ICARDA
Science for resilient livelihoods in dry areas

Continuum between conservation and use of plant genetic resources: strengthening pre-breeding at ICARDA

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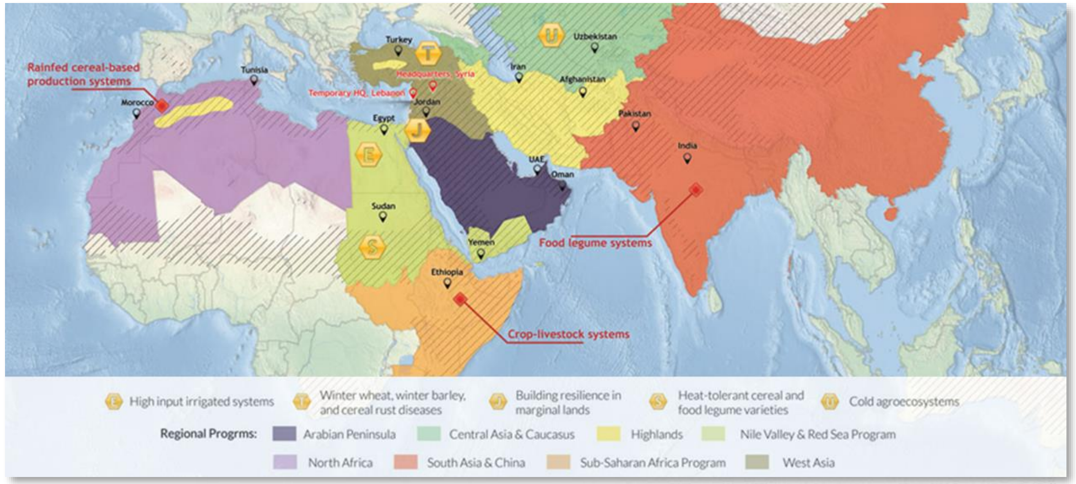
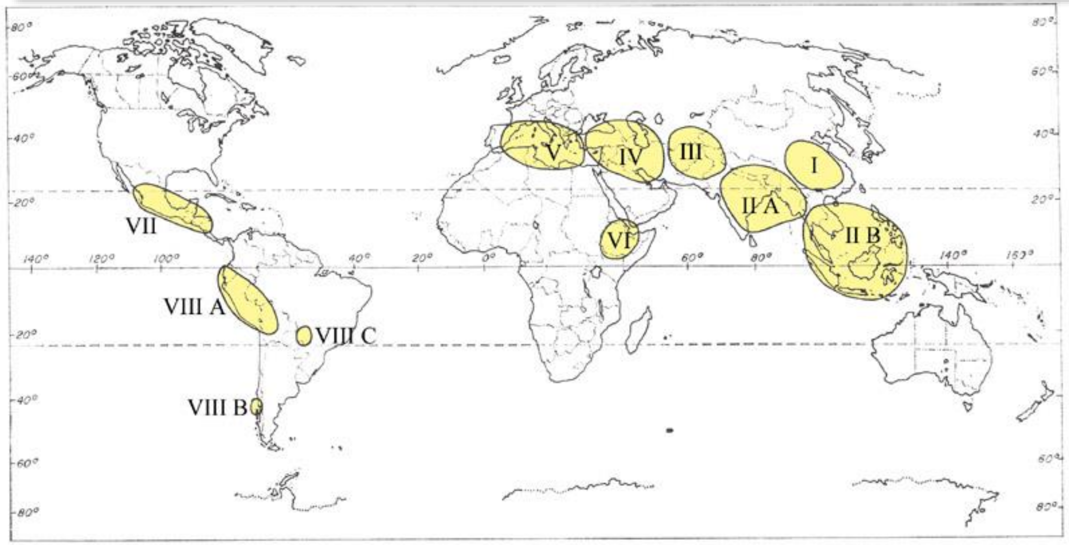
icarda.org
International Center for Agricultural Research in the Dry Areas

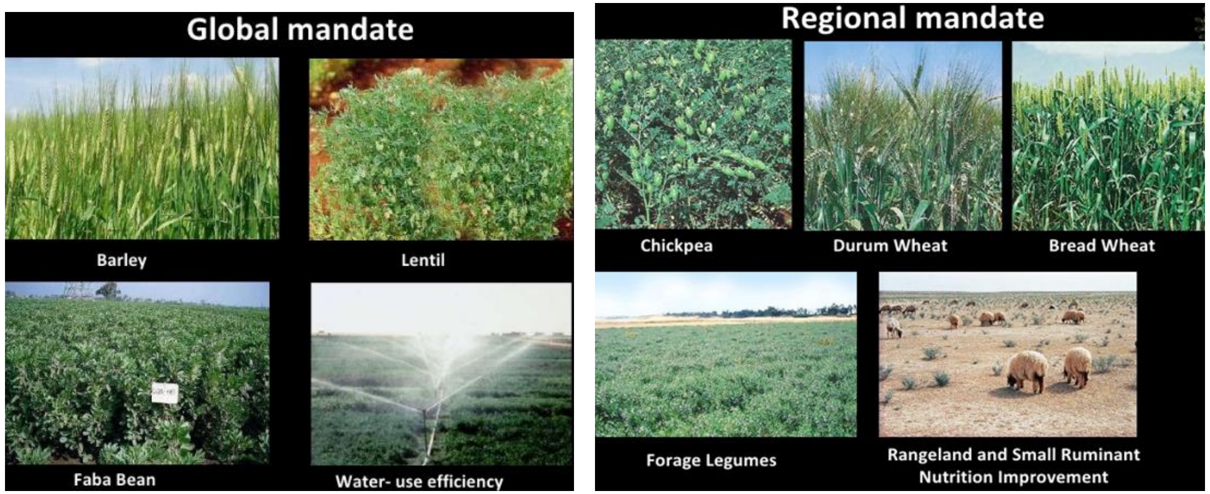
cgiar.org
A CGIAR Research Center

ICARDA at a glance

Reduce poverty and enhance food, water, and nutritional security and environmental health in the face of global challenges including climate change.





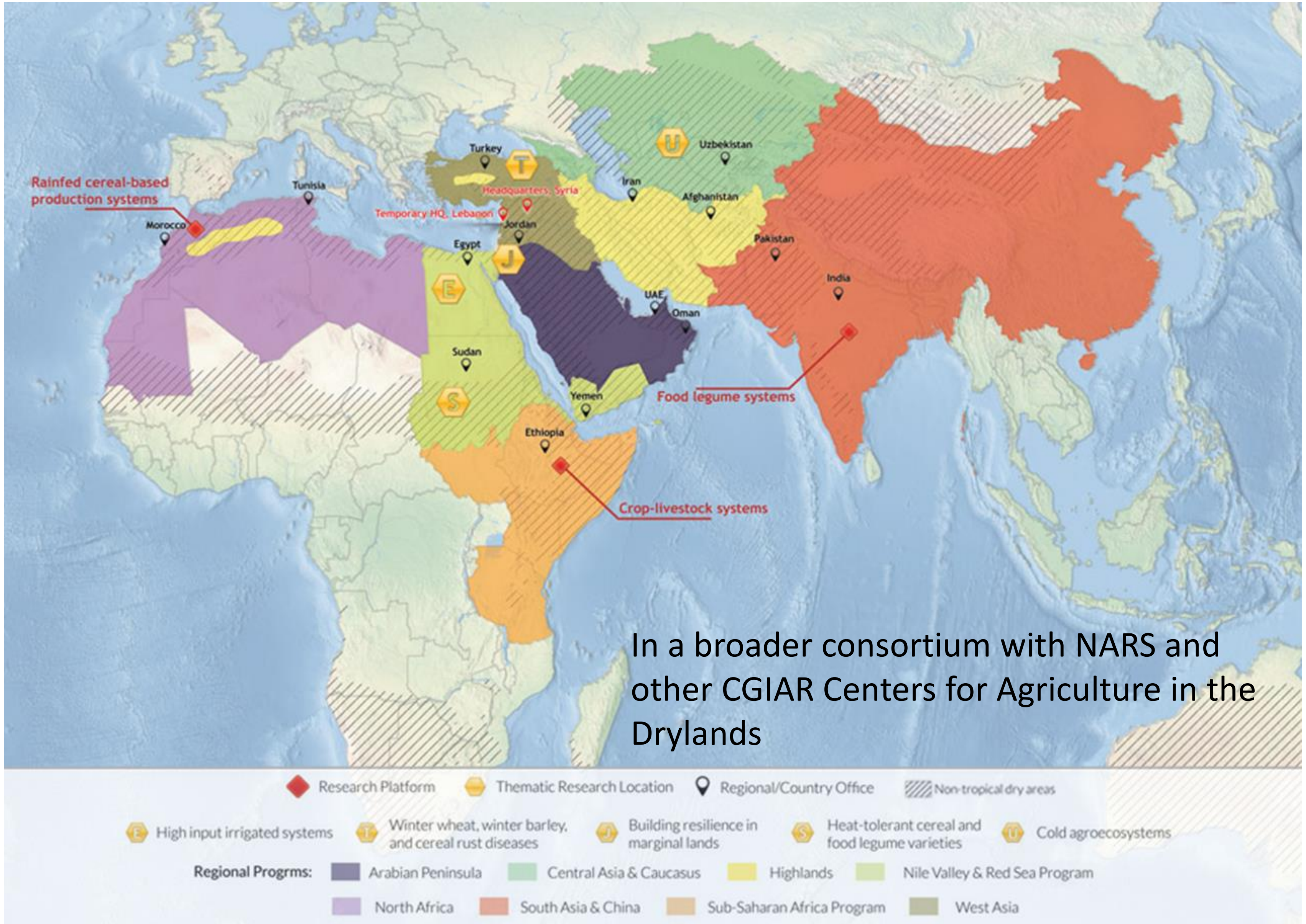


Global and regional mandates of ICARDA

ICARDA operates within four major centers of diversity and contributes to conservation of genetic resources of crops and forages of global importance

ICARDA is a Decentralized Global R4D Center on Dryland Agriculture combining Component Research and Systems Research

Staff: 400
Scientists: 80



In a broader consortium with NARS and other CGIAR Centers for Agriculture in the Drylands

Genetic Resources Activities at ICARDA

collect | conserve | characterize | evaluate/use | document | distribute

Second level Safety duplication at Svalbard

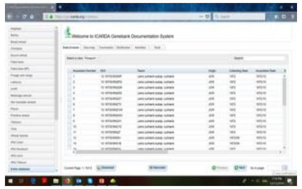
Lebanon: Collections of faba bean, forage Lathyrus, and range species and crop wild relatives (90,000)

Morocco: Collections of cultivated species of barley, wheat, lentil and chickpea (150,000 acc.)

- **Genetic diversity, Collected, analyzed and conserved**
- **Gap analysis**
- **FIGS development**
- **Research on best practices**
- **Evaluation of germplasm**
- **Pre-breeding**





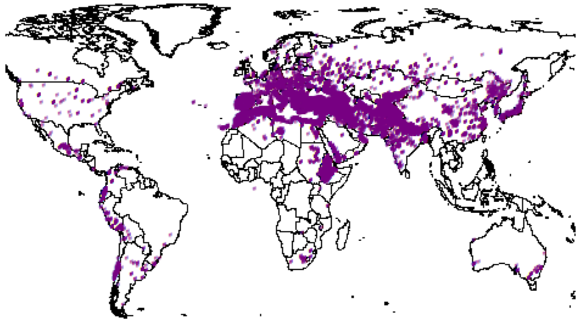



- ***In situ* conservation of agro-biodiversity**
- **Development of field guides**
- **Herbarium maintenance**
- **Rhizobium collection**
- **Participation to GRFA Global System**

Preserving the past for the future

Taxon	Syria Up to 2012	Morocco up to Feb. 2020	Lebanon Up to Feb. 2020	Total accessions in Feb. 2020	Total unique in 2 location Feb. 2020
Bread wheat	14,100	14138	2034	15090	14423
Durum wheat	19,635	19825	1529	20516	19852
Primitive wheat	912	570	491	1280	1041
Aegilops	4057		4444	5157	4371
Wild *Triticum*	1584	117	1824	1829	1824
Barley	28,465	29517	3710	30210	29595
Wild *Hordeum*	1989		2050	2580	2050
Chickpea	14,214	11871	698	15195	12558
Wild *Cicer*	270		477	554	477
Lentil	10,496	13265	655	13978	13746
Wild *Lens*	587		553	619	617
Faba bean	9542		8671	10034	8511
Lathyrus	3996		3350	4451	3350
Pisum	6106		4152	6132	4152
Medicago	8398		7529	9133	7529
Trifolium	4536		5602	5900	5602
Vicia	6144		5733	6561	5733
Range and pasture	5802		5843	7351	5843
Others	219	77	160	310	236
Total	141,052	89380	59505	156929	141510

Crop genepool	Global Ranking	% acc. globally
Barley	2nd	19.0
Wheat	4th	14.6
Chickpea	2nd	23.2
Faba bean	1st	89.1
Lentil	1st	43.5
Lathyrus	1st	63.6
Medicago	2nd	15.0
Pisum	3rd	12.1
Trifolium	3rd	9.0
Vicia	1st	23.7
Overall	4th	4.0

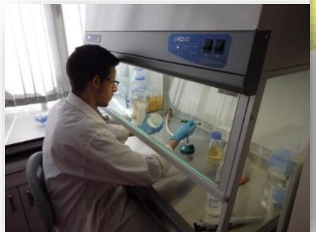


Total taxa	**865**
Perennial	**> 100**
Cross-pollinated	**> 130**
% unique accessions	45
% landraces and native species	65-85
% characterized	78
% safe duplicated	98
% stored in Svalbard	80
Number of Rhizobium strains	1,380

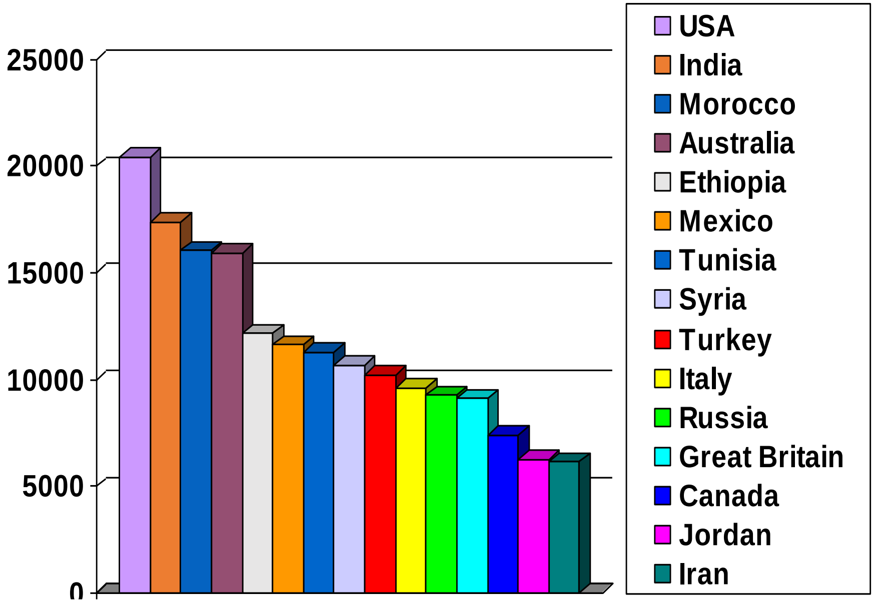
1,468 Rhizobia strains conserved at ICARDA (lyophilized)

