosus*

Diseases can significantly lower sunflower seed yield

Wild sunflower species can be used as a source of resistance

1979: INRA Versailles, new F.A.O. subnetwork established: **Collection, evaluation and conservation of wild species and their use in sunflower breeding programmes**

IFVCNS designated as Liaison center of this subnetwork



1962: Industrial crops department established

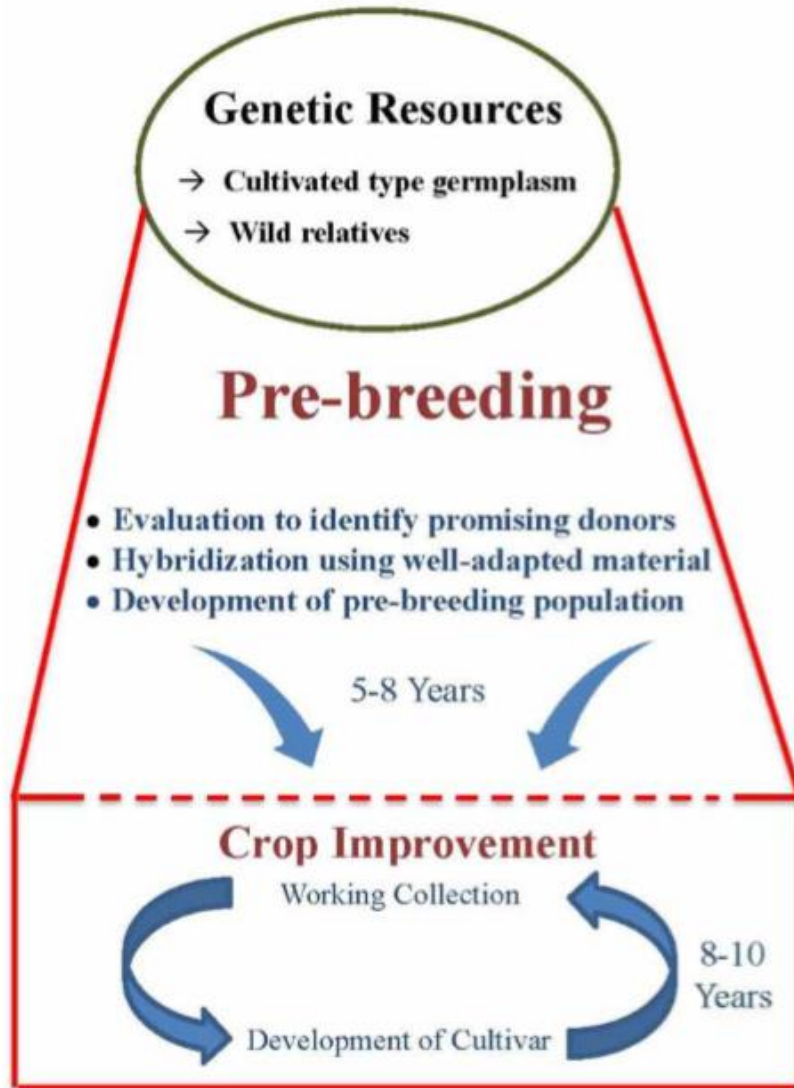
1978: IFVCNS among the first to introduce sunflower hybrids for commercial production

1980: IFVCNS collection of wild *Helianthus* species founded

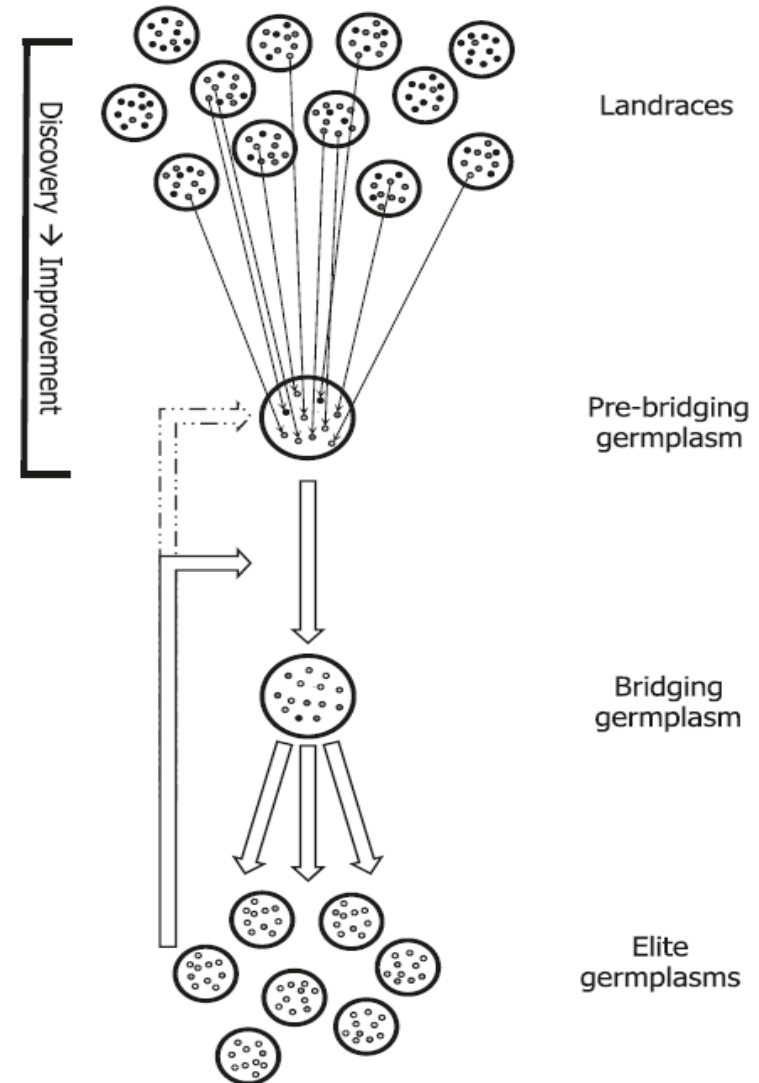


Helianthus maximiliani

Pre-breeding



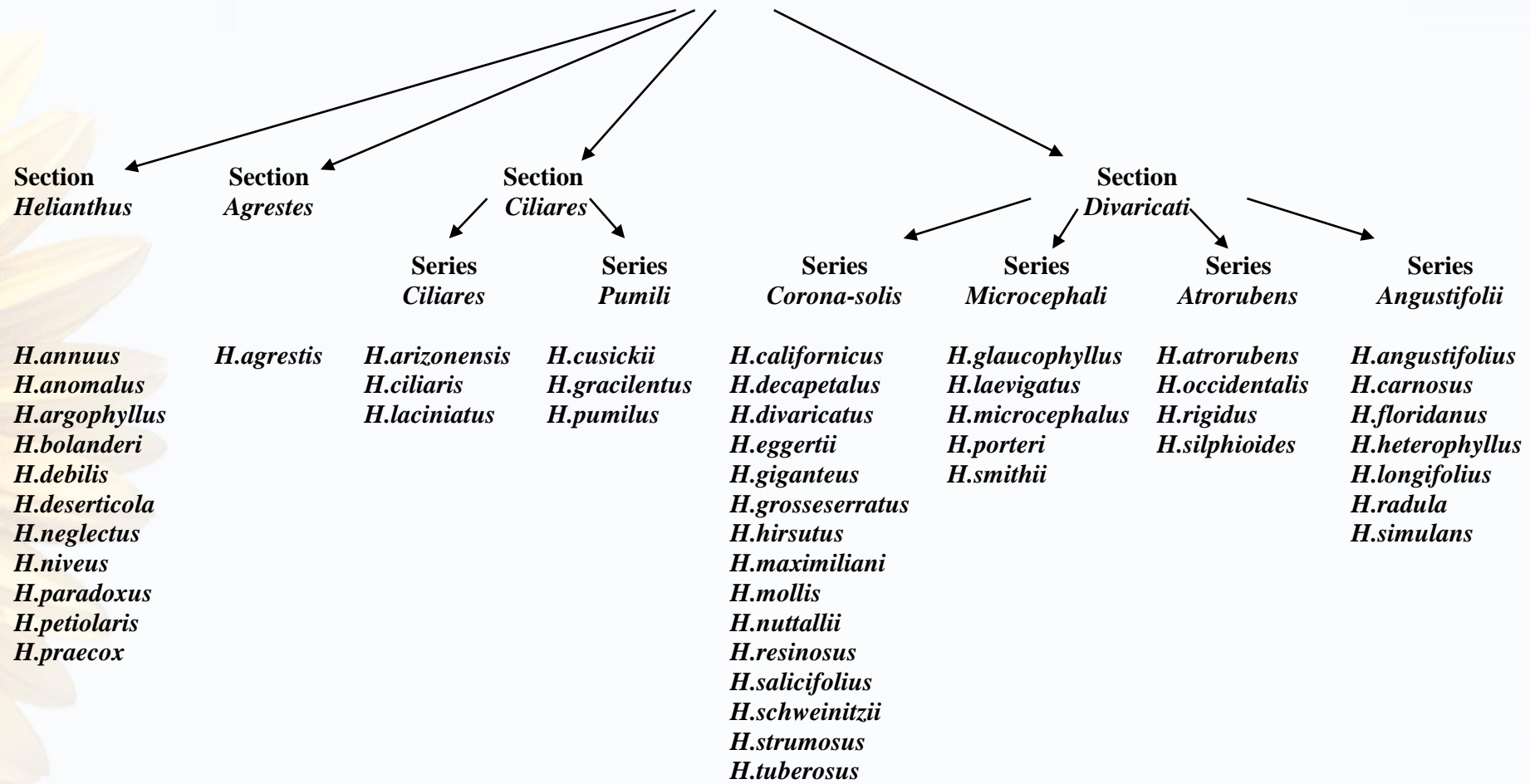
Sharma et al. 2013 Grain legumes pre-breeding...