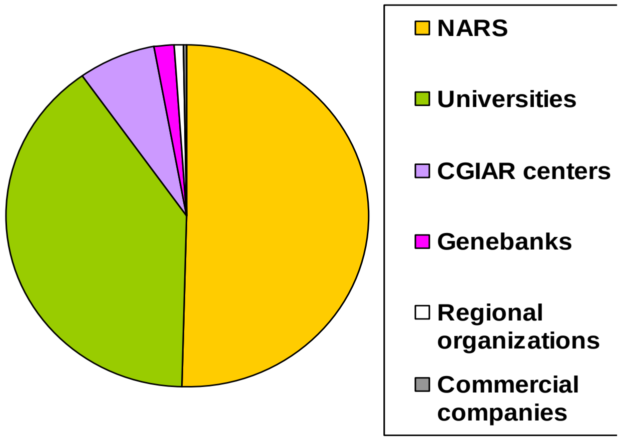
Taxon	Strains	Origin (Region)
Rhizobium ciceri	99	18 countries (49-WANA, 10-America, 20-Asia, 13-Europe, 7-Unknown)
Rhizobium meliloti	685	9 countries (677-WANA, 6-Australia, 2-Unknown)
Rhizobium trifolii	244	4 countries (243-WANA, 1-Unknown)
Rhizobium leguminosarum	440	18 countries (387-WANA, 8-Africa, 28-America, 7-Asia, 4-Europe, 1-Australia, 5-Unknown)

Strains originated at ICARDA - 1298
Strains donated to ICARDA – 170 : AUS(3), CYP(2), DZA(1), ESP(6), FRA(21), GBR(1), IND(12), ITA(2), LBY(1), MAR(52), NZL(1), SYR(1), TUN(7), TUR(6), USA(47), THA(3)



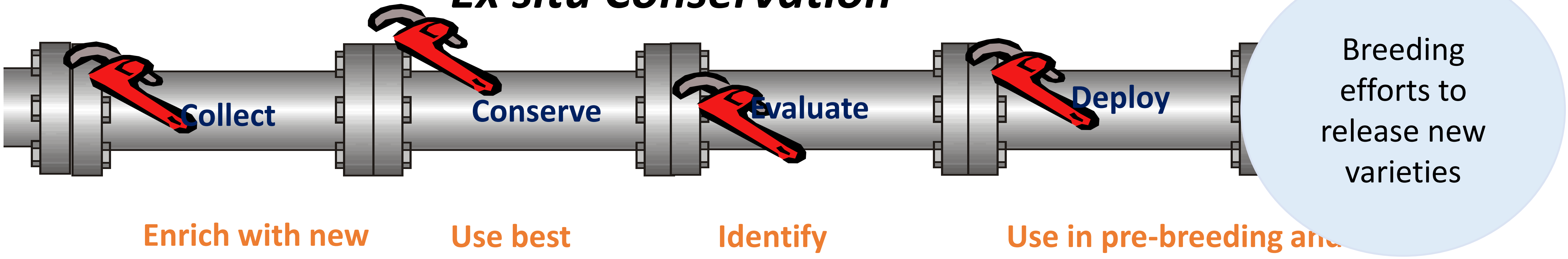
ICARDA distributes more than 20,000 accessions on average annually Up to 2017


Top 15 country recipients of material


Main users

Activities of ex situ and in situ conservation approaches

Ex situ Conservation



Collect

Conserve

Evaluate

Deploy

Breeding efforts to release new varieties

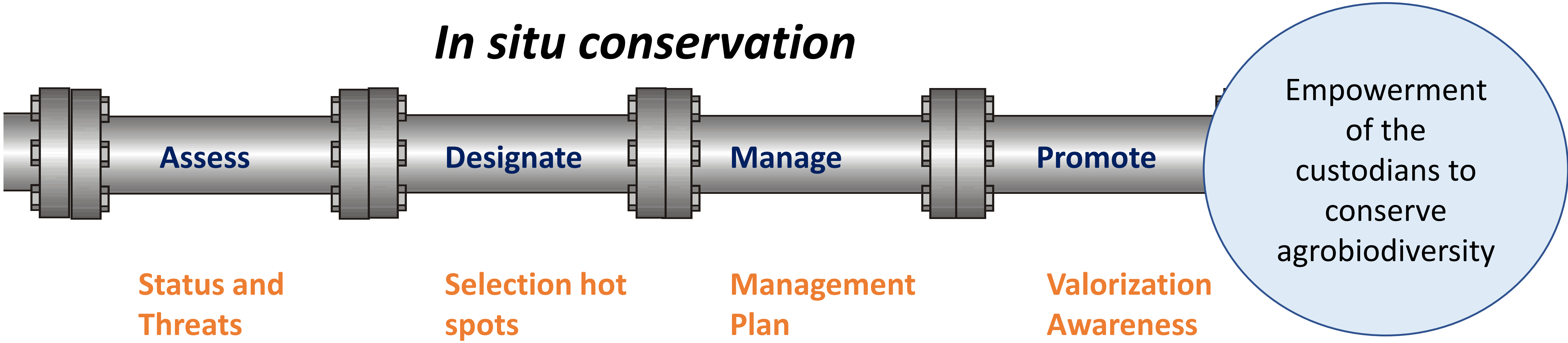
Enrich with new accessions

Use best practices

Identify valuable traits

Use in pre-breeding an breeding

In situ conservation



Assess

Designate

Manage

Promote

Empowerment of the custodians to conserve agrobiodiversity

Status and Threats

Selection hot spots

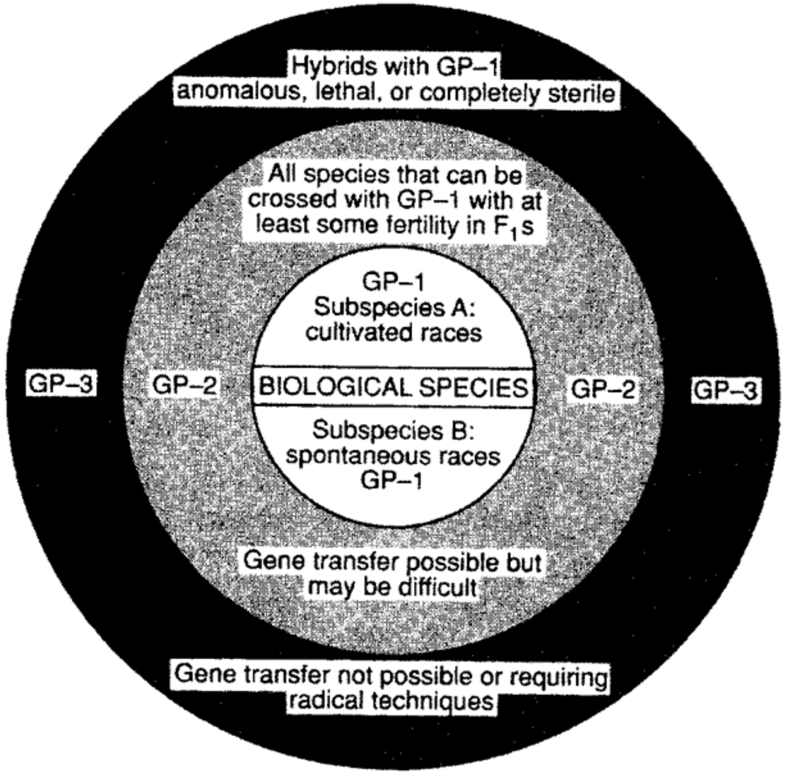
Management Plan

Valorization Awareness

Making genebanks more useful

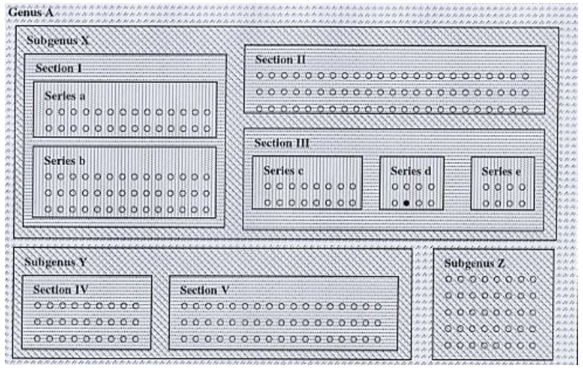
- Traits targeted collecting to fill the gaps
- Mining collections for useful traits including efficient sub-setting targeting traits
- Gene discovery: Phenotyping and genotyping
- Strong pre-breeding
- Gene deployment strategy

The value of conserved genetic resources is in their ability to supply continuously novel diversity needed by breeders and for rehabilitation of degraded systems



Genetic approach
Genepool concept (Harlan and De Wet, 1971)

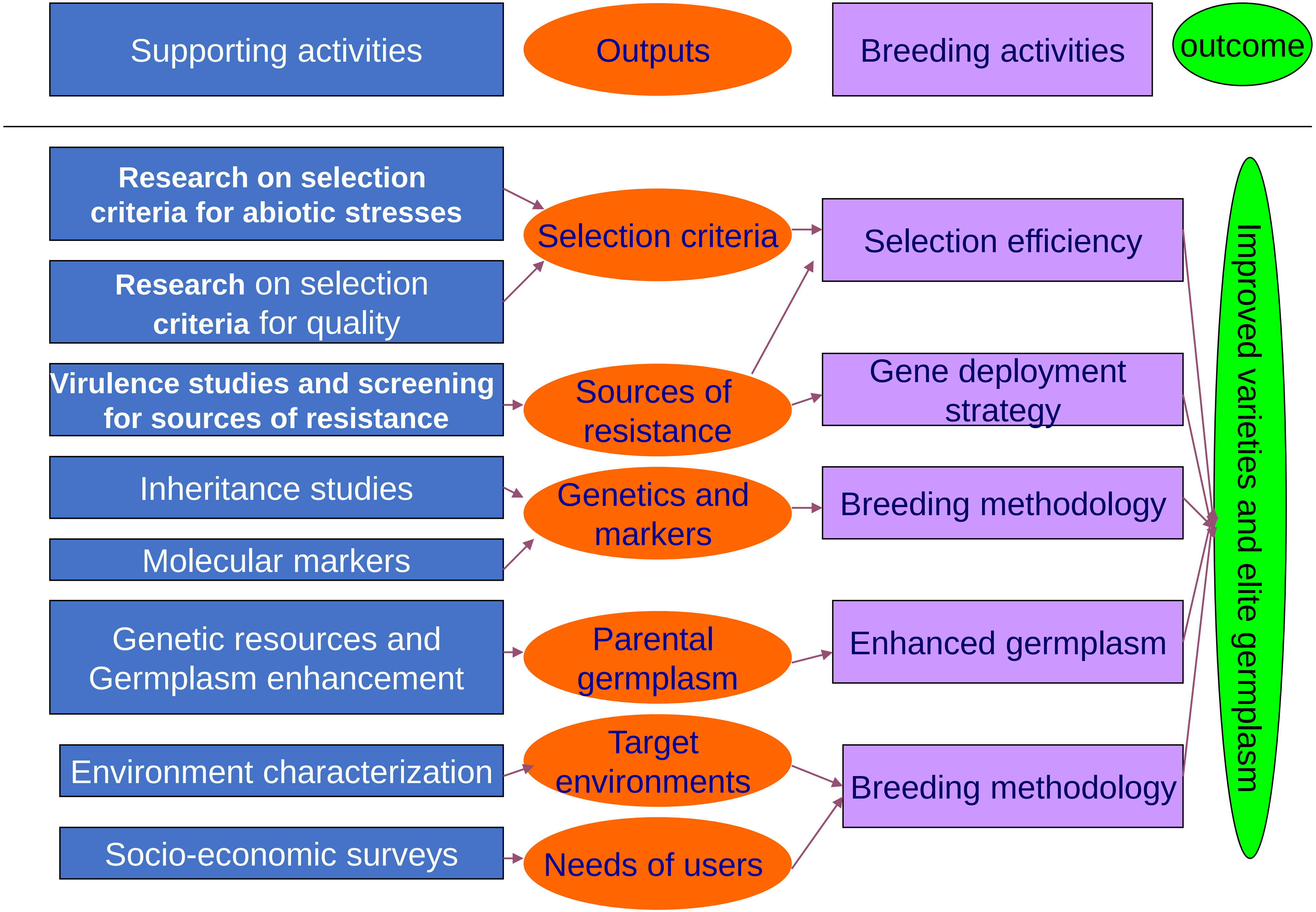
Taxon	
Group 1a	Crop
Group 1b	Same species as crop
Group 2	Same section as a crop
Group 3	Same sub-genus as a crop
Group 4	Same genus as a crop
Group 5	Different genus



Taxonomic approach
Taxon group concept (Maxted et al., 2006)

Efficient breeding program depends on:

- Definition of clear and priority objectives
- Understanding of genetics of traits;
- Availability of genetic variability and of parental material including pre-breeding component;
- Selection effectiveness including team work, quality testing, agronomic and use of molecular markers,…;
- Breeding methodologies and population characteristics;
- Team work and team spirit;
- Multi-institutional and International collaboration;
- Adequate funding and respect of breeders property rights;
- Adequate gene deployment strategy.



Supporting activities

Outputs

Breeding activities

outcome

Research on selection criteria for abiotic stresses

Research on selection **criteria** for quality

Selection criteria

Selection efficiency

Virulence studies and screening for sources of resistance

Sources of resistance

Gene deployment strategy

Inheritance studies

Molecular markers

Genetics and markers

Breeding methodology

Genetic resources and Germplasm enhancement

Parental germplasm

Enhanced germplasm

Environment characterization

Target environments

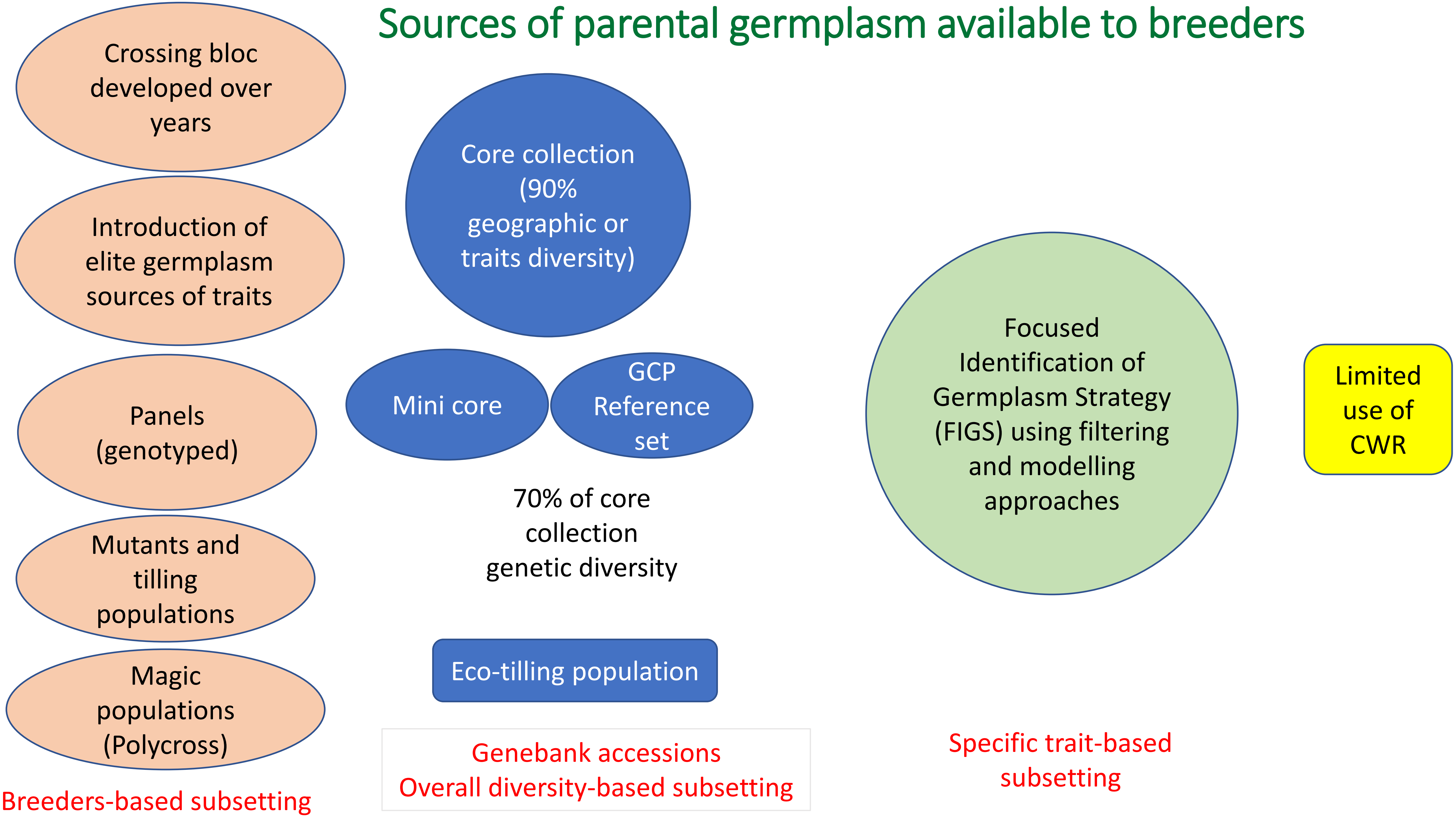
Socio-economic surveys

Needs of users

Breeding methodology

Improved varieties and elite germplasm

Sources of parental germplasm available to breeders



Crossing bloc developed over years

Introduction of elite germplasm sources of traits

Panels (genotyped)