Gorjanc et al. 2016 Maize pre-breeding...

1. Collecting
2. Maintenance
3. Characterisation
4. Biotechnology
5. Interspecific crosses

Helianthus



Infrageneric classification of *Helianthus* (Compositae), Schilling, E. E., Heiser, Ch. B., (1981)

Sunflower germplasm explorations – 1976-2004:

Joint efforts between the USDA-ARS and:

Food and Agriculture Organization of the United Nations (FAO)

Wild Species Working Group, The International Plant Genetic Resources Institute, European Cooperative Program for Genetic Resources (IPGRI/ECPGR)

European Cooperative Research Network (ESCORENA)

US Agency for International Development (USAID), USDA Office of International Cooperation and Development (OICD)

The National Bureau of Plant Genetic Resources (NBPGR) New Delhi, India



Expeditions (1980-1991)

Collected by	Year	No. of states	No. of species	No. of accessions
Seiler, G. (USDA-ARS) Ćuk, L. (YUGIFVC)	1980	21 (USA)	37	384
Marinković, R. (YUGIFVC) Miller, J. (USDA-ARS)	1984	1 (Canada)	7	88
Škorić, D. (YUGIFVC), Seiler, G. (USDA-ARS) Rooth, W. (USDA-ARS)	1985	12 (USA)	13	88
Seiler, G. (USDA-ARS), Pomeroy, J. (USDA-ARS) Marinković, R. (YUGIFVC)	1987	6 (USA)	7	52
Dozet, B. (YUGIFVC), Seiler, G. (USDA-ARS) Pomeroy, J. (USDA-ARS), Gavrilova, V. (SUNWIR)	1989	6 (USA)	12	84
Dozet, B. (YUGIFVC) Marinković, R. (YUGIFVC)	1990	1 (Montenegro)	1	81
Marinković, R. (YUGIFVC), Seiler, G. (USDA-ARS) Stauffer, C. (USDA-ARS), Duhoon, S. (NBPGR)	1991	7 (USA)	9	140

Exchange

Prior to 1980: Exchange of breeding material

1980: IFVCNS received:

59 samples of 36 wild species from France

9 samples of 9 wild species from Bulgaria

1981: 24 samples of 24 wild species from Romania

8 samples of 7 wild species from Bulgaria

5 samples of 2 wild species from Argentina

1981: Wild sunflower species sent to other collections:

11 samples of 11 wild species to France

12 samples of 7 wild species to Bulgaria



Maintainance

The collection of wild
sunflower species in Novi Sad
(1984)



Dense populations, 2008



Weed control fabric - since 2010



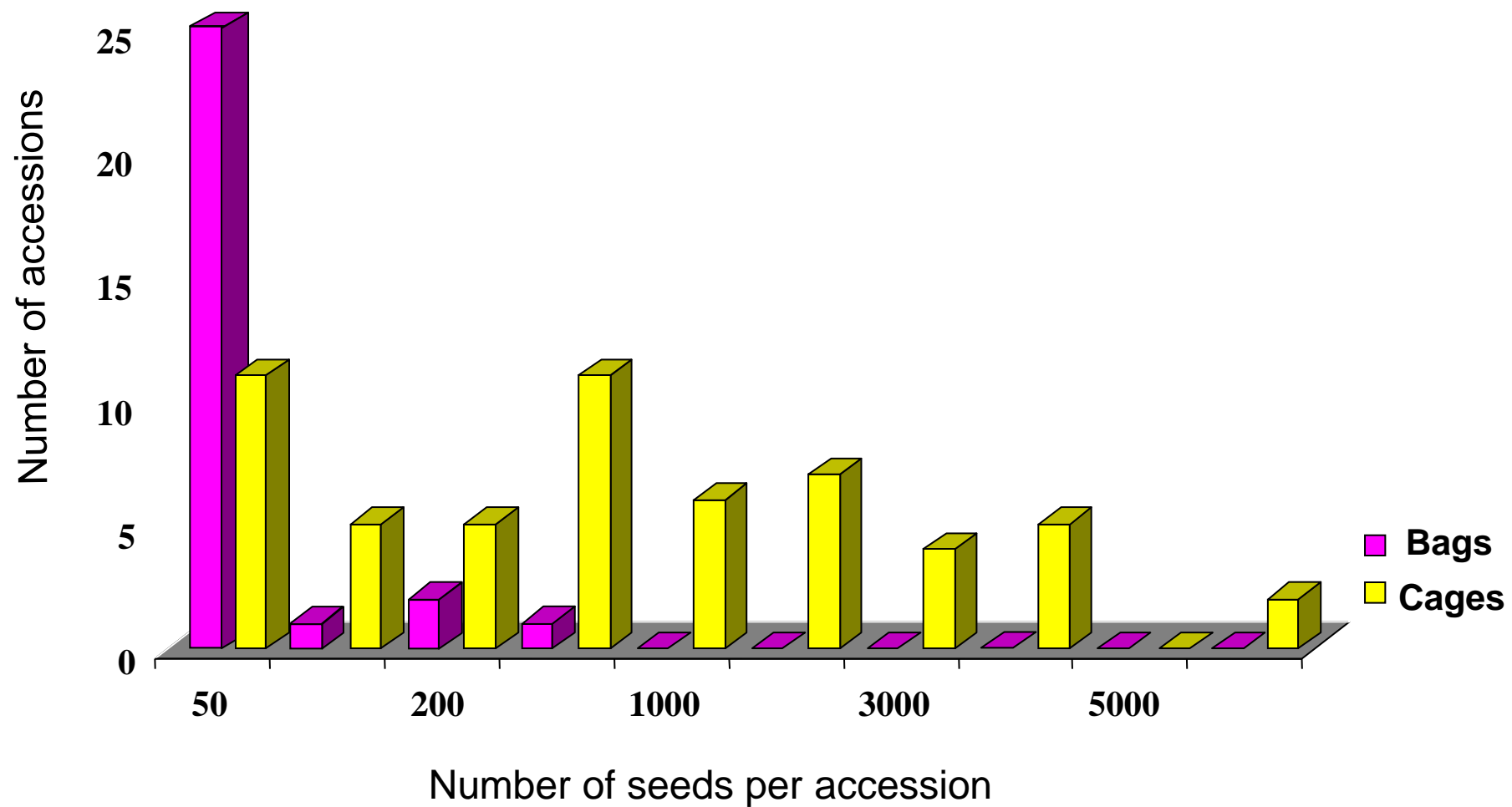
The IFVCNS collection of annual wild species (7/14)

Species	Number of accessions		Number of seeds
	in gene bank data base	with seed reserves	
<i>H.annuus</i>	323	74	10-2539
<i>H.petiolaris</i>	80	25	80-9130
<i>H.praecox</i>	27	26	335-10710
<i>H.debilis</i>	25	24	33-5490
<i>H.argophyllus</i>	23	6	1616-10396
<i>H.neglectus</i>	18	17	1564-4838
<i>H.niveus</i>	12	8	259-5910

The IFVCNS collection of perennial species (21/37)

Species	Number of accessions		Number of seeds	Number of accessions in the field
	in gene bank data base	with seed reserves		
<i>H.tuberosus</i>	158	20	1-650	112
<i>H.maximiliani</i>	48	36	1-8630	36
<i>H.grosseserratus</i>	44	20	2-399	32
<i>H.strumosus</i>	40	12	2-354	21
⋮				
<i>H.silphioides</i>	2	1	13	1
<i>H.salicifolius</i>	2	1	20	2
<i>H.glaucophyllus</i>	1	1	38	1
<i>H.californicus</i>	1	1	1	1

The seed production of annual species in relation with the type of isolation



Cage pollination with bumblebees...



The effect of seed scarification on germination

Perennial species	Number of accessions	Germination of non scarified seeds (%)	Germination of scarified seeds (%)	Increase (%)
<i>H.grosseserratus</i>	1	4	38	34
<i>H.tuberosus</i>	1	0	30	30
<i>H.maximiliani</i>	2	4	29,5	25,5
<i>H.atrorubens</i>	2	11	32	21
<i>H.strumosus</i>	1	18	30	12
<i>H.mollis</i>	3	27	36	9,3
<i>H.hirsutus</i>	2	0	9	9
<i>H.rigidus</i>	2	0	8	8
<i>H.laevigatus</i>	1	6	12	6

Average increase = 17,2%

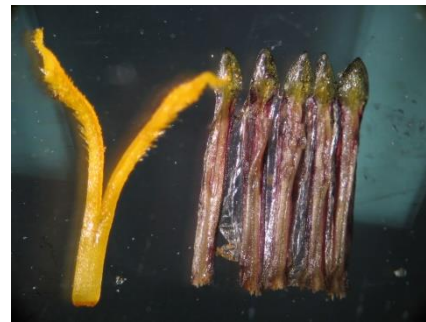
Conserving F₁ hybrids with perennial species in the field

Hybrid plants keep the ability of vegetative reproduction in F₁ generation

Conserved in the field for 30 years under the same growing conditions as wild species

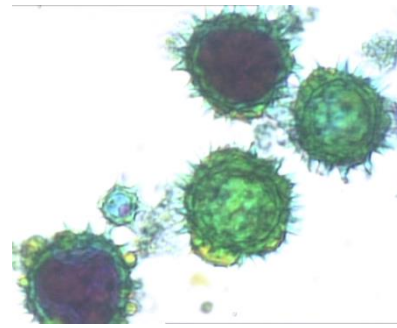


F1 EGG 1626



0%
pollen viability

Chromosome
configurations
32^{II}1^{IV}; 28^{II}3^{IV}



28%
pollen viability

Chromosome
configurations
32^{II}1^{IV}; 30^{II}2^{IV}



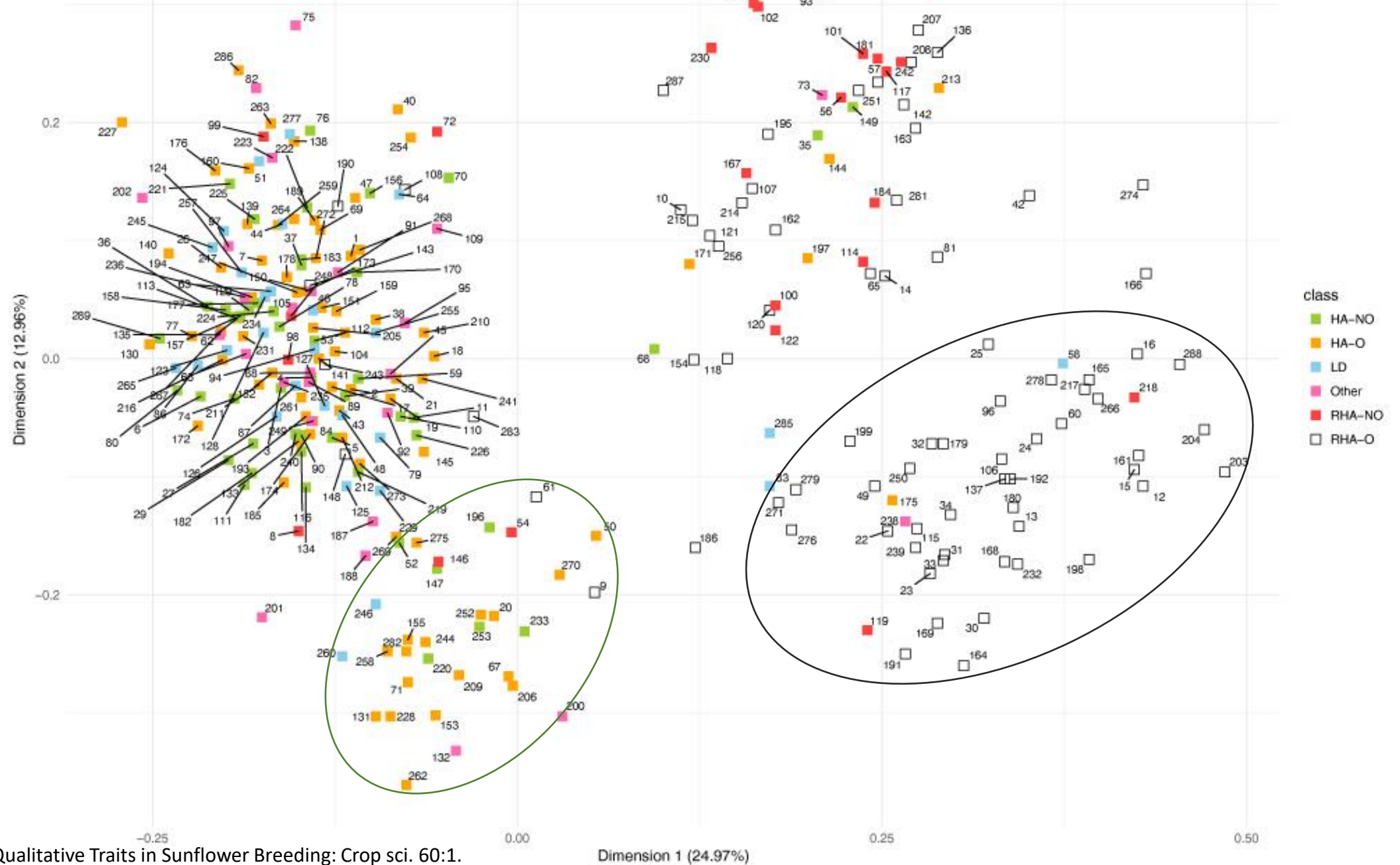
F1 RES 1545




Characterisation

59% of worldwide use of CWR for pest and disease resistance
13% abiotic stress tolerance
11% quality improvement
10% yield increase
4% sterility and fertility restoration

Homogeneity analysis plot of UGA SAM1 accessions based on morphological traits





Orphan/alternative crops...
Helianthus tuberosus

- 141 accessions
- Morphological comparison
- Mineral composition of tubers and leaves
- Total tuber sugar content
- Photoperiod and vegetation phases
- Climatic variables and yield components
- 2 cultivars registered
- New national DUS test guideline developed

Provincial project, 2017-2020 Anatomic characterization of wild sunflower collection as a potential gene pool for cultivated sunflower breeding

7 annual, 21 perennial species;
19 cultivated sunflower inbred lines of various background

All accessions phenologically screened and evaluated for oil content upon introduction to the collection

Phenotypic diversity

Root phenotyping - EPPN²⁰²⁰

COIT WG1 / EPPN2020 workshop, Novi Sad, Serbia, 29-30 September 2017
Current and future applications of phenotyping for plant breeding

Comparative phenotypic analysis of wild and cultivated sunflower for improved crop resilience

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The collection of wild annual and perennial sunflowers in the Institute of Field and Vegetable Crops is one of the largest sunflower collections in the World. Collection was founded for the purpose of sunflower breeding program and first phenotypic evaluation were made in 1970s.

The program was further developed and access collection was established in 1990. The first hybrids resistant to *Phomopsis helianthi* in the world have been created crossing cultivated sunflower genotypes with wild relatives from this collection.

The collection is continuously used in IFVCNS sunflower breeding program, but also as the source of accessions for other research and breeding centers all over the world.

WEBSITE
<http://www.nisem.com/about/invc/collections/wild.php>

Comparative phenotypic analysis of wild sunflower species, along with a parallel analysis of the same traits in cultivated sunflower could enable identification of morphological parameters of various plant organs that could be useful tools for detection of genotypes tolerant to different environmental stresses. We have analyzed the morphological specificity of the plant organs, as well as the molecular diversity of 7 annual, 21 perennial wild sunflower species and 19 genotypes of cultivated sunflower, with the aim to find out if observed characteristics have an effect on seed germination and nutrient use efficiency in stress conditions.

We have also carried out comparative morphological analysis of various vegetative organs of tested *Helianthus* species in order to determine phenotypic indicators of stress tolerance. Preliminary results showed that there is significant phenotypic variability in observed morphological traits between tested genotypes indicating that some of them could be useful in pre-breeding and breeding for increased stress tolerance and identification of genotypes that could be used in sunflower crop improvement.

Part of flower variability of tested accessions

Part of morphological variability of tested accessions

ACKNOWLEDGMENTS
This study was supported by Ministry of Education, Science and Technological Development of Republic of Serbia, project TR31020, and Provincial Secretariats for Higher Education and Science of Vojvodina, project 514-451-2126/2016-03.