Mutants and tilling populations

Magic populations (Polycross)

Breeders-based subsetting

Core collection (90% geographic or traits diversity)

Mini core

GCP Reference set

70% of core collection genetic diversity

Eco-tilling population

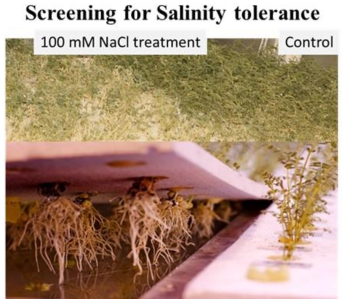
Genebank accessions
Overall diversity-based subsetting

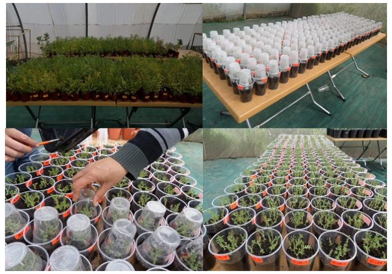
Focused Identification of Germplasm Strategy (FIGS) using filtering and modelling approaches

Specific trait-based subsetting

Limited use of CWR

Results of the evaluation of chickpea FIGS subsets





Crop	Sought traits	Total accessions	Resistant/tolerant accessions
10 FIGS subsets developed with a total of 1908 accessions evaluated	Fusarium wilt	192	15
	Beet western yellows virus	182	9
	Chickpea chlorotic stunt virus	182	2
	Alfalfa mosaic virus	182	1
	Aschocyta blight	200	0
	Cold tolerance	150	18
	Drought tolerance	150	46
	Salinity tolerance	200	15
	Pod borer	375	0
	Leaf minor	200	2

Mining of new genetic resources
Using FIGS, new subsets (150-200) of chickpea accessions for each of biotic (AB, FW, Viruses and BGM) and abiotic (Cold, drought, salinity) stresses identified and assembled.

GRDC Grains Research & Development Corporation
Your GRDC working with you

New biparental crosses
Developing of 40 new crosses

Pre-emptive chickpea pre-breeding for biotic stresses and germplasm enhancement for abiotic stresses

Screening for biotic and abiotic stresses
- Cold tolerance
- Drought tolerance
- Salt tolerance
- BGM
- Ascochyta blight (Terbol station and Tunisia)
- Fusarium wilt.
- viruses resistance [(BWYV), (CpCSV), (AMV) and (CMV)]

Genetic mapping and QTL analysis:
Five RIL population will be developed for:
- Cold
- Drought
- Salt tolerance
- Ascochyta blight
- Fusarium wilt.

- Six accessions with good cold tolerance
- Ten accessions with good levels of drought tolerance

IG
132879
124049
70447
128632
70455

IG
73390
131985
70401
70384
70393
117697
70408
70434
70789
75029

Three Genotypes showed 0% infection for different FW races in Ethiopia, Lebanon and Tunisia

Pre-emptive chickpea pre-breeding for biotic stresses and germplasm enhancement for abiotic stresses

Screening for Fusarium wilt resistance in chickpea FW-subset

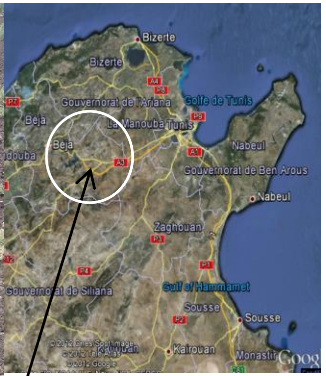
Three genotypes (0% of infection)

Terbol, Lebanon

Only one (0% of infection)

Debre Zeit, Ethiopia

Nine genotypes (0% of infection)



Race 0 (Foc-0).

Bija, Tunis

Three Genotypes showed 0% infection for different FW races in different locations

Pre-emptive chickpea pre-breeding for biotic stresses and germplasm enhancement for abiotic stresses

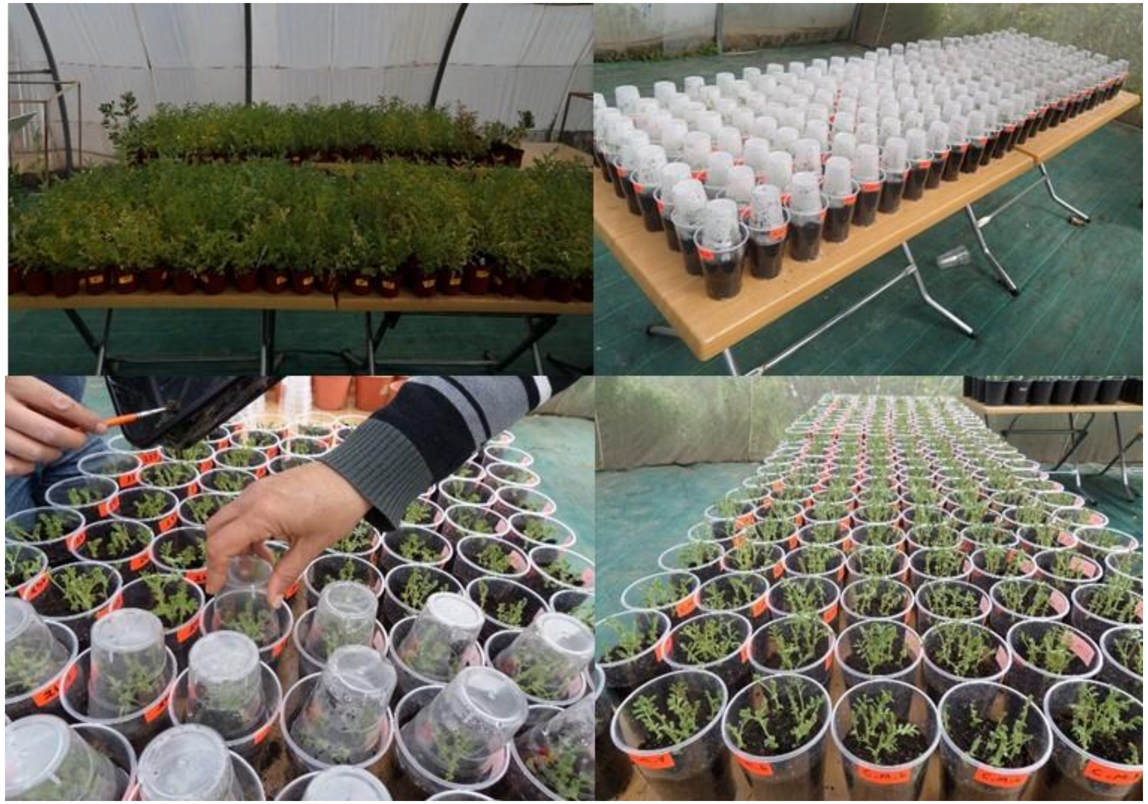
Chickpea accessions for their reaction to three viruses under greenhouse conditions

- 182 chickpea genotypes (16 countries) selected by FIGS system
- Evaluation for: Beet western yellows virus (BWYV), Chickpea chlorotic stunt virus (CpCSV) and Alfalfa mosaic virus (AMV)

Preliminary evaluation of 182 chickpea accessions for their reaction to BWYV, CpCSV and AMV infection after artificial inoculation with the virus during the 2014/2015 growing season under greenhouse conditions, at INRAT station, Tunis.

Number of resistant genotypes

% of infection	Virus/ Chickpea genotypes (IG#)		
	BWYV	CpCSV	AMV
0	6	1	1
0.1-10.0	3	1	0



Chickpea screening for CpCSV, BWYV and CMV, under greenhouse, INRAT station, Tunis, 2014/2015 growing season

Donors identified in lentil

Partners: IIPR, IARI, RAK college, HPAU

Donors for	
Fusarium wilt	14
Heat	17
Drought	2
Salinity	5
Early	13
High biomass	3
Large seeds	21
Rust	3
Powdery mildew	2

Pusa Ageti released by IARI, using landrace from ICARDA

Early maturing derivatives generated using ICARDA-supplied germplasm

Screening for drought and Al toxicity at IARI

Results of the evaluation of faba bean and lentil FIGS subsets

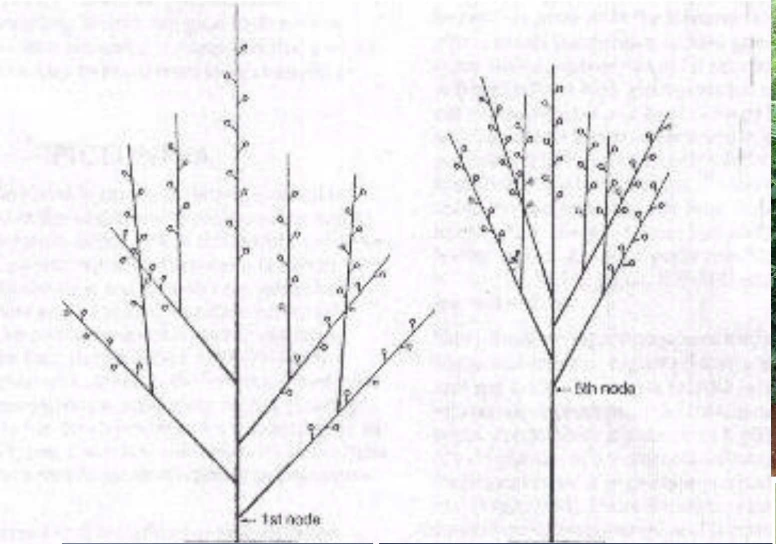
100 wild accessions of lentil screened

17 identified as salt tolerant

	IG/ILWL
1	297
2	301
3	317
4	326
5	348
6	359
7	368
8	371
9	417
10	426
11	455
12	475
13	479
14	480
15	485
16	487
17	136670

FIGS subsets	Trait sought	Total accessions	Resistant/tolerant accessions
Faba bean (4 FIGS subsets and 1 GCP set)	2 sets for drought	400	38
	FBYNV	150	28
	Heat tolerance (GCP)	100	9
Lentil (3 FIGS subsets and 1 GCP set)	Salt tolerance (GCP)	100	17
	Heat tolerance	200	22

For a major breakthrough in productivity, restructuring the plant type is a must in pulses



Pre-breeding for Earliness

	Ist Sowing (Oct 21, 2011)	
	Parent ILWL-118	Selection IPLWS-118
Flower initiation	98	30
Pod initiation	105	37
Days to maturity	182	62
Pods/plant	60-90	10-12

Accession	IIPR 2013-14	RS-IIPR 2014	IIPR 2014-15	Mean (days)
ILWLS – 118	40	42	37	40
IPLS – 09 – 17	41	47	39	42
IPLS – 09 – 05	46	43	44	44
IPLS – 09 – 34	44	43	50	46

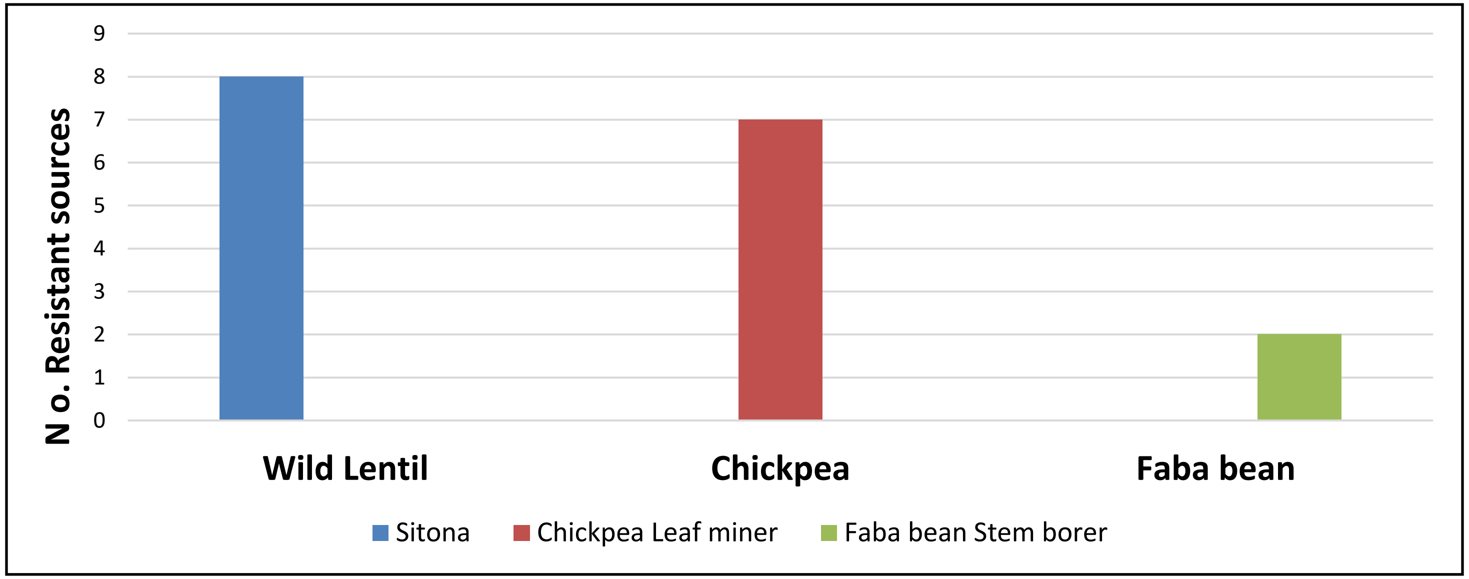
Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun

Monsoon rice
June/July-Oct/Nov

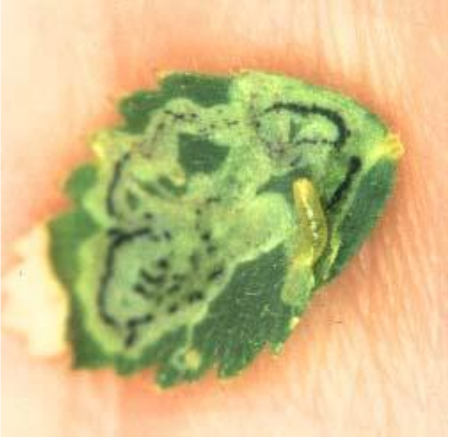
Super-early lentil
Fits in <90 days window

Spring rice
(Feb-May/June)

A new cropping pattern is recommended : **Rice-Lentil-Rice** for Bangladesh, eastern Indian states and eastern Nepal



N o. Resistant sources
0
1
2
3
4
5
6
7
8
9
Wild Lentil
Chickpea
Faba bean
Sitona
Chickpea Leaf miner
Faba bean Stem borer