Agronomic uses and traits in US CWR

Taxon	Trait	Taxon	Trait
<i>Corylus americana</i>	Eastern filbert blight resistance and other traits	<i>Juglans major</i>	Rootstock for high pH soil
<i>Helianthus anomalous</i>	Fertility restoration genes	<i>Juglans microcarpa</i>	Rootstock for high pH soil
<i>Helianthus argophyllus</i>	Downy mildew resistance	<i>Juglans nigra</i>	Anthracnose resistance
<i>Helianthus bolanderi</i>	Genetic stock	<i>Malus fusca</i>	Graftstock
<i>Helianthus debilis</i>	Powdery mildew resistance	<i>Prunus andersonii</i>	Graftstock
<i>Helianthus deserticola</i>	Downy mildew resistance	<i>Prunus pumila</i>	Graftstock
<i>Helianthus divaricatus</i>	Broomrape resistance	<i>Prunus rivularis</i>	Graftstock
<i>Helianthus giganteus</i>	Fertility restoration genes	<i>Ribes nigrum</i>	Pest and disease resistance. Other useful agronomic traits.
<i>Helianthus grosseserratus</i>	Broomrape resistance	<i>Ribes uva-crispa</i>	Gall mite resistance
<i>Helianthus hirsutus</i>	Fertility restoration genes	<i>Solanum stoloniferum</i>	Late blight resistance
<i>Helianthus maximiliani</i>	Broomrape resistance	<i>Tripsacum dactyloides</i>	Corn leaf blight resistance
<i>Helianthus neglectus</i>	Fertility restoration genes	<i>Vitis acerifolia</i>	Graftstock
<i>Helianthus paradoxus</i>	Salt tolerance	<i>Vitis aestivalis</i>	Graftstock
<i>Helianthus pauciflorus</i>	Cytoplasmic male sterility	<i>Vitis cinerea</i>	Graftstock
<i>Helianthus petiolaris</i>	Verticillium resistance	<i>Vitis cinerea var. helleri</i>	Graftstock
<i>Helianthus praecox</i>	Downy mildew, rust, verticillium wilt and broomrape resistance	<i>Vitis labrusca</i>	Cold tolerance
<i>Helianthus resinusus</i>	Fertility restoration genes	<i>Vitis monticola</i>	Graftstock
<i>Helianthus strumosus</i>	Fertility restoration genes	<i>Vitis mustangensis</i>	Graftstock
<i>Helianthus tuberosus</i>	Broomrape resistance	<i>Vitis riparia</i>	Phylloxera vitifoliae resistance



Disease incidence observed in a seven year period on **perennial *Helianthus* species** in a naturally infected field

<i>Helianthus</i> species	Number of acc.	Powdery mildew	Alternaria leaf spot	Stem canker	Sclerotinia head rot
<i>H. californicus</i>	1				
<i>H. decapetalus</i>	8	1	1		1
<i>H. divaricatus</i>	10	1			
<i>H. eggertii</i>	2	1			
<i>H. giganteus</i>	16	11	2		
<i>H. glaucophyllus</i>	1				
<i>H. grosseserratus</i>	32	20	8		
<i>H. hirsutus</i>	4	3			
<i>H. laevigatus</i>	6	2			
<i>H. maximiliani</i>	37	25		3	1
<i>H. microcephalus</i>	2				
<i>H. mollis</i>	9	6	1		
<i>H. x multiflorus</i>	1				
<i>H. nuttallii</i>	23	17	5		
<i>H. rigidus</i>	14	11			
<i>H. resinusus</i>	2				
<i>H. salicifolius</i>	2				
<i>H. silphioides</i>	1				
<i>H. smithii</i>	2				
<i>H. strumosus</i>	21	9		1	
<i>H. tuberosus</i>	141	135		2	1
Total:	336	242	17	6	3

Disease incidence observed in a seven year period on **annual *Helianthus* species** in a naturally infected field



Annual species	Total acc.	Powdery mildew <i>Erysiphe chichoracearum</i>	Black stem <i>Phoma macdonaldii</i>	Sclerotinia rot <i>Sclerotinia sclerotiorum</i>	Stem canker <i>Phomopsis Helianthi</i>	Charcoal rot <i>Macrophomina phaseolina</i>	Alternaria leaf spot <i>Alternaria helianthi</i>	Broomrape <i>Orobanche cumana</i>
ANN	121	34	104	32	96	10	4	75
ARG	8	3	7	2	4			1
DEB	29	7	13	3	4	1	5	
DES	1							
NEG	17	3	11	2	4	1	3	
NIV	8	1			2		2	
PET	34	5	22	4	22		1	7
PRA	26	7	14	4	2	4	1	1
Total:	244	60	171	47	134	16	16	84

Find new sources of resistance genes to the new broomrape races

Long-term program
(wild relatives)



Short-term program
(inbred lines in gene bank)



Testing wild species



Testing F_1 hybrids



Backcrossing F_1 with cultivated line
Sowing F_1 and producing F_2



- Wild species evaluated in a long term characterization program since 1990s
- Greenhouse controlled conditions and infested fields
- Most recent resistance test included 7 annual *Helianthus* species and 182 accessions
- Highest resistance found in *H. petiolaris* and *H. niveus*

Helianthus spp.	Total No. of accessions	Resistant accessions within species	Resistant plants within accessions
<i>H. petiolaris</i>	31	0.81	0.98
<i>H. niveus</i>	6	0.67	0.94
<i>H. argophyllus</i>	6	0.67	0.86
<i>H. debilis</i>	24	0.58	0.85
<i>H. praecox</i>	25	0.52	0.84
<i>H. neglectus</i>	17	0.47	0.77
<i>H. annuus</i>	73	0.14	0.37
Susceptible check AD66		0	0

- F1 interspecific crosses with perennial species had almost 100% resistance
- Interspecific crosses with annuals species used to develop pre-breeding genepools

White head rot (*Sclerotinia sclerotiorum*)

Mid-stalk rot, head rot
Artificial inoculation
Screening of wild species in the field



Tolerance to capitula rot found in sunflower species *H. debilis* and *H. argophyllus*

Charcoal rot (*Macrophomina phaseolina* (Tassi) Goid.)

The results indicated that *H. annuus*, *H. tuberosus* and *H. petiolaris* can be used as a source of resistance to *M. phaseolina*



Downy mildew (*Plasmopara Halstedii*)

According to Seiler (2012), complete resistance to the downy mildew pathogen can be found in several annual and perennial wild sunflower species

When the donor lines are used in commercial breeding programs they have to be crossed with inbred lines which have desirable agronomical traits (Jocić et al. 2010)



IFVC trial:
6 annual species, 29 accessions
Plasmopara race 4 (730)
Resistance: *H. annuus* and *H. argophyllus*

Black stem disease (*Phoma macdonaldii*)

Tested in controlled conditions, high level of resistance confirmed



Phomopsis Stem canker (*Phomopsis helianthi*)

Tolerance to Phomopsis stem canker was found in the perennial species *H. maximiliani*, *H. pauciflorus*, *H. hirsutus*, *H. resinosus* and *H. tuberosus* (Škorić 1985; Dozet 1990)

141 accessions of *Helianthus tuberosus* from the IFVCNS collection were tested

Accessions TUB2046, TUB2062 and TUB CG 65 were most tolerant



The effects of a full treatment with Express total herbicide
(active ingredient - tribenuron methyl)
7 annual species, 73 accessions tested



Sensitive plants of
Helianthus annuus



Resistant plants of
Helianthus argophyllus

Biotechnology

Natural interspecific hybridisation in the genus *Helianthus*...

GENETIC DISTANCE

- Difference in chromosome number
- Difference in chromosome structure

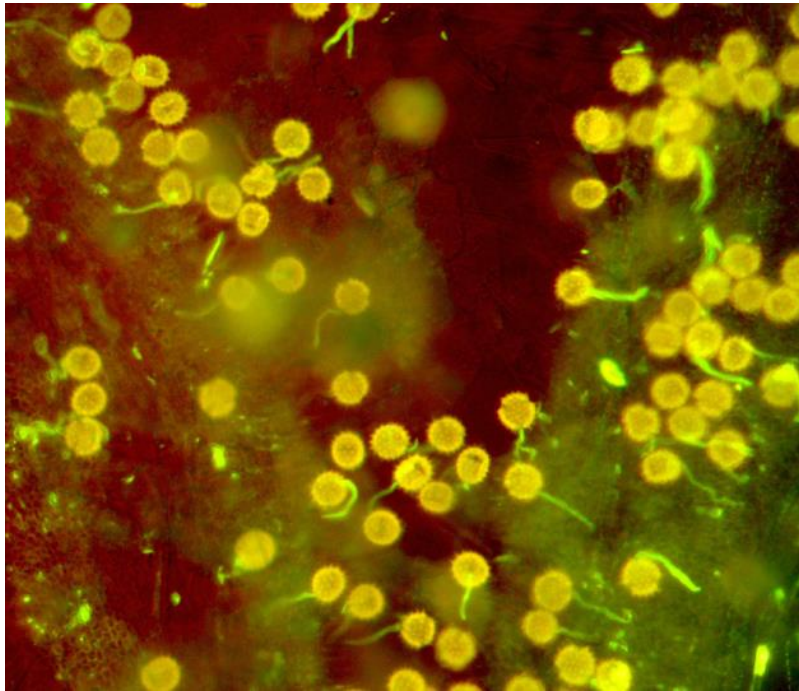
PROBLEMS

- Poor viability of seeds of wild species
- Long growing season and non uniform flowering
 - Auto sterility
 - Incompatibility
 - Abortion of hybrid embryo
- Sterility of F₁ and F₂ interspecific hybrids