FIGS successes

Sunn pest – first time in bread wheat

RWA resistance – new gene indicated

Hessian fly - resistance to Syrian bio-type

Powdery mildew – 2 new funcitonal genes

Salinity – 20% of salinity set showed resistance compared to only 3% of core set

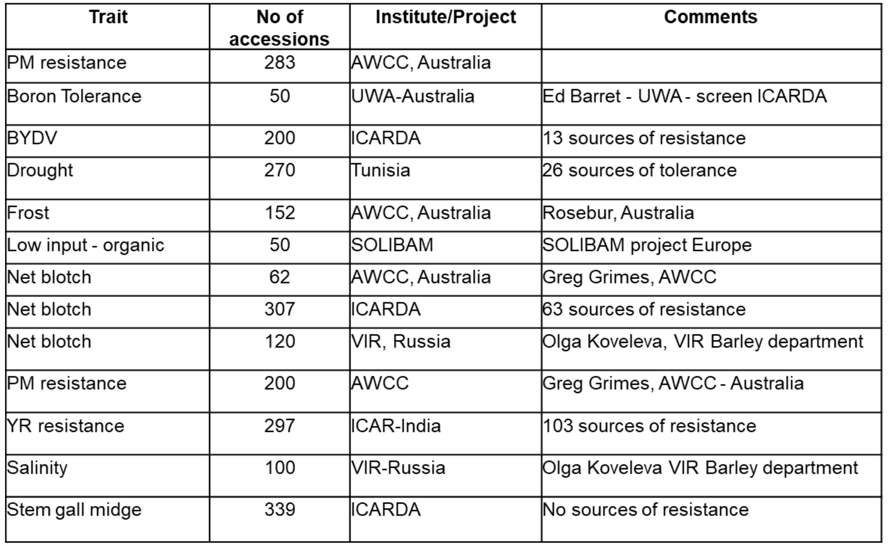
Drought – FIGS performed better than core

Summary of screening FIGS subsets for resistance to major diseases

		Resistant lines							
	# of lines	NB	SB	SC	YR	PM	LR	BYDV	SS/FS
FIGS- Net blotch	96	18	02	-	-	-	-	-	SS
Powdery mildew	352	-	-	-	-	98	-	-	SS
FIGS- Leaf rust	84	-	-	-	-	-	45	-	FS
FIGS- Yellow rust	293	-	-	-	129	-	-	-	FS
GCP	192	10	02	-	-	-	-	16	SS
FIGS- BYDV	100	-	-	-	-	-	-	27	SS

SS= seedling screening
FS= Field screening

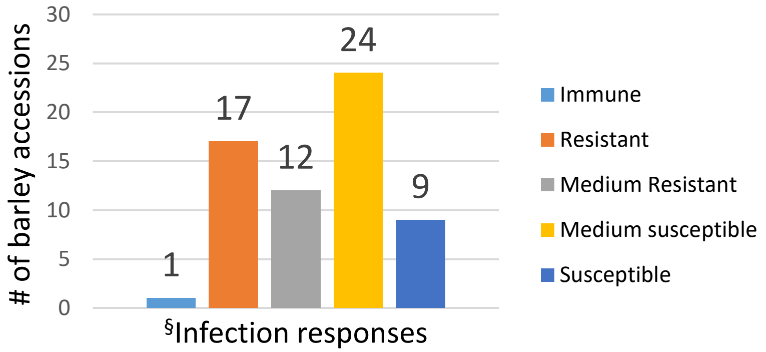
10 FIGS subsets totaling 2500 accessions of barley and 628 sources of resistance (280 accessions and 348 elite barley lines) shared with Australian breeders.



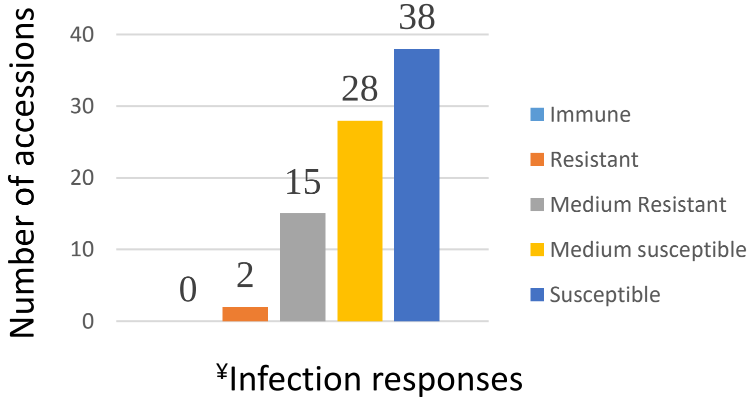
Trait	No of accessions	Institute/Project	Comments
PM resistance	283	AWCC, Australia	
Boron Tolerance	50	UWA-Australia	Ed Barret - UWA - screen ICARDA
BYDV	200	ICARDA	13 sources of resistance
Drought	270	Tunisia	26 sources of tolerance
Frost	152	AWCC, Australia	Rosebur, Australia
Low input - organic	50	SOLIBAM	SOLIBAM project Europe
Net blotch	62	AWCC, Australia	Greg Grimes, AWCC
Net blotch	307	ICARDA	63 sources of resistance
Net blotch	120	VIR, Russia	Olga Koveleva, VIR Barley department
PM resistance	200	AWCC	Greg Grimes, AWCC - Australia
YR resistance	297	ICAR-India	103 sources of resistance
Salinity	100	VIR-Russia	Olga Koveleva VIR Barley department
Stem gall midge	339	ICARDA	No sources of resistance

Screening of NB-FIGS and GCP with Net blotch and Spot blotch

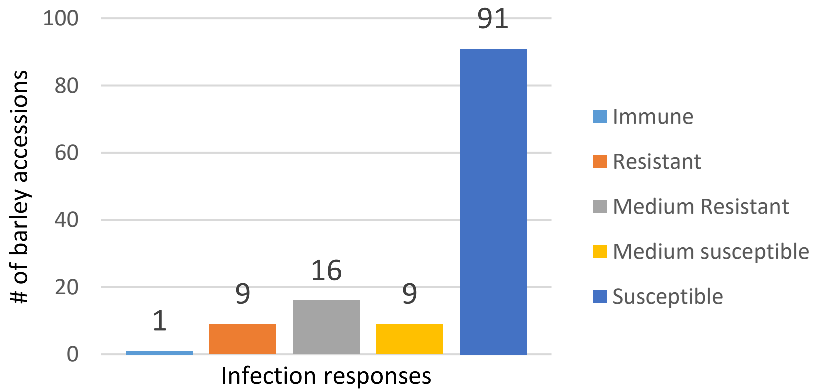
Response of NB-FIGS subset to Net Blotch



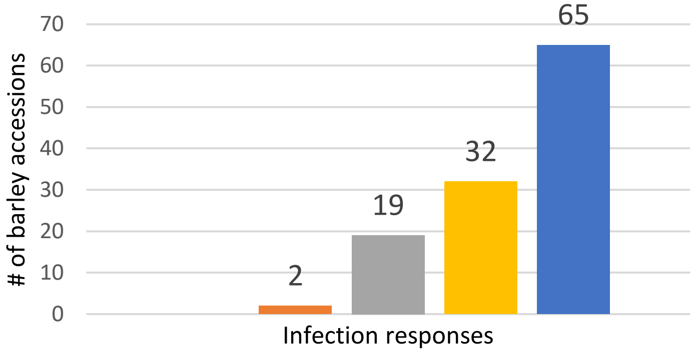
Response of NB-FIGS subset to Spot Blotch



Response of GCP subset to Net Blotch



Response of GCP subset to spot Blotch



Infection response scoring (0 Immune, 1-3 R, 4-5 MR, 6-7 MS, > 7 S)

Infection with a mixture of 20 isolates for Net blotch and with a mixture of 19 isolates for spot blotch)

- To enlarge genetic base for all crops including those suffering from inbreeding depression and from lack of useful genes;
- Adaptation to harsh conditions such as drought, salinity, heat,…;
- Looking for tolerance mechanisms and resistance genes for major and complex pests and diseases (most widely used);
- Quality and nutritional attributes not found in the cultivated genetic resources;
- Need for cytoplasmic and genetic male sterility genes

- Enlarge genetic diversity;
- Production of haploids in breeding programs;
- Bridging crosses;
- Sources of cytoplasmic and genetic male sterility;
- Study the genome structure, crop evolution and phylogeny;
- Generating new species like Triticale and Tritordeum in case of cereals.
- (use as rootstocks)

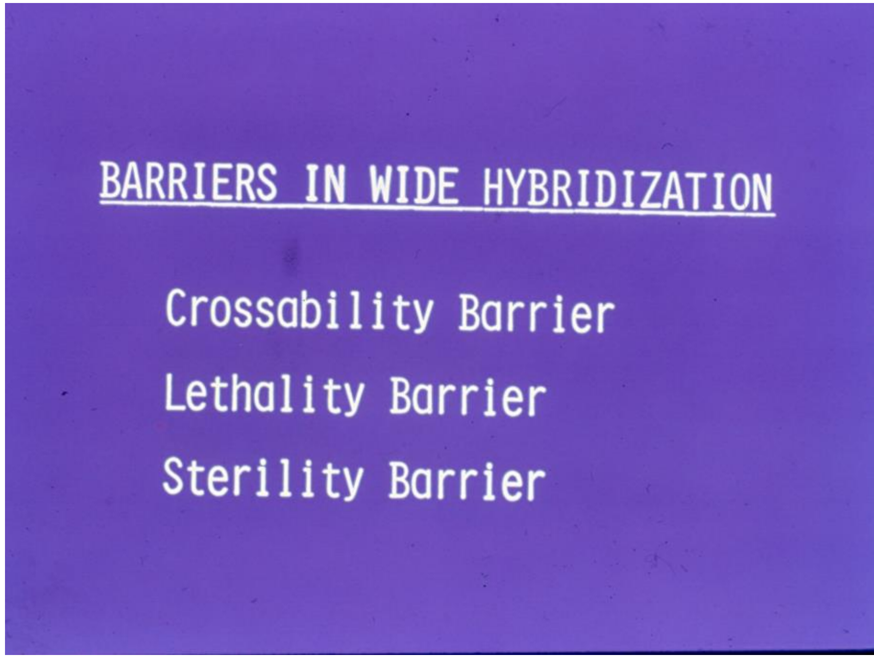
Pre-breeding (narrow sense definition)

Pre-breeding is the most promising alternative to link genetic resources and breeding programs. Pre-breeding refers to all activities designed to identify desirable characteristics and/or genes from unadapted (exotic or semi-exotic) materials, including those that, although adapted have been subjected to any kind of selection for improvement. As pre-breeding is being carried out , the resulting materials are expected to have merit to be included in ordinary breeding programs.

Pre-breeding can be extended to pyramiding genes using molecular markers, different races, …

1. Barriers in stigma and style:

- Effects of S genes for incompatibility;
- Difficulty in pollen tube penetration and growth
- Structural and functional properties of the style
- Solutions: pollen manipulation through correct timing and placement, use of mixture of viable and mentor pollen; use of proteases and plant growth hormones, changing temperature, direct pollination after removal of stigma and style, reciprocal crosses, use of immature style,….

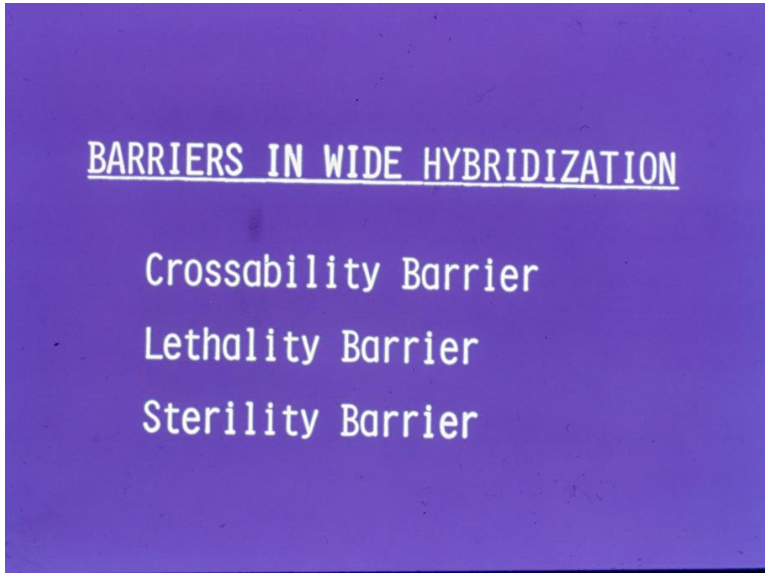


BARRIERS IN WIDE HYBRIDIZATION

Crossability Barrier
Lethality Barrier
Sterility Barrier

Barriers to inter-specific crosses

2. Fertilization: abortion of the embryos can be overcome by in vitro fertilization and use of exogenous plant growth regulators;
3. Barriers acting during seed development leading to abortion of the embryo can be overcome by reciprocal crosses, removal of competing sinks, use of plant growth regulators, embryo rescue and manipulation of ploidy level;
4. Partial or total sterility of the resulting hybrids: backcrossing.



BARRIERS IN WIDE HYBRIDIZATION

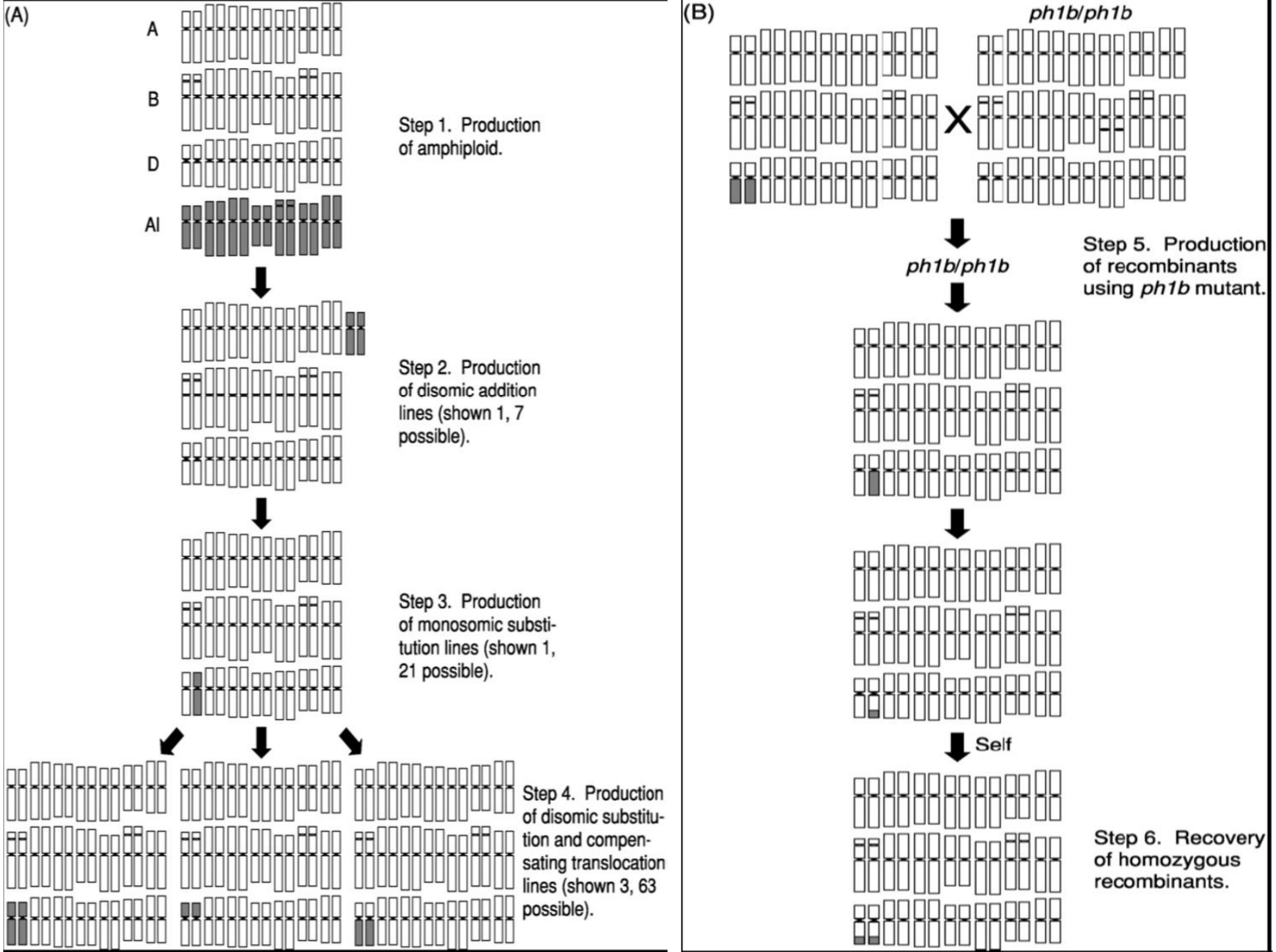
Crossability Barrier

Lethality Barrier

Sterility Barrier

- Choice of the parents from cultivated varieties with favorable genes for crossability.
- Use the recurrent parent as female at least in one cross to transfer the cytoplasm from the cultivated species.
- Select the species with high affinity with the cultivated species by analyzing the gene pools.
- Select among accessions of the wild relatives those with less undesirable traits while having the needed attribute.
- Use backcross or top cross to varieties of cultivated species to transfer the desirable characteristics while recovering the background of the cultivated species.
- Design a sound gene deployment strategy.