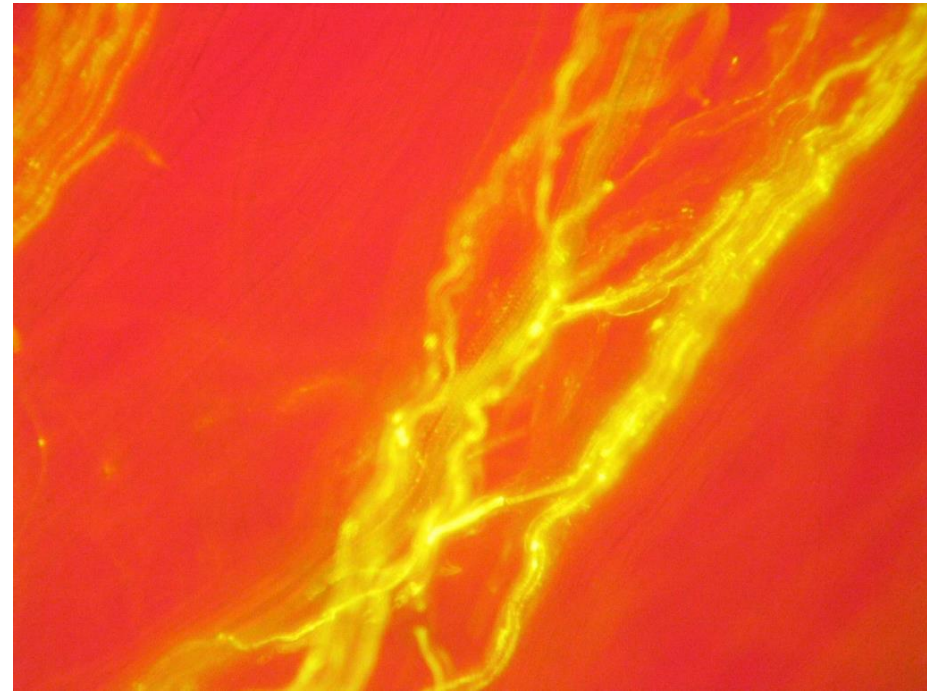
SOLUTIONS

- Chromosome doubling
- Tissue culture
- Embryo culture

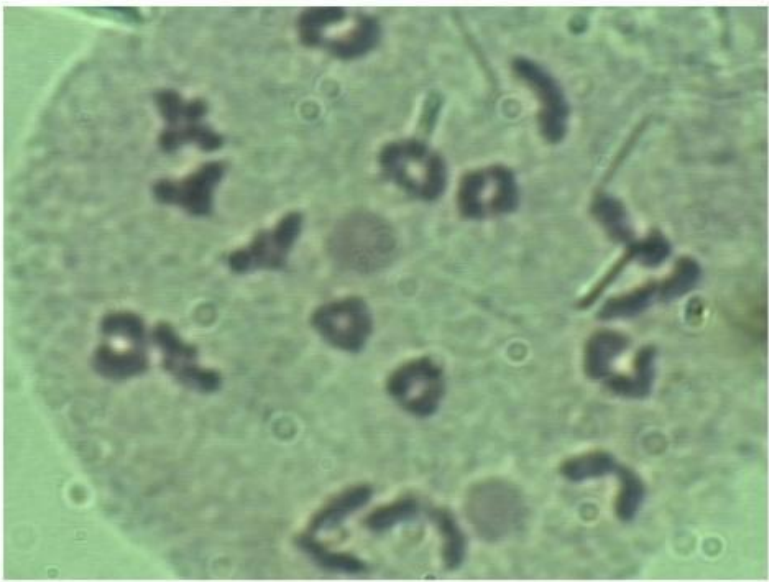
Fluorescent microscopy



Pollen germination



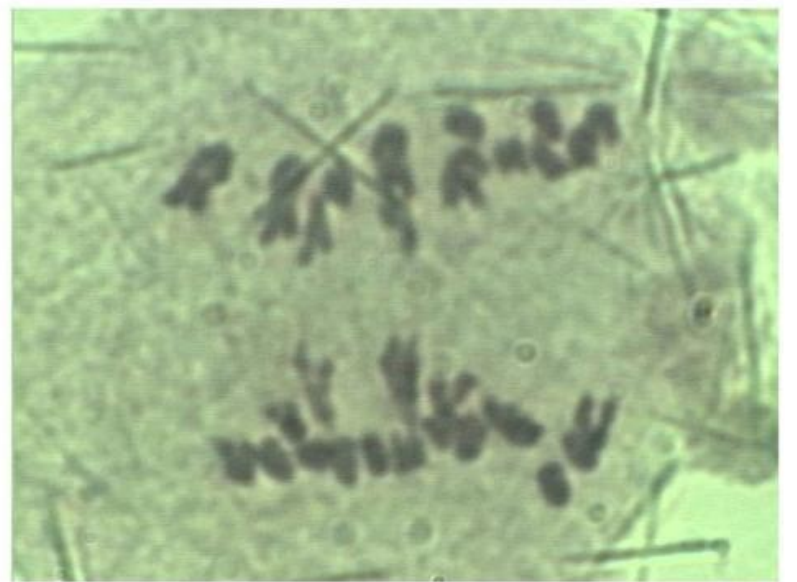
Pollen tube growth



A) DIAKINESIS

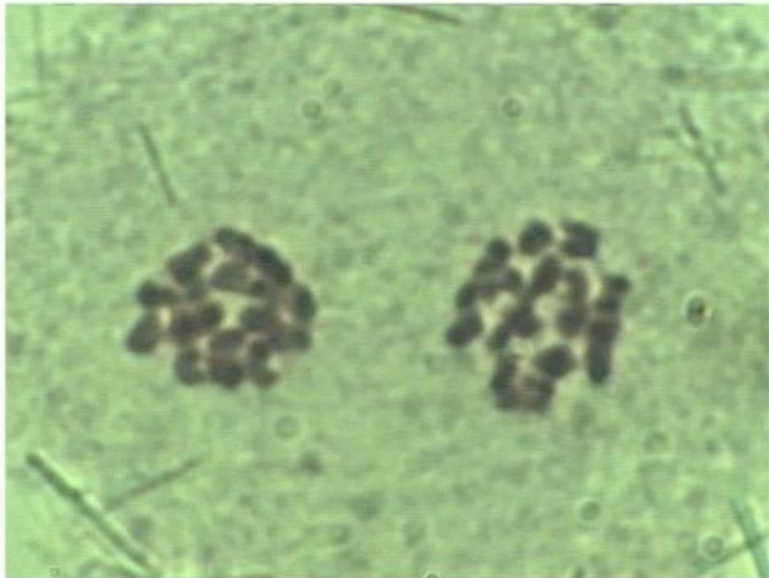


B) METAPHASE I

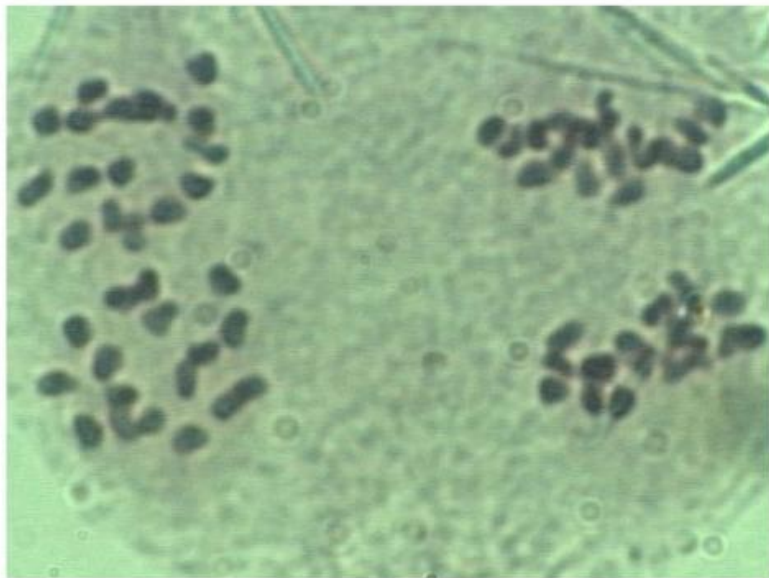


C) ANAPHASE I

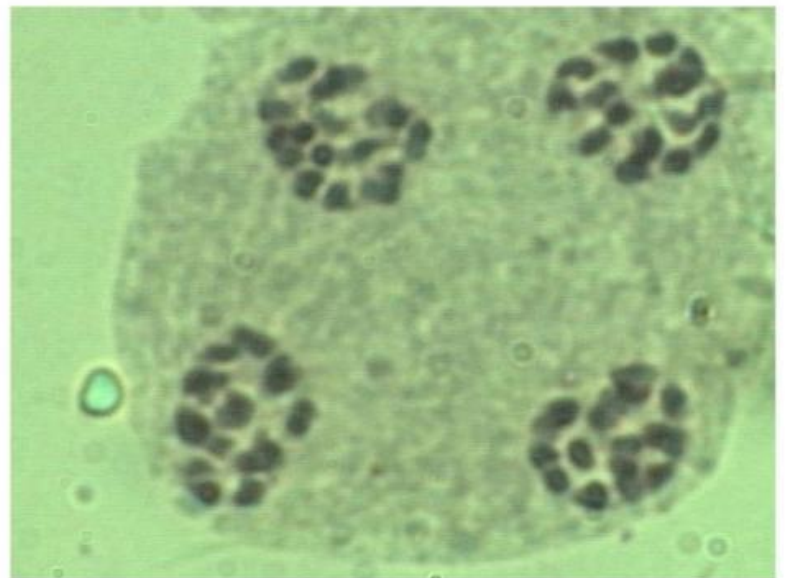
Regular phases of meiosis



D) TELOPHASE I

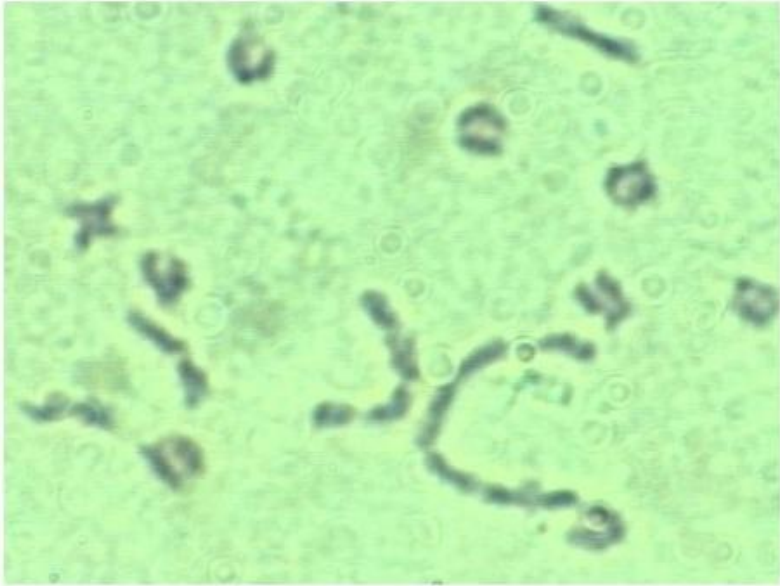


E) ANAPHASE II



F) TELOPHASE II

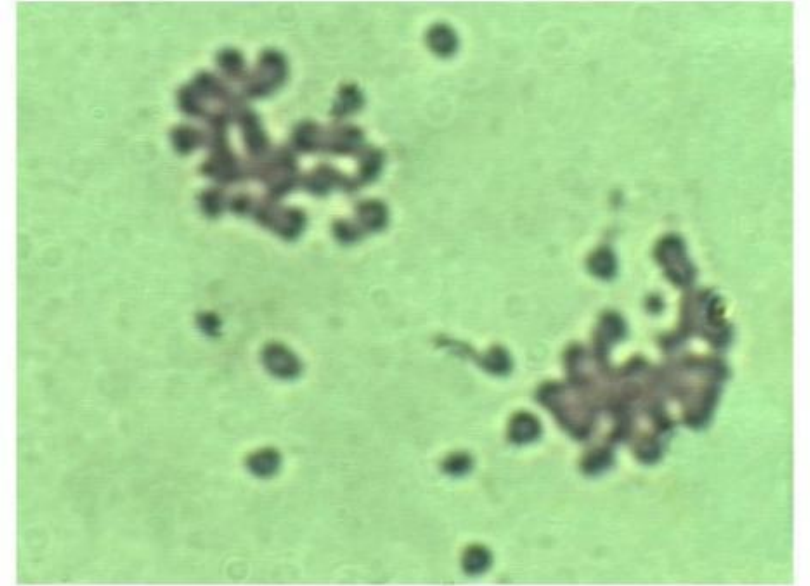
Irregular phases of meiosis



A) Diakinesis with a quadri and a hexavalent



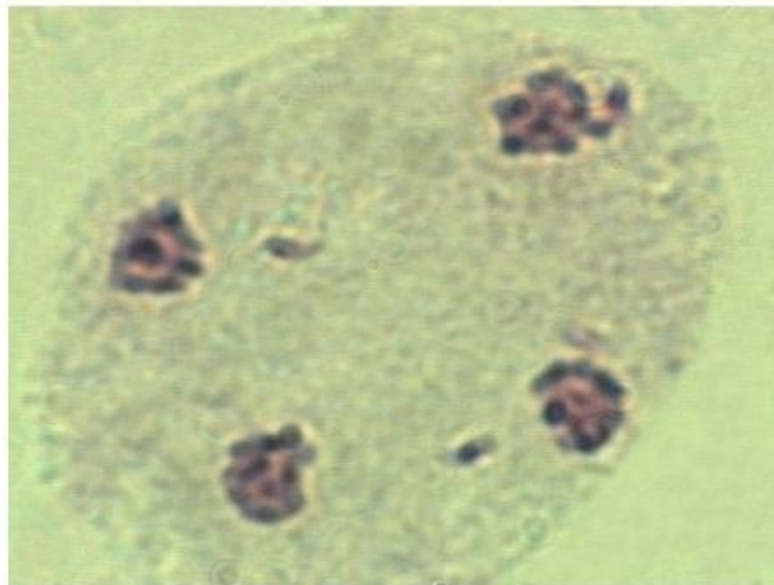
B) Metaphase I with fast chromosomes



C) Anaphase I with lagging chromosomes



D) Anaphase I with a chromosome bridge

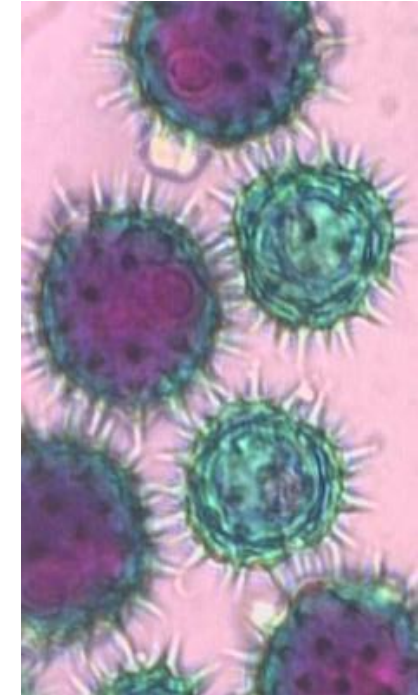
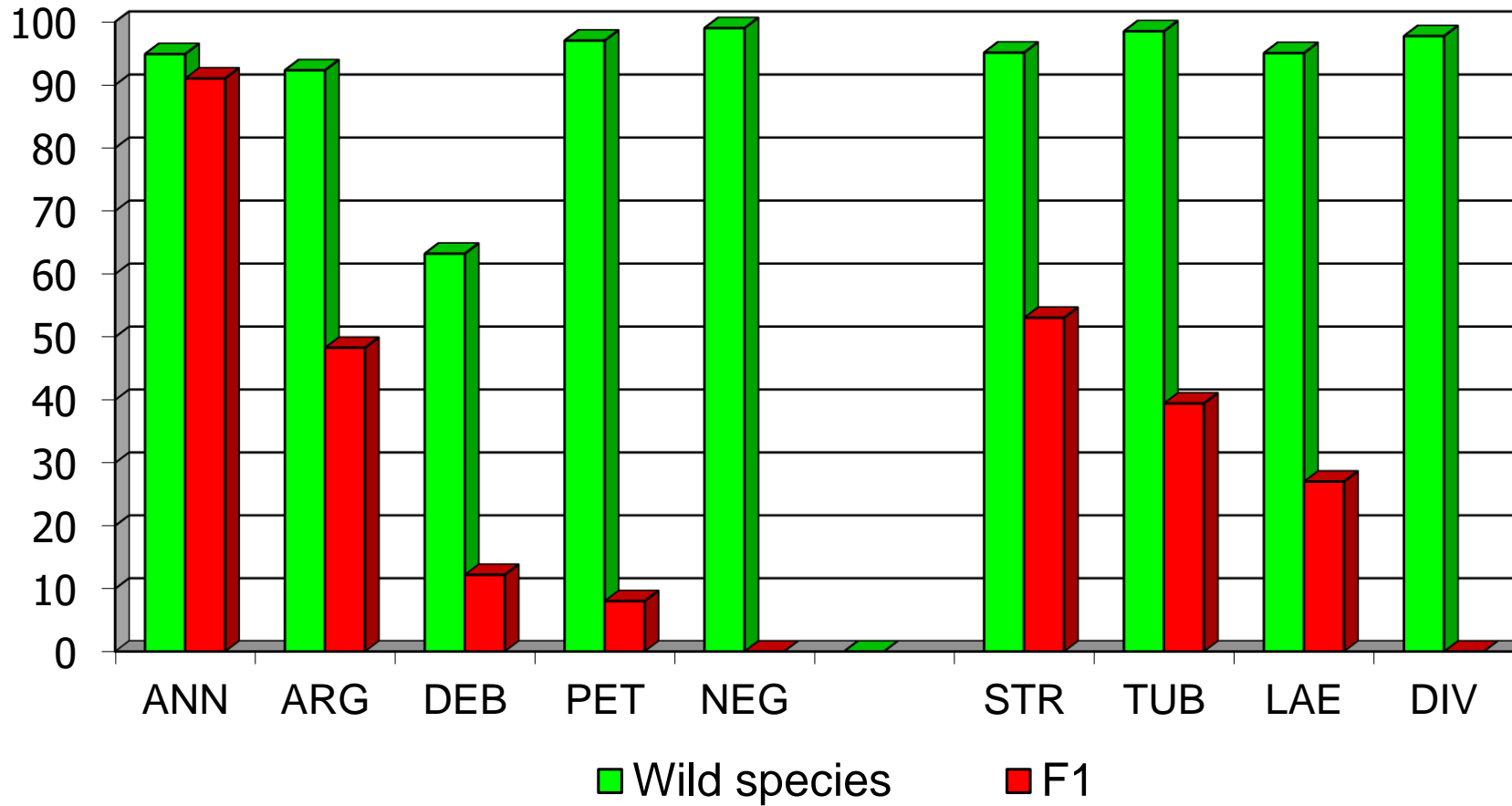