- Creation of amphyploids;
- Creation of chromosome addition lines through backcrossing (not sufficiently stable for variety requirements);
- Creation of chromosome substitution lines or trisomics using aneuploid stocks (more stable but indesirable linkages);
- Transferring part of the alien chromosome through irradiation, tissue culture, induced translocation using homeologous pairing facilitator systems;
- Use of autopolyploids and bridging crosses;
- Use of varieties with crossability genes;
- Natural hybridization occurring in mixtures or field edges.



Step 1. Production of amphiploid.

Step 2. Production of disomic addition lines (shown 1, 7 possible).

Step 3. Production of monosomic substitution lines (shown 1, 21 possible).

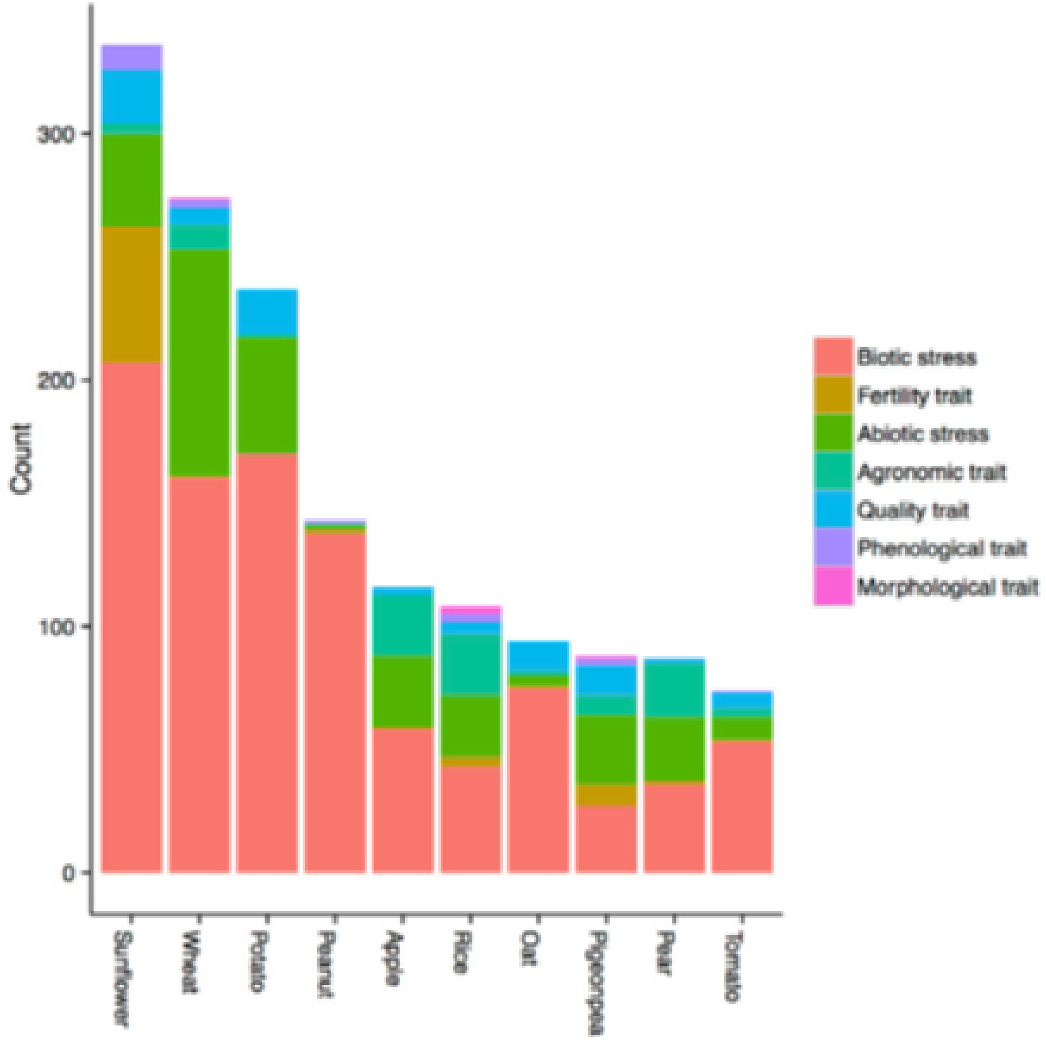
Step 4. Production of disomic substitution and compensating translocation lines (shown 3, 63 possible).

Step 5. Production of recombinants using *ph1b* mutant.

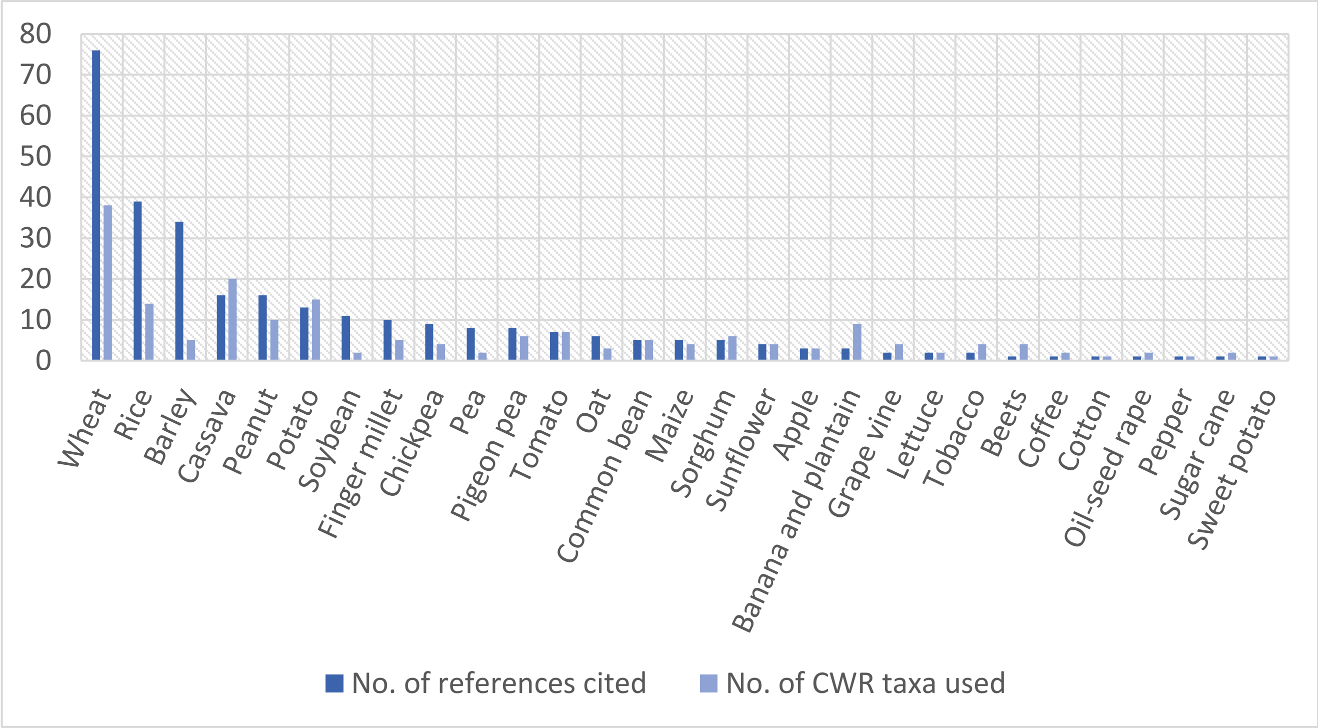
Step 6. Recovery of homozygous recombinants.

- Special techniques might be needed to increase the success of the crosses such as embryo rescue, the use of aneuploid stocks to develop addition or substitution lines or to allow homeologous pairing and the use of intermediary species and synthetic species as bridges.
- Irradiation and tissue culture techniques might be needed to develop translocations leading the transfer of the desirable genes.
- Part of the generated material from interspecific crosses of all generations should be kept for further screening and evaluation for other traits to avoid duplication of the crossing phases.
- The monitoring of the transfer of genes from wild relatives can be done through, banding techniques, *in situ* hybridization techniques and molecular techniques.
- The success of forming viable grains may require the pollination of large number of spikes and the use of growth hormones.

Use of crop wild relatives for different crops and purposes



Confirmed and potential breeding uses of crop wild relatives of the 10 crops with most "breeding use" citations in the literature, categorized in trait classes. (Dempewolf et al. 2017)



Source: Maxted et al. 2010

Citations:
- 2% <1970
- 13% 1970s
- 15% 1980s
- 32% 1990s
- 38% >1999

Use:
- 39% pest resistance
- 17% abiotic stress resistance
- 13% yield increase

Species in chickpea gene pools

Primary gene pool species

(cultivated forms)

Cultivated forms of *Cicer arietinum*

Secondary gene pool species

(progenitors)

C. reticulatum and C. echinospermum

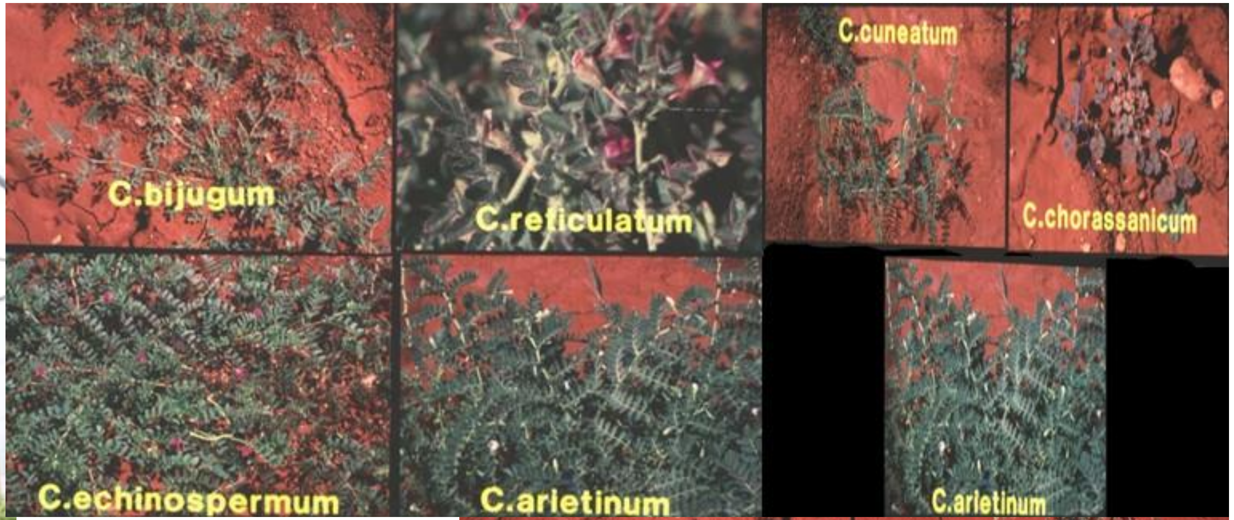
Tertiary gene pool species

(other species)

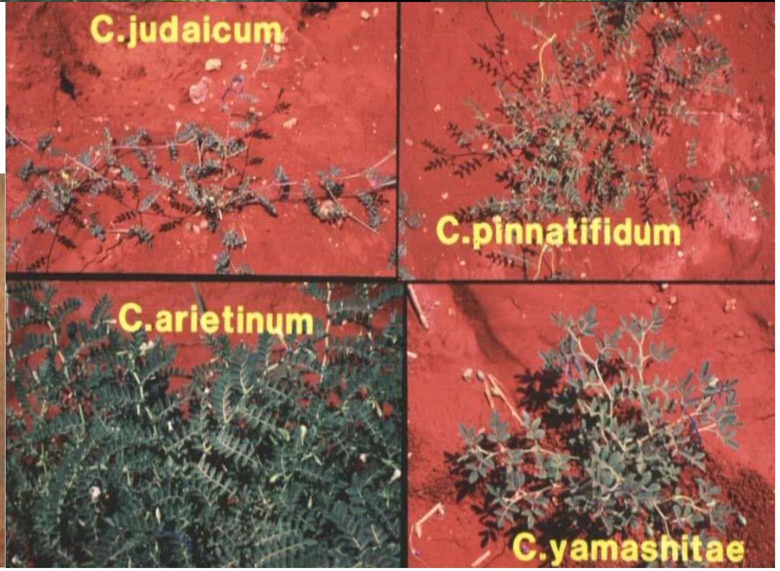
All remaining annual and perennial Cicer species