E) Telophase II with lagging chromosomes



F) Telophase II with chromosome bridges

Pollen viability:



Genotyping in sunflower - Mapping traits, describing the diversity of germplasms and genomic prediction

Sequencing the sunflower genome - XRQ inbred line
Described in Nature 546, 148–152 (2017)

To date, three high quality genomes are available: XRQ, HA412 and PSC8

In 2019, a pan genome (gene content variation across the cultivated gene pool) based on re-sequencing of 287 cultivated sunflower lines (UGA SAM1) 17 Native American landraces and 189 wild accessions across three gene pools:

Primary: *H. annuus*

Secondary: *H. petiolaris*, *H. neglectus*, *H. argophyllus*, *H. anomalus*, *H. debilis*, *H. paradoxus* and *H. praecox*

Tertiary: *H. divaricatus*, *H. grosseserratus* and *H. giganteus*

The International Consortium on Sunflower Genomics, grouping 4 public research institutes and 8 private partners, aims to sequence reference genomes for wild sunflowers and wild relatives

Interspecific crosses

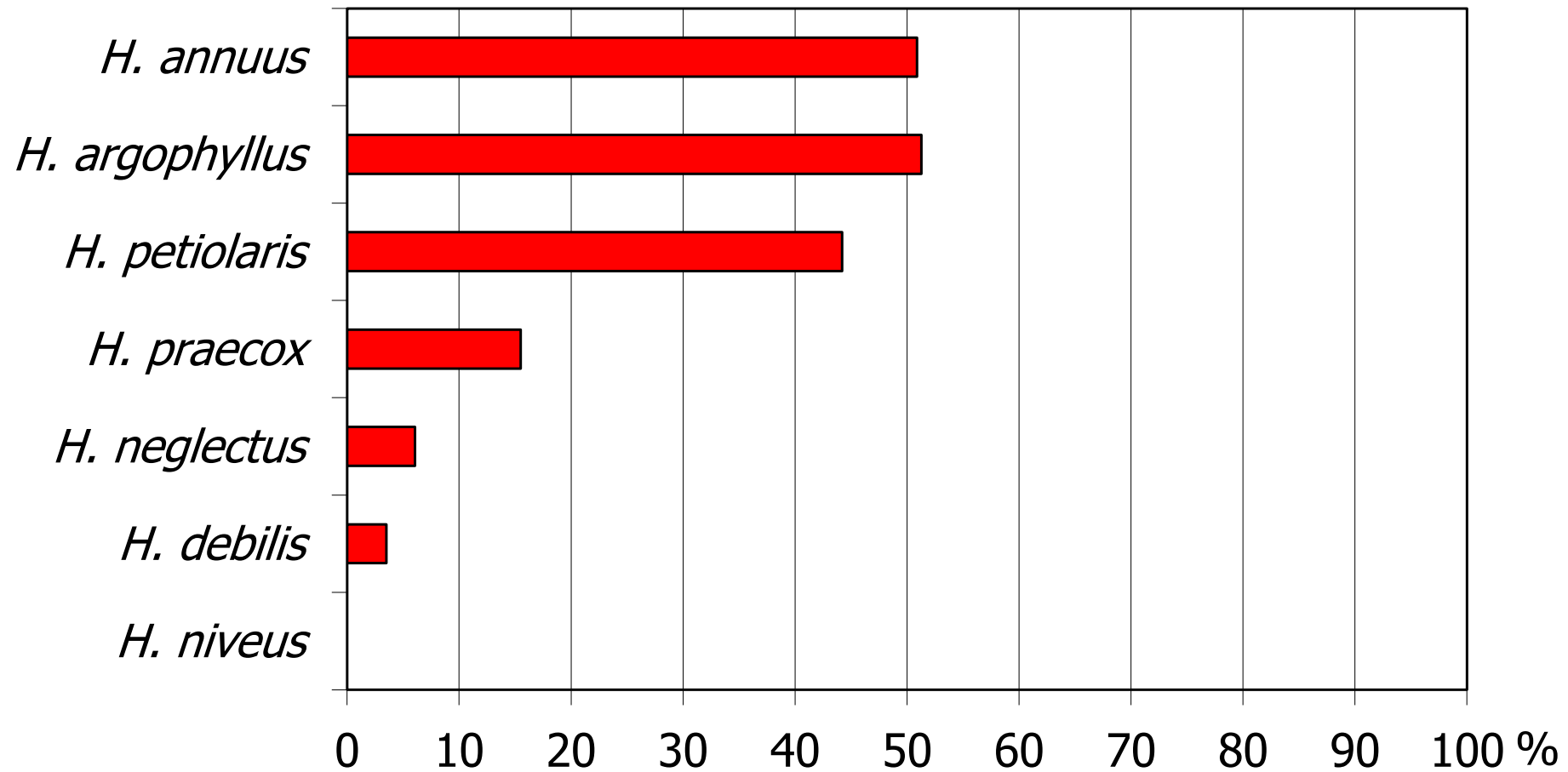
Interspecific crosses:

Introduction of unwanted phenotypic traits can not be avoided in classical interspecific crosses

- Hybridization methods: classical-pollination, protoplast fusion, somatic hybridisation. . .
- 7 annual and 16 perennial species crossed with cultivated sunflower at IFVCNS
- Perennial species are harder to cross, but interspecific hybrids are obtainable

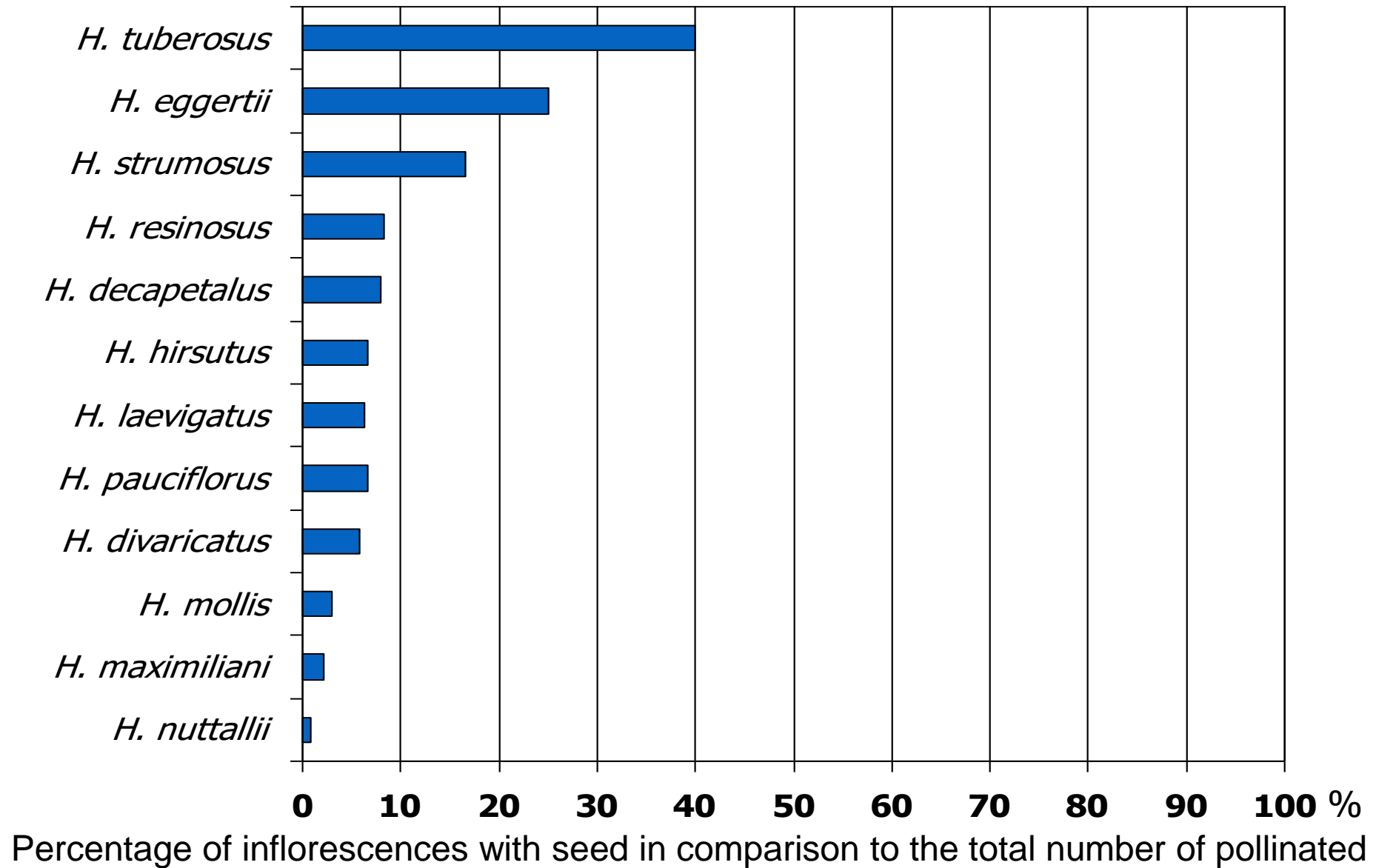


The success of interspecific crosses with annual species



Percentage of inflorescences with seed in comparison to the total number of pollinated