Chickpea CWR at ICARDA

Cultivated: 15086
Wild: 307



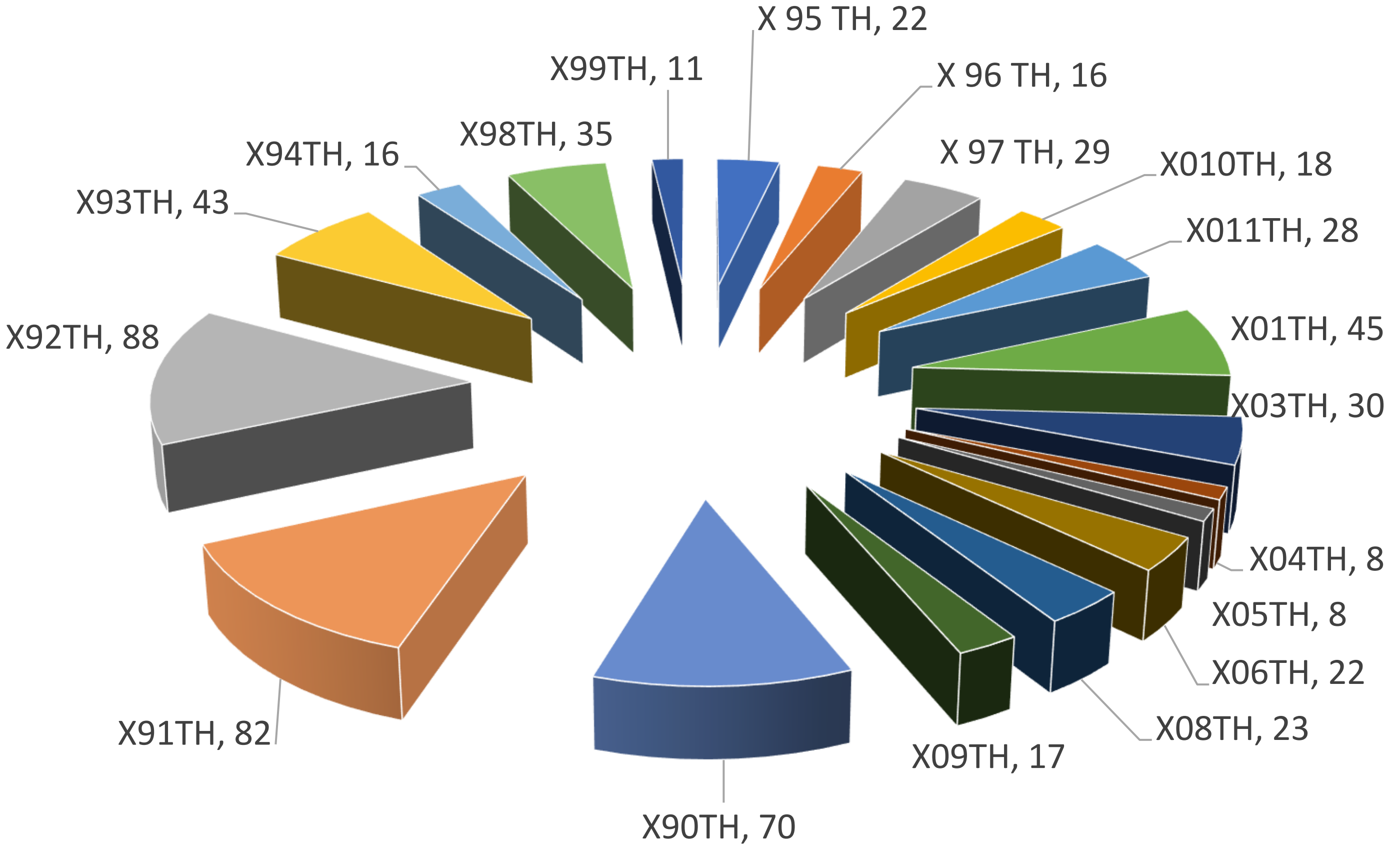
Interspecific Cross
(*C. arietinum* x *C. bijugum*)



Chickpea: A total of 611 of interspecific crosses have been developed

Wild species used

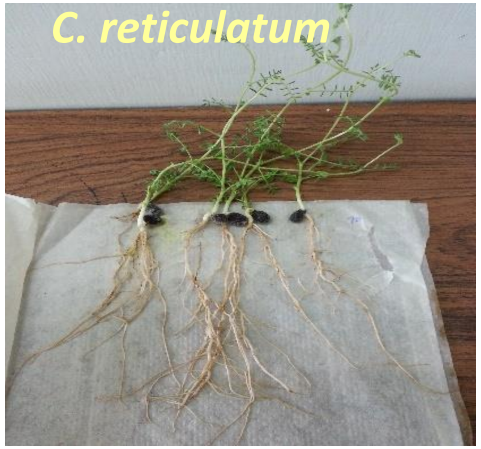
C. echinospermum
C. arietinum
C. bijugum
C. chorassanicum
C. cuneatum
C. echinospermum
C. judaicum
C. pinnatifidum
C. reticulatum
C. bijugum
C. echinospermum
C. judaicum
C. pinnatifidum
C. reticulatum



Wild Cicer: Promising sources

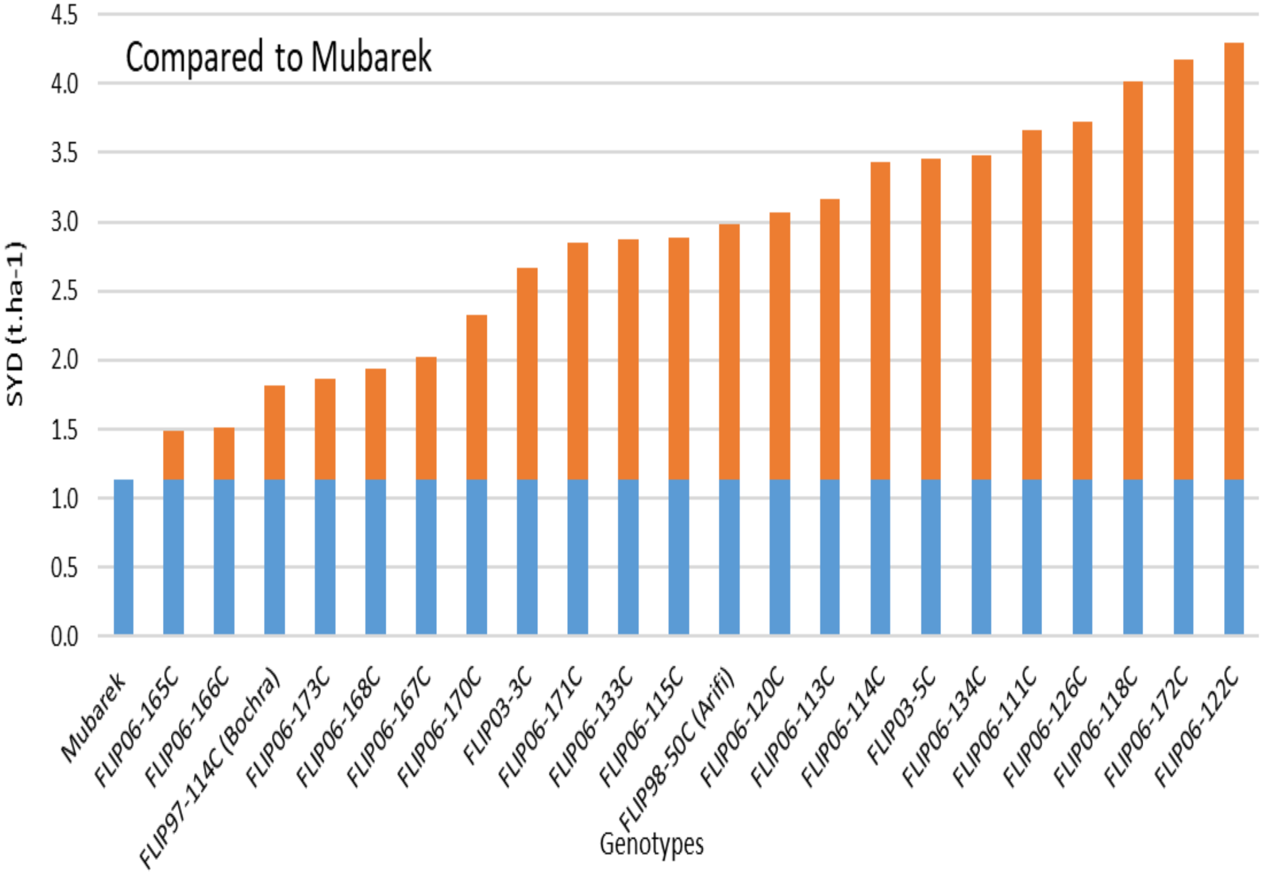
Species	Genepool	Number of accessions	Useful traits
C. reticulatum	Primary	36	Resistance/tolerance to dry root rot, ascochyta blight, botrytis gray mold, *H. armigera*, leaf minor, cyst nematode, drought and cold
C. echinospermum	Secondary	18	
C. judaicum, *C. bijugum*, *C. pinnatifidum*, *C. cuneatum*, *C. chorassanicum*, and *C. yamashitae*	Tertiary	177	

Very few accessions used in chickpea improvement

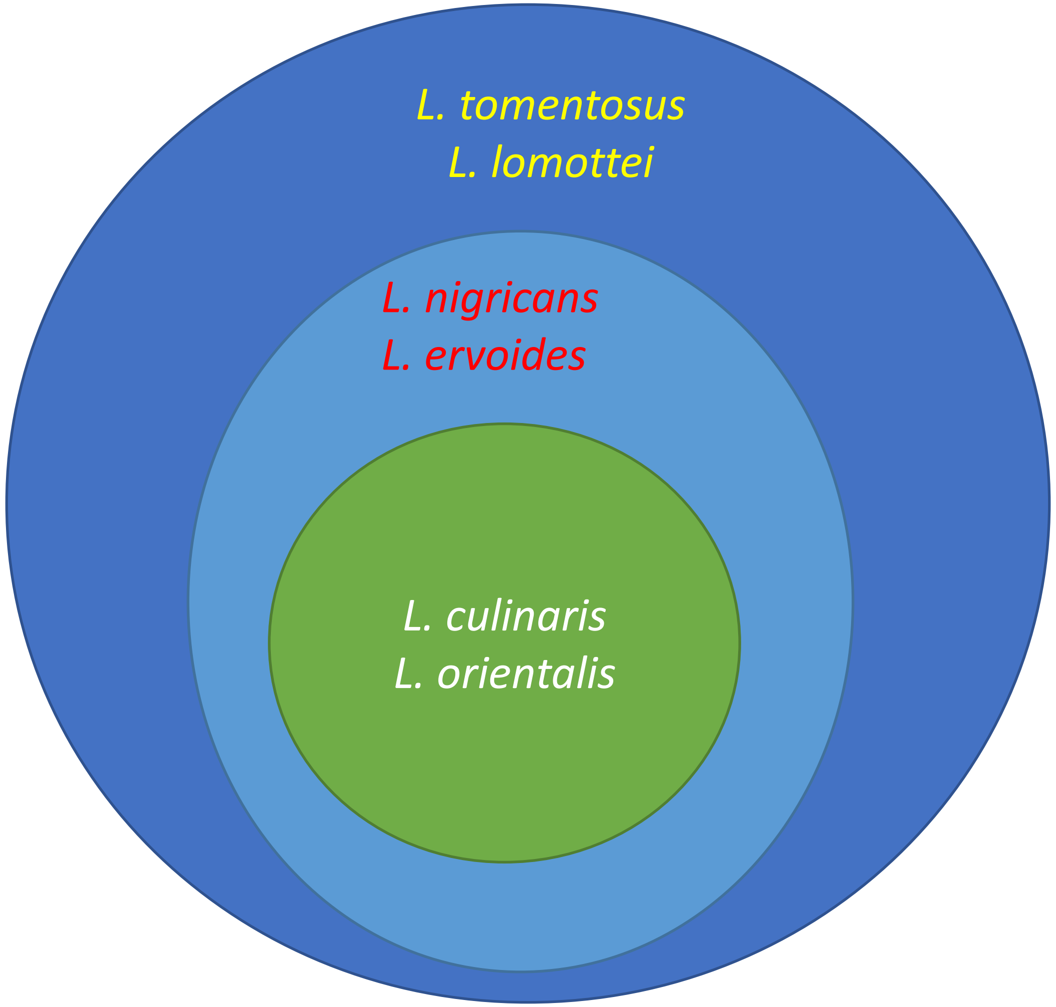


Performance of Prebred Chickpea

- ~10% of 996 crosses have *C. reticulatum* as one of the parents in order to introgress resistance to cold, drought, heat, and fusarium wilt into cultivated chickpea.
- 20 improved lines with high yield and resistance/tolerance to major diseases and abiotic stresses are in final stage of MET.
- Yield advantage – up to 3 tonnes



Species in lentil gene pools



L. tomentosus
L. lomottei

L. nigricans
L. ervoides

L. culinaris
L. orientalis

Lentil Wild Relatives - precious source of traits

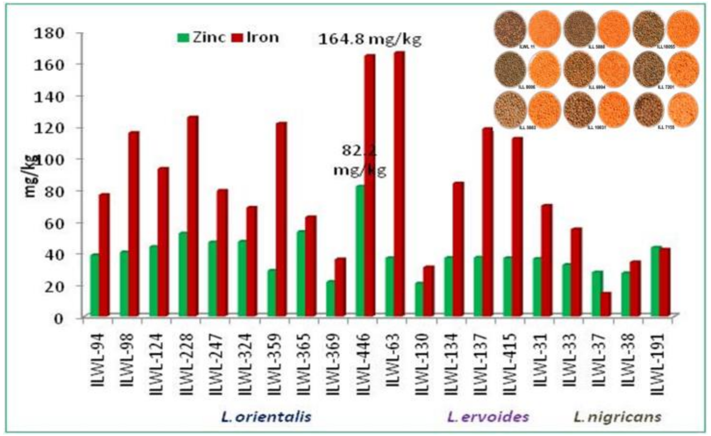
Species	Accession	Origin countries
Lens culinaris ssp. culinaris	11876	78
L. culinaris ssp. odemensis	66	5
L. culinaris ssp. orientalis	259	15
L. culinaris ssp. tomentosus	21	2
L. ervoides	170	16
L. lamottei	10	3
L. nigricans	62	8

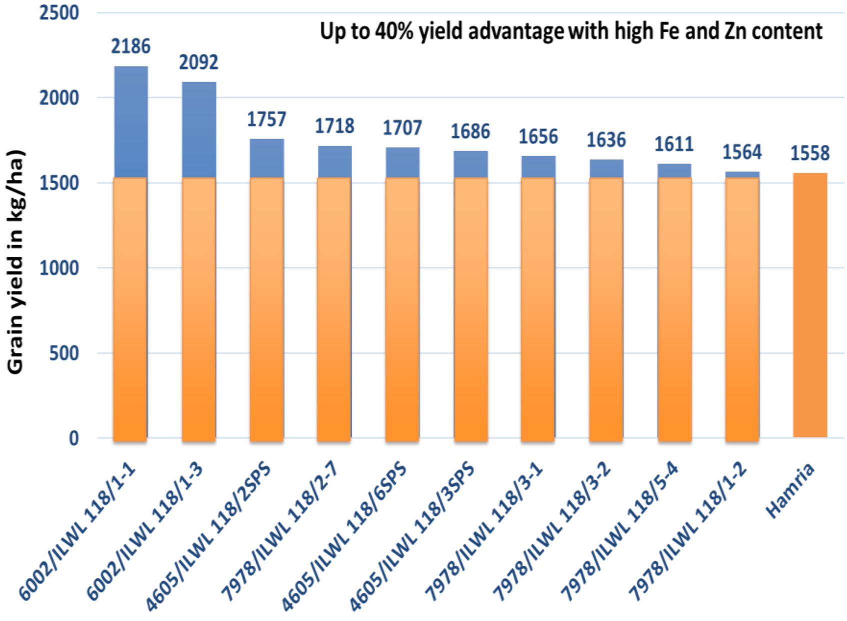
Traits of interest from CWR- Lentil

Biotic Stresses	Progress
Anthracnose	good
Ascochyta	good
Stemphylium	good
Botrytis	?
Sclerotinia	?
Rust	?
Orobanche	some
Abiotic Stresses	**Progress**
Drought tolerance	some
Heat stress	?
Flooding tolerance	?
Frost tolerance	some
Others	**Progress**
Nitrogen fixation	starting
Growth habits	some
Seed biochemistry	some
Productivity traits	some

Value of genetic resources in lentil improvement

Trait of interest	CWR screened	Donors identified
Fusarium wilt	435	ILWLs76, 79 37, 113, 138
Salinity tolerance	100	ILWL297, ILWL368, ILWL371, ILWL417, IG136670
Earliness	285	ILWL 118
Fe and Zn contents	285	ILWL74, IG135395, IG 135403
Orobanche	31	ILWL367, ILWL240





Lens orientalis derivative lines

Gene pool concept of *Lathyrus*

Primary gene pool
GP1

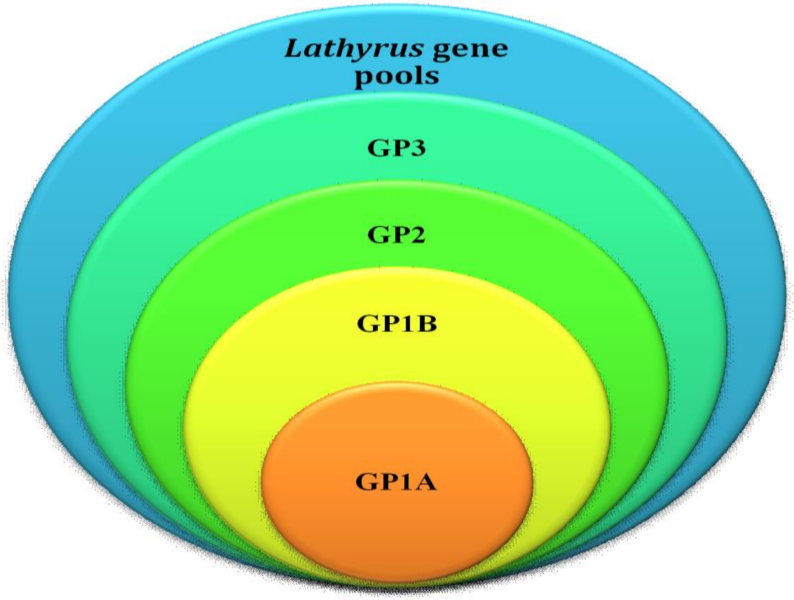
- GP1A (Cultivated forms of L. sativus)
- GP1B (Wild forms of L. sativus)

Secondary gene pool
GP2

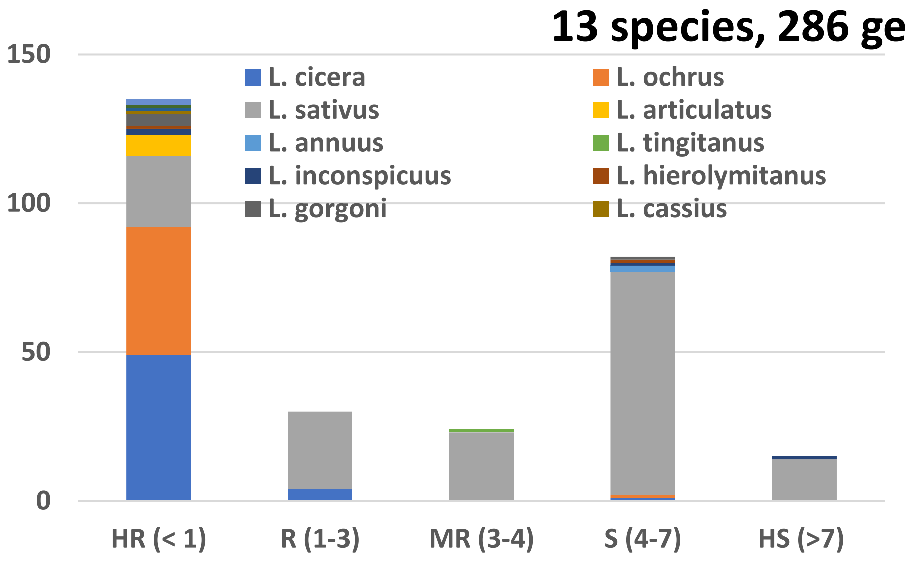
- *L. chrysanthus*
- *L. gorgoni*
- *L. marmoratus*
- *L. pseudocicera*
- *L. amphicarpos*
- *L. blepharicarpus*
- *L. chloranthus*
- *L. cicera*
- *L. hierosolymitanus*
- *L. hirsutus*

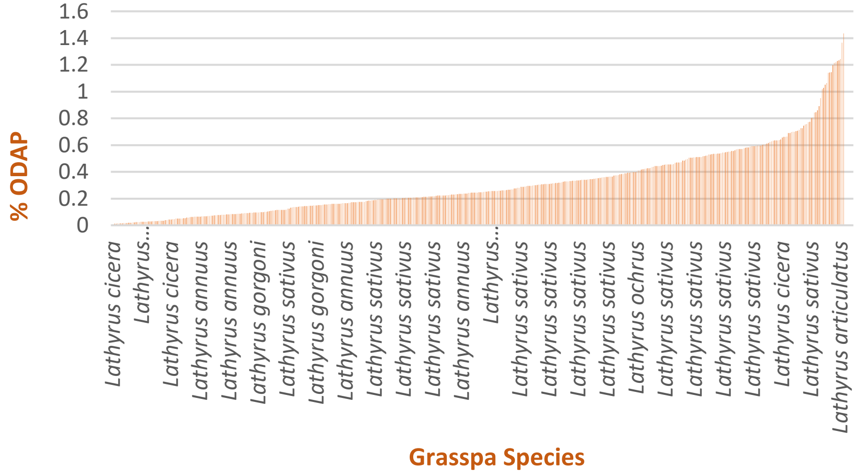
Tertiary gene pool
GP3

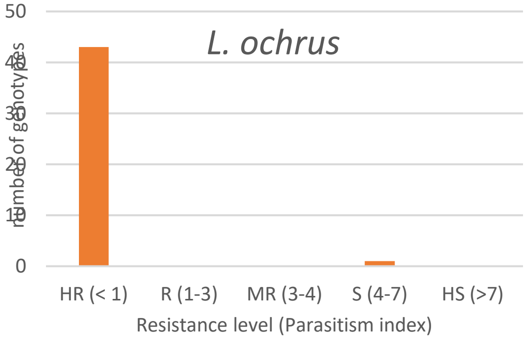
- Other *Lathyrus* species

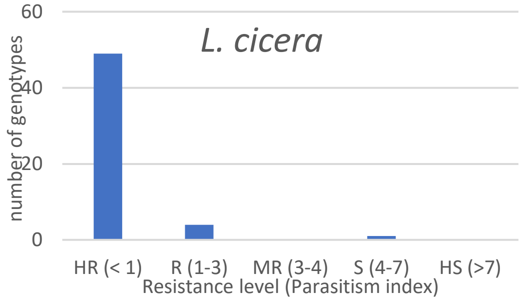


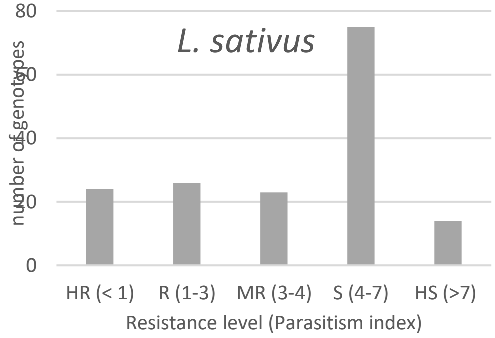
Screening Grass pea for Resistance to *Orobanche crenata*

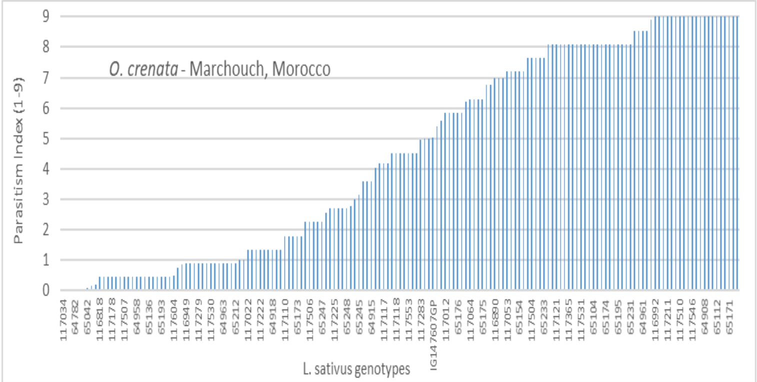






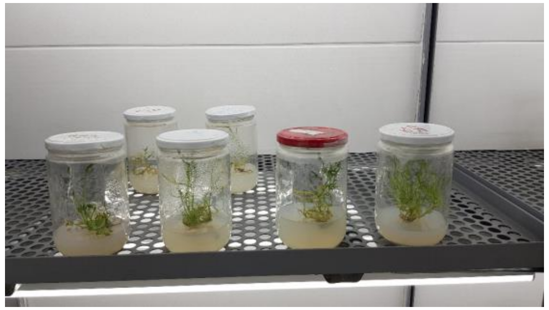






Strengthening pre-breeding efforts through interspecific crosses

- First successful interspecific crosses between grass pea and five *Lathyrus* species: a total of 450 F_5 from interspecific crosses using *Lathyrus cicera* and F_3 and F_3 BC2 and BC3 seeds from crosses with *L. articulatus*, *L. cicera, L. heirosolymitanus, L. inconspicuous, L. marmoratus* and *L. ochrus* were successfully produced.



Species in wheat gene pools

Primary gene pool species

(one or more genomes in common with wheat)

- *T. aestivum*
  - *ssp. aestivum*
  - *compactum*
  - *macha*
  - *spelta*
  - *sphaerococcum*
- *T. turgidum*
  - *ssp. dicoccoides*
  - *carthlicum*
  - *dicoccum*
  - *durum*
  - *paleocolchicum*
  - *polonicum*
  - *turanicum*
- *Ae. tauschii*

Secondary gene pool species

(one genome in common with wheat)

- *T. m. aegilopoides*
- *T. m. monococcum*
- *T. urartu*
- *T. t. armeniacum*
- *T. t. timopheevii*
- *T. zhukovskyi*
- *Ae. crassa*
- *Ae. cylindrica*
- *Ae. juvenalis*
- *Ae. vavilovii*
- *Ae. ventricosa*
- *Ae. searsii*
- *Ae. bicornis*
- *Ae. longissima*
- *Ae. sharonensis*
- *Ae. speltoides*

Tertiary gene pool species

(no genome in common with wheat)

- *Ae. biuncialis*
- *Ae. columnaris*
- *Ae. comosa*
- *Ae. geniculata*
- *Ae. kotschyi*
- *Ae. markgrafii*
- *Ae. neglecta*
- *Ae. peregrina*
- *Ae. triuncialis*
- *Ae. umbellulata*
- *Ae. uniaristata*
- *Am. muticum*
- *Dasypyrum villosum*
- *Hordeum chilense*

Source: Bikram Gill, WGRC KSU

Genepools of wheat (by M. van Slageren)

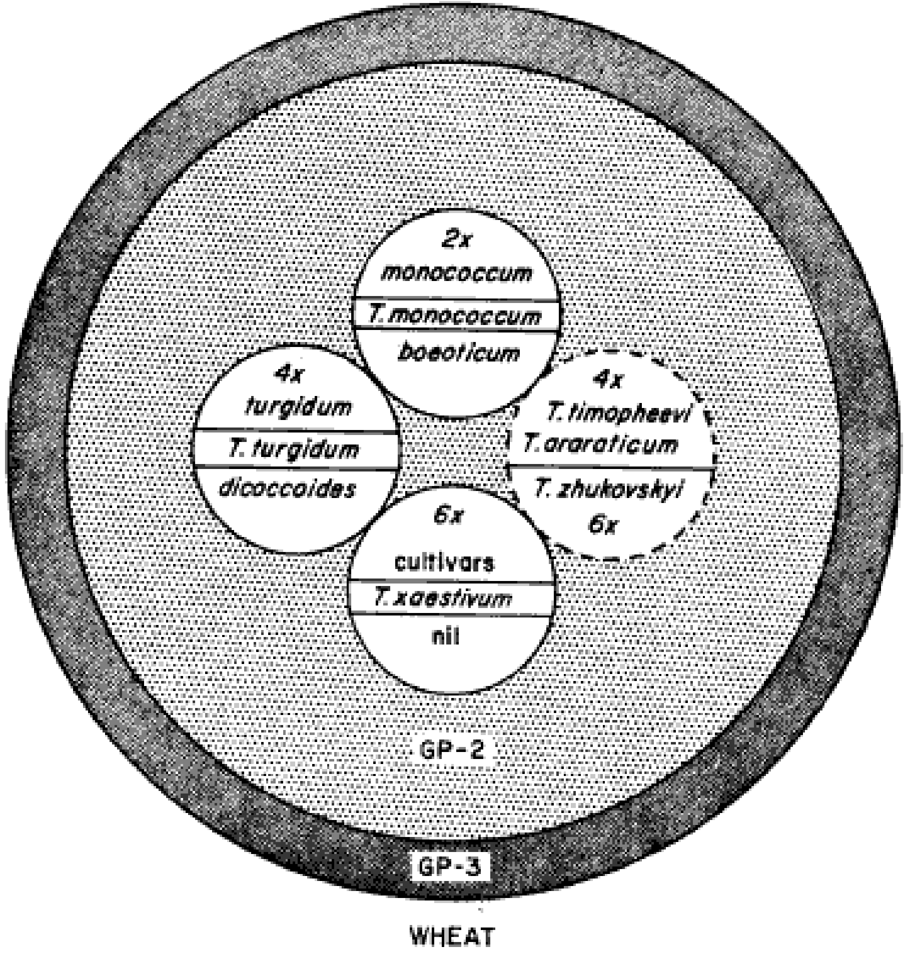
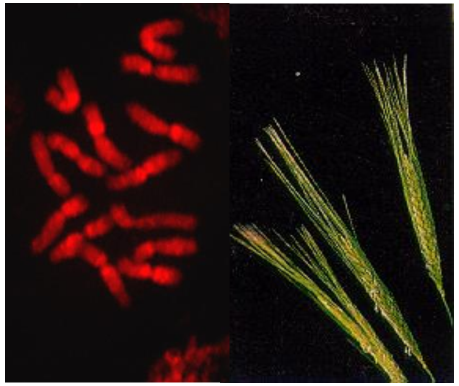


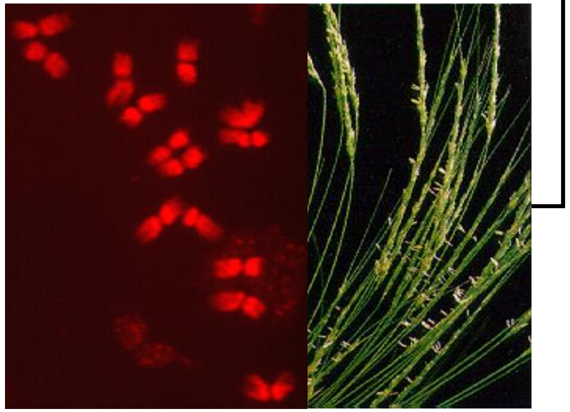
Fig. 2. The gene pools of wheat. The secondary gene pool is very large and includes all species of *Aegilops*, *Secale*, and *Haynaldia*, plus at least *Agropyron elongatum*, *A. intermedium*, and *A. trichophorum*. The tertiary gene pool includes several species of *Agropyron* and several of *Elymus*.