The success of interspecific crosses with perennial species



H. rigidus



F₁ hybrid

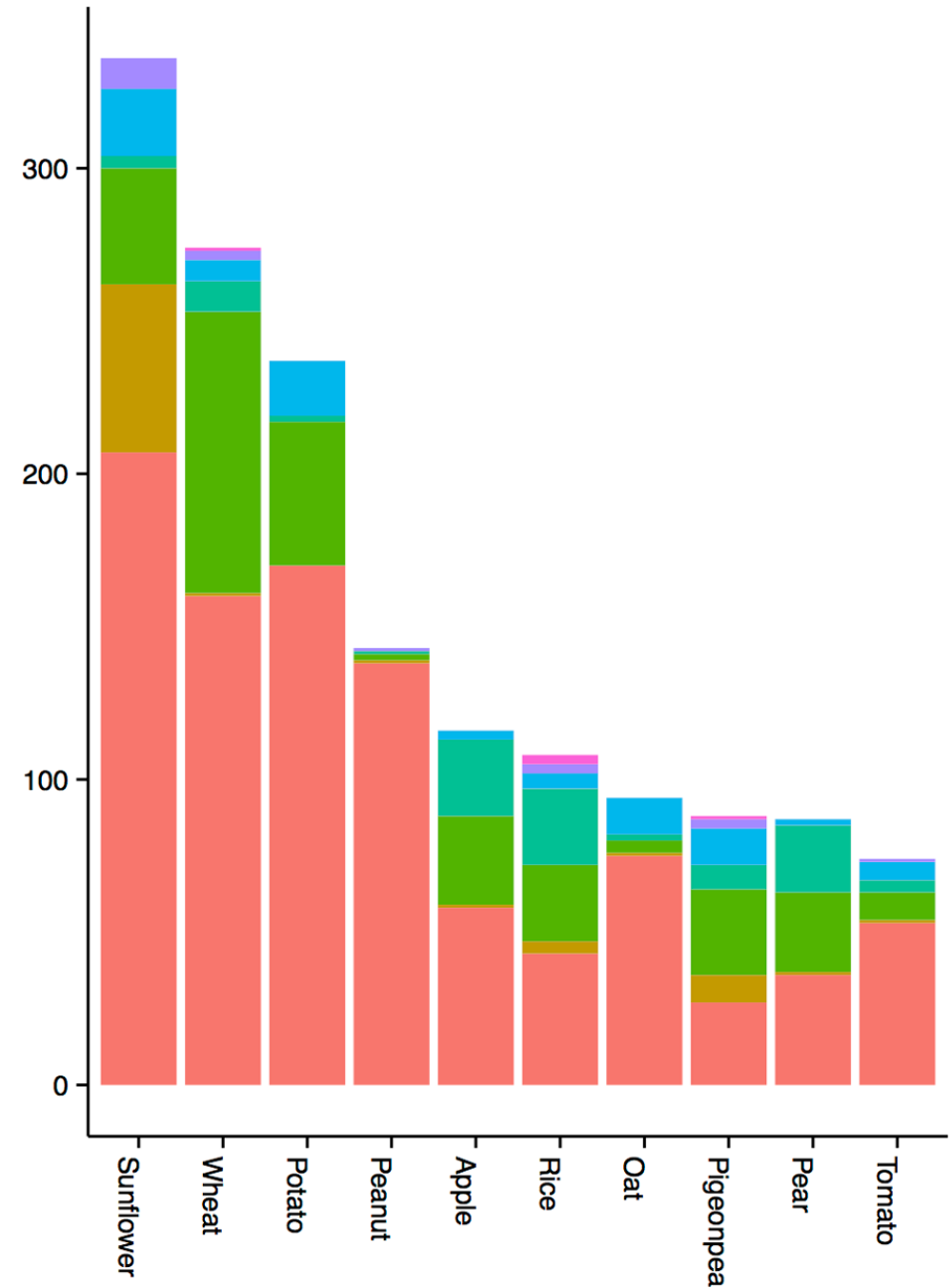


Cultivated line



Confirmed and potential “breeding uses” of the 10 crops with most “breeding use” citations in the literature, categorized in trait classes

- 5 Agronomic traits
- 10 Phenological traits
- 25 Quality characters
- 40 Abiotic stresses
- 60 Male fertility restoration
- 210 Biotic stresses



High-throughput phenotyping – Low information sharing!?

Accessions are populations, not inbred lines...!

Species diverse in vegetation phases, habitus... Making automated phenotyping demanding
Greenhouse platforms, unmanned aerial or ground based vehicles...

Information portals should be used more to share the results/improve the usage of CWR

Eurisco (The European Search Catalogue for Plant Genetic Resources)

AEGIS (A European Genebank Integrated System)

U.S. National Plant Germplasm System

France: The PhenoDB INRAE database <https://sunrise.toulouse.inra.fr/phenoDB/>

Prebreeding – specific traits

***H. mollis* – sessile leaves**

cms9 x *H. mollis*

Sterile F₁

2 back crosses with rf line

Pedigree selection producing
new lines

Crosses with testers and paralel
tests for sclerotinia resistance

Shorter leaf petiole

Oil content variable

Inflorescence not inclining...

Broomrape resistance

1. Annuals and perennials, F₁ hybrids with perennials
2. Annual wild acc, F₁ with annual species
3. BC₁ produced and tested
4. BC₂ followed by selfing and further tests

Highest percentage of resistant plants in F₁ and BC₁F₁

Sclerotinia – head rot tolerance

1. 44 interspecific progenies with 6 annual wild
2. Field test and selfing of selected plants, 3-4 cycles
3. Pedigree selection producing new lines

Material from *H. debilis* with highest tolerance

Interspecific lines obtained from USDA, Seiler (1991)

6-7 years, pre-breeding

RES-834-1 (cms HA 89*2/H. resinosus 834) F5)

PRA-RUN-1329-1 (nms P21*3/H. praecox 1329) F3)

DEB-SIL-367-2 (cms HA 89*3/H. debilis 367) F3)

DES-1474-2 (cms89*2/H. deserticola 1474)//RHA 274 F4)

3 years of selfing
Field observations and
pedigry selection

16 selected male fertile lines

H. resinosus: 1RES, 2RES, 5RES

H. debilis : 8DEB-SIL, 9DEB-SIL 10DEB-SIL

H. praecox : 11PRA-RUN, 12PRA-RUN, 13PRA-RUN, 14PRA-RUN

H. deserticola: 16DES, 17DES D, 18DES D, 19DES D, 20DES



8 years
CMS form

Three IFVC Rf lines
with good GCA
utilized as testers

Confectionary sunflower lines

Interspecific lines produced at IFVCNS, Terzić (2006)

HA-26 (hand emasculatation)



- *H. debilis* 1848
- *H. praecox* 1341
- *H. petiolaris* 2119
- *H. annuus* 2168
- *H. neglectus* 1181



Prebreeding material

- F1 S1 DEB 1848
- F1 S1 DEB 1848
- F1 S1 PRA 1341
- F1 S1 PRA 1341
- F1 S1 PRA 1341
- BC2 PET 2119
- BC2 PET 2119
- BC2 S2 ANN 2168
- BC2 S2 ANN 2168

3-6 years

Pedigree selection

RHA lines

- Ts-s-1-17
- Ts-s-1-22
- Ts-s-1-192
- Ts-s-1-200
- Ts-s-1-202
- Ts-bc-30
- Ts-bc-31
- Ts-bc-44
- Ts-bc-45

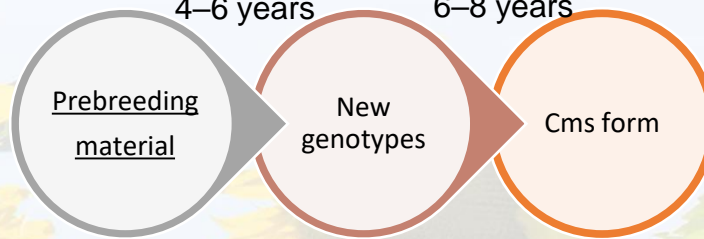
3-5 years

3-5 years

B-lines

Pedigree selection
4-6 years

6-8 years



Oil sunflower lines

Future prospects

The evolving field of phenomics will help accelerate sunflower CWR exploitation for introgression breeding by increasing the number of evaluated traits and accessions – thus more understanding their diversity

Existing sunflower collections could benefit from closer cooperation to improve the quality and availability of materials conserved: tackle issues like local gene bank standards, germplasm availability and characterisation data, genetic drift, pollination... *Gene bank peer review - AEGIS*

Intellectual property rights imposed by the funding body sometimes put further constraints... But international cooperation is possible and for major tasks like Sclerotinia and broomrape resistance it is necessary!

Gene banks for wild and cultivated sunflower genetic resources [☆]

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Thank you for your attention !!!