Genera in the wheat genepools

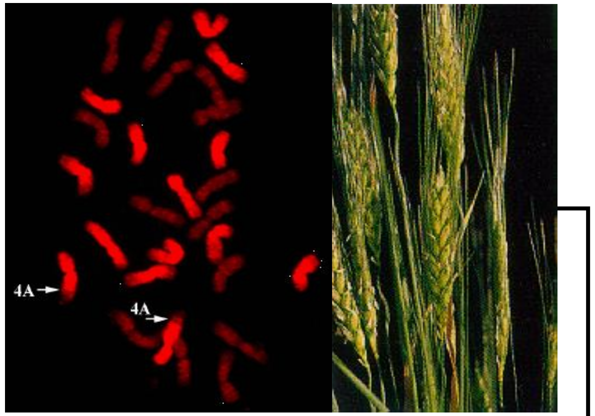
Genus	Ploidy levels	Number of species	Number of genomes	Genomes
Triticum	2X, 4X, 6X	4	3	A,B or G, D
Aegilops	2X, 4X, 6X	22	6	C,D,M,N,S,U
Amblypyron	2x	1	1	T
Secale	2X	7	1	R
Agropyron	2X, 4X, 6X, 8X	100	8	H,C*,S,J,Ju,E,X,Y
Haynaldia	2X, 4X	2	1	Ha
Elymus	2X, 4X, 6X, 8X, 12X	60	4	H,S,J,X
Hordeum	2X, 4X, 6X	30	1	H



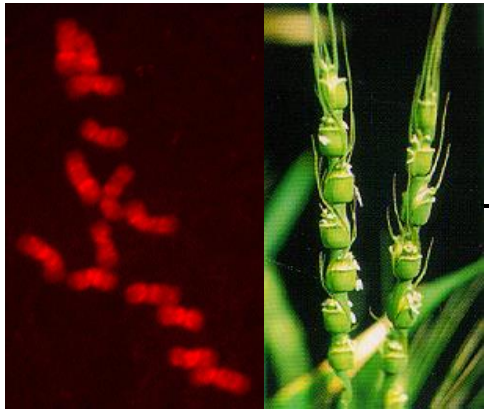
Triticum urartu
(2n=2x, AA)



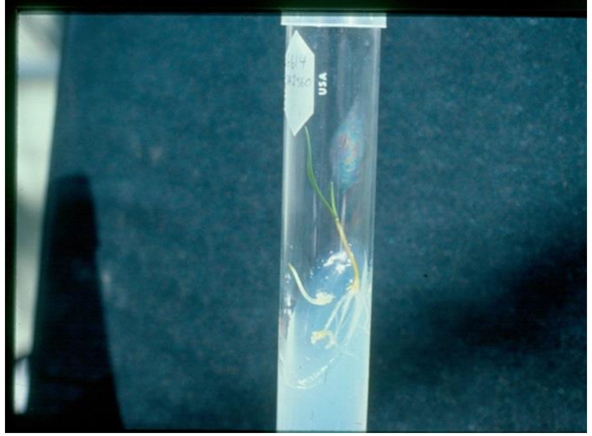
Aegilops speltoides
(2n=2x, SS)

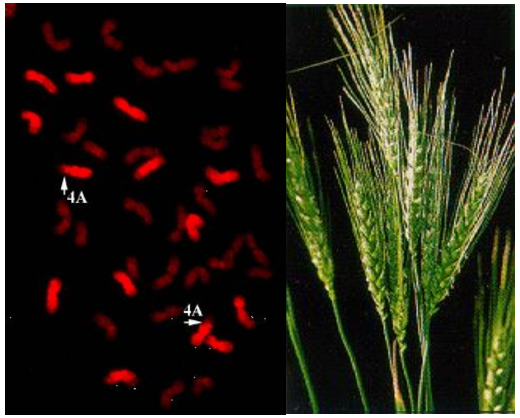


Triticum turgidum
(2n=4x, AABB)



Aegilops tauschii
(2n=2x, DD)





Triticum aestivum
(2n=6x, AABBDD)


Aegilops tauschii
F1
Bread wheat
Durum wheat

Useful traits transferred from synthetic hexaploid wheat

- **Synthetics have exponentially increased genetic diversity in wheat**
  1. **Yield under drought and irrigated conditions**
  2. **Multiple disease**
     - **Leaf, stem, and yellow rusts**
     - **Yellow Leaf Spot (= tan spot) resistance**
     - **Nematode resistance**
     - ***Septoria tritici* blotch resistance**
  3. **Salinity tolerance**
  4. **Pre-harvest sprouting tolerance**
  5. **Insect pests tolerance**
- **After introducing a novel DD genome (*Ae. tauschii*), now work starting on using novel AABB genome (*. dicoccoides* and *T. dicoccum*) in new synthetics.**

Genotype	YR response	Yield (t/ha)	% of Arrehane
KAUZ/PASTOR/3/ALTAR 84/AEGILOPS SQUARROSA (TAUS)//OPATA	5R	6.93	131
TINAMOU-3/BANA-4	40MS	6.59	125
NESSER/SERI/3/SHUHA-2//NS732/HER	40MS	6.51	123
MUNIA//CHEN/ALTAR 84/3/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/4/MARCHOUCH-8	10MR	6.37	121
NESSER/SERI//TEVEE-1/SHUHA-6	15MR	6.33	120
KAUZ/PASTOR/3/ALTAR 84/AEGILOPS SQUARROSA (TAUS)//OPATA	5R	6.32	120
YEBROUD'S'//DOVE'S'/SERI/3/SAFI-1	10MR	6.17	117
SHUHA-4/FLORKWA-4//HUBARA-3	5MR	6.07	115
KAUZ/PASTOR/3/ALTAR 84/AEGILOPS SQUARROSA (TAUS)//OPATA	10MR	6.05	115
TEVEE-1/SHUHA-6//MASSIRA	5R	5.99	114
CHILERO-1/STAR'S'//SHUHA-2/FOW-2	15MR	5.93	112
NESSER/SERI/3/SHUHA-2//NS732/HER	10MR	5.92	112
NESSER/SERI//TEVEE-1/SHUHA-6	40MS	5.92	112
MUNIA//CHEN/ALTAR 84/3/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/4/MARCHOUCH-8	5R	5.87	111
KAUZ/PASTOR/3/ALTAR 84/AEGILOPS SQUARROSA (TAUS)//OPATA	10MR	5.70	108
QIMMA-12/PASTOR-6//QIMMA-12	30MS	5.65	107
KARAWAN-1/TALLO 3//REGRAG-1	5R	5.64	107
ALTAR 84/AE.SQUARROSA (219)//SERI/3/MASSIRA	5R	5.63	107
ALTAR 84/AE.SQUARROSA (219)//SERI/3/MASSIRA	5R	5.62	107
KARAWAN-1/TALLO 3//JADIDA-2	5R	5.58	106
Arrehane (check)	15MR	5.27	100

New genetic diversity for wheat identified in wide crosses

● *T. boeoticum*

● *T. urartu*

● *T. dicoccoides*

● *Ae. speltoides*

yellow rust resistance

leaf rust resistance

earliness

high productive tillering

spike productivity

plant productivity

plant height

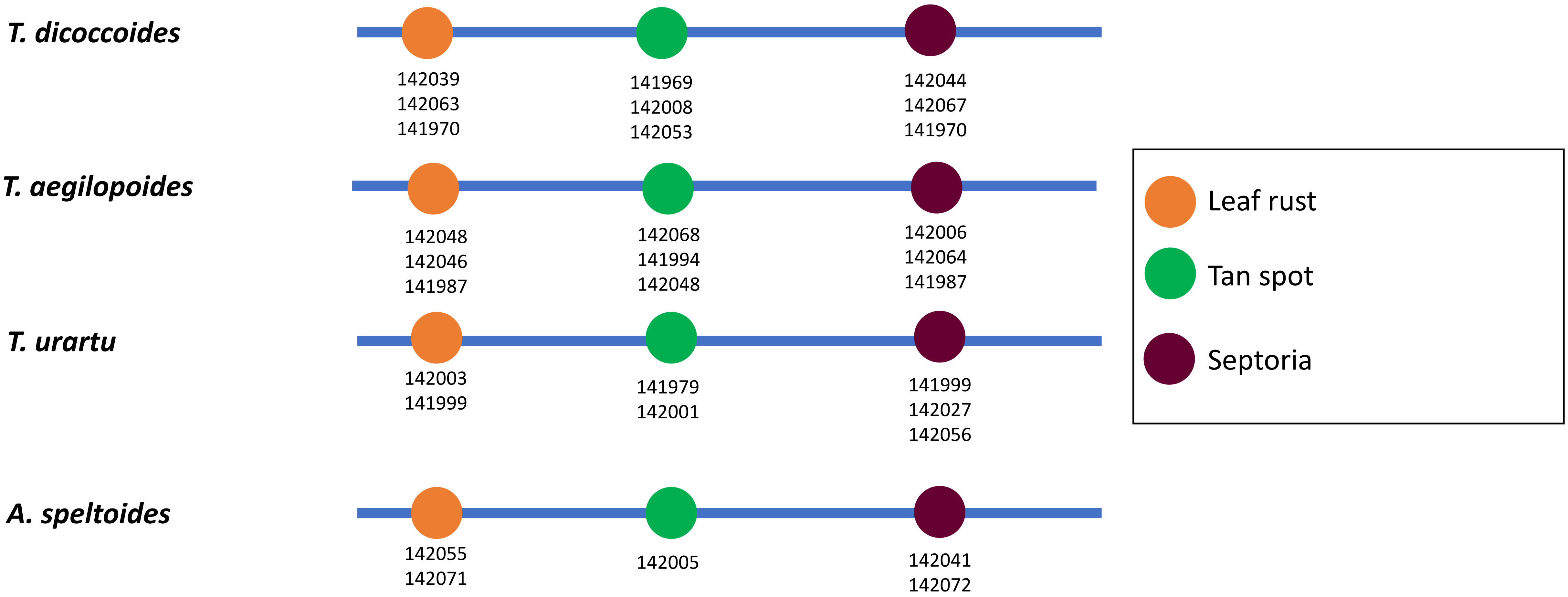
drought tolerance

Sunn pest resistance

Russian wheat aphid resistance

Septoria tritici resistance

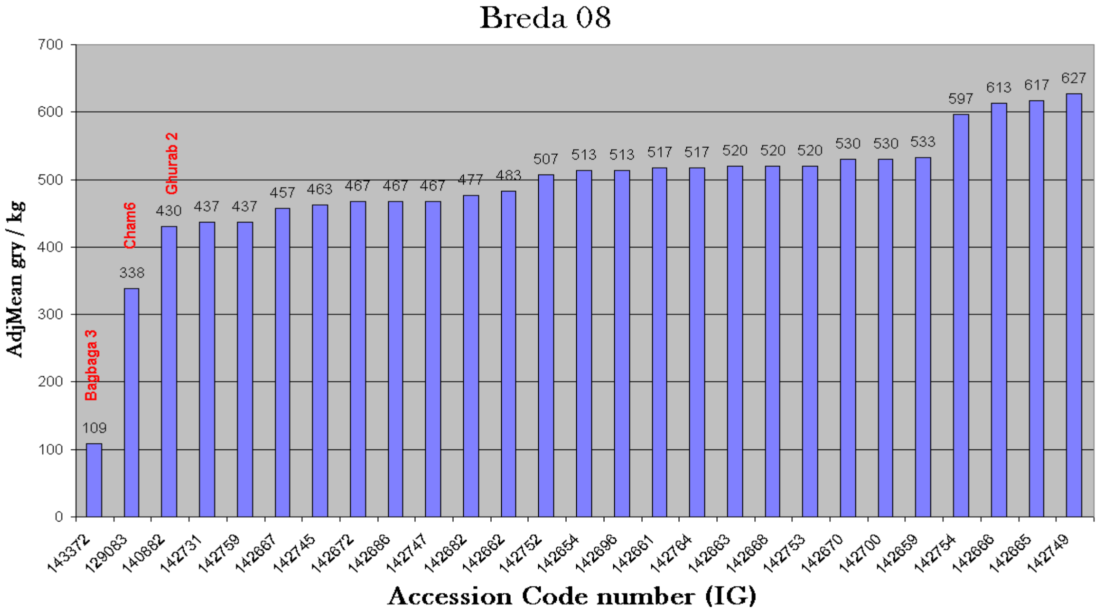
Sources of resistance from durum wheat derivatives

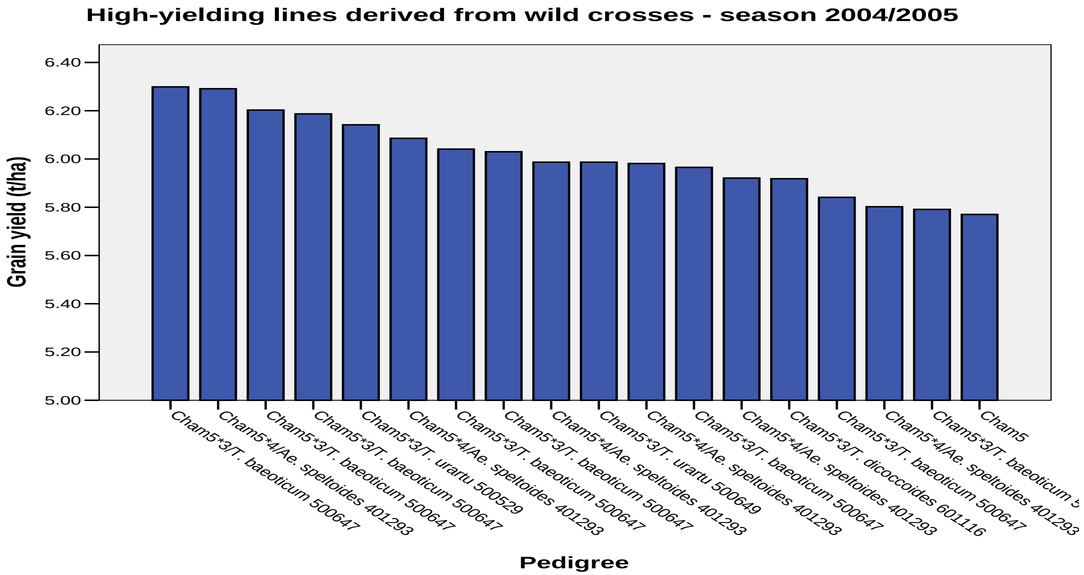


	Leaf rust	Tan spot	Septoria
T. dicoccoides	142039 142063 141970	141969 142008 142053	142044 142067 141970
T. aegilopoides	142048 142046 141987	142068 141994 142048	142006 142064 141987
T. urartu	142003 141999	141979 142001	141999 142027 142056
A. speltoides	142055 142071	142005	142041 142072

IG number of durum wheat lines derived from interspecific crosses with Cham5 and Haurani

Grain yield (kg/ha) of promising lines of bread and durum wheat compared to best checks at Breda (2007-08 dry season) and Tel Hadia (2004-05 wet season)





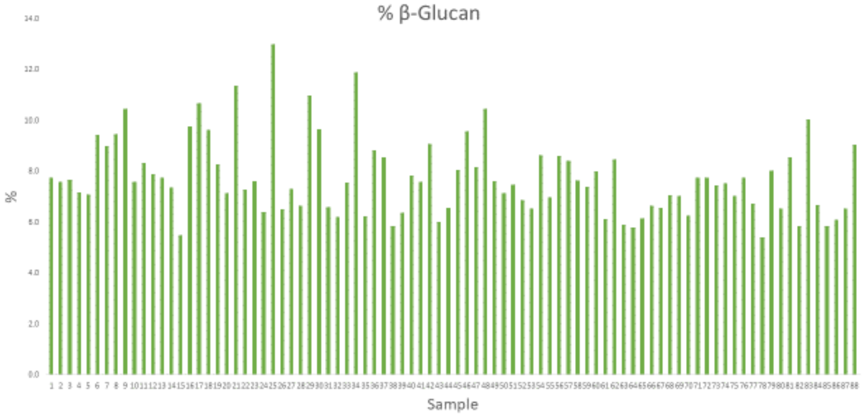
Importance de la résistance aux maladies et insectes

Hessian Fly Resistant

Pre-breeding efforts in barley

- Disease resistance
  - powdery mildew
  - leaf rust
  - net blotch
  - Septoria speckled leaf blotch
  - spot blotch
  - stem rust
  - leaf scald

- Other traits
  - drought tolerance
  - photothermal response
  - protein content
  - Beta glucans, Iron, Zinc and Selenium
- QTLs (*H. spontaneum* 41-1 x 'Arta')
  - tall plants under drought stress (7 QTLs)
  - prostrate growth habit
  - cold tolerance



Crop varieties released by the NARS partners using ICARDA germplasm between 2006 - 2018

Year	All	Wheat	Barley	Faba bean	Chickpea	Lentil	Grass-pea
2006	21	2	6	3	2	6	2
2007	27	9	6	1	4	5	2
2008	17	3	5		6	3	
2009	7	1				6	
2010	5	1	3			1	
2011	26	13	6	3	2	1	1
2012	27	8	8	1	5	5	
2013	43	12	10	3	9	9	
2014	23	5	4	4	5	4	1
2015	22	5	4	4	5	4	
2016	13	1	5		5	2	
2017	28	8	6	6	4	4	
2018	31	12	10		2	7	
Total	**290**	**79**	**73**	**25**	**49**	**57**	**6**