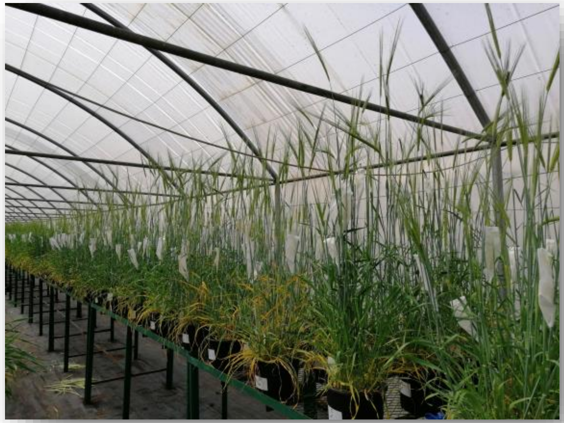
ICARDA

Science for resilient livelihoods in dry areas

WIDENING THE GENETIC BASE OF CULTIVATED GERMPLASM THROUGH PRE-BREEDING ACTIVITIES

A.L. Tsivelikas and GRS team



Trends on Genetic Diversity

Fortunately, existing varieties of most crops have quite a broad genetic base. Farmer-accepted, adapted varieties will continue to provide most of the genes that breeders need.

Theor Appl Genet (2010) 120:1241–1252
DOI 10.1007/s00122-009-1252-6

ORIGINAL PAPER

Genetic diversity trends in twentieth century crop cultivars: a meta analysis

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Received: 10 March 2009 / Accepted: 14 December 2009 / Published online: 7 January 2010
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Abstract In recent years, an increasing number of papers has been published on the genetic diversity trends in crop cultivars released in the last century using a variety of molecular techniques. No clear general trends in diversity have emerged from these studies. Meta analytical techniques, using a study weight adapted for use with diversity indices, were applied to analyze these studies. In the meta analysis, 44 published papers were used, addressing diversity trends in released crop varieties in the twentieth century for eight different field crops, wheat being the most represented. The meta analysis demonstrated that overall in the long run no substantial reduction in the regional diversity of crop varieties released by plant breeders has taken place. A significant reduction of 6% in diversity in the 1960s as compared with the diversity in the 1950s was observed. Indications are that after the 1960s and 1970s breeders have been able to again increase the diversity in released varieties. Thus, a gradual narrowing of the genetic base of the varieties released by breeders could not be observed. Separate analyses for wheat and the group of other field crops and separate analyses on the basis of regions all showed similar trends in diversity.

Communicated by A. Charcosset.

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Introduction

In the last century, scientific plant breeding has made an enormous impact on the agricultural landscape. In the early twentieth century knowledge about hybrids and mutations, and the application of Mendel's work on inheritance was instrumental in a dramatic leap forward in plant breeding (Murphy 2007). Breeders have continuously introduced new varieties with higher yields and which are adapted to changing farming systems and user demands. This has contributed to a large extent to the major increases in agricultural productivity which have been observed in the twentieth century (Dudley 1994). Especially the Green Revolution of the 1960s and 1970s was a very important achievement of plant breeders, contributing to global food security (Evenson and Gollin 2003).

However, concern has been raised that the major breeding efforts in the twentieth century have been a strong force in the reduction of crop genetic diversity (Gepts 2006). It is generally thought that continuous selection among crosses of genetically related cultivars has led to a narrowing of the genetic base of the crops on which modern agriculture is based, contributing to the genetic erosion of the crop gene pools on which breeding is based (Plucknett et al. 1987).

In the past, genetic uniformity of crops has led to several devastating attacks of pests and diseases. Well-known examples are the potato blight epidemic in Ireland in the 1840s, and the corn leaf blight which devastated maize production in the USA in the 1970s (Lopez 1994). New strains of old diseases might threaten future agriculture productivity. A new strain of stem rust is now a cause of concern to wheat growers (Singh et al. 2006b) and it is feared that the global banana production will face severe losses in the near future due to a new strain of Panama

Indications are that after the 1960s and 1970s breeders have been able to again increase the diversity in released varieties. Thus, a gradual narrowing of the genetic base of the varieties released by breeders could not be observed.

van de Wouw et al. (2010) Theor Appl Genet, 120:1241–1252.

On the other hand…

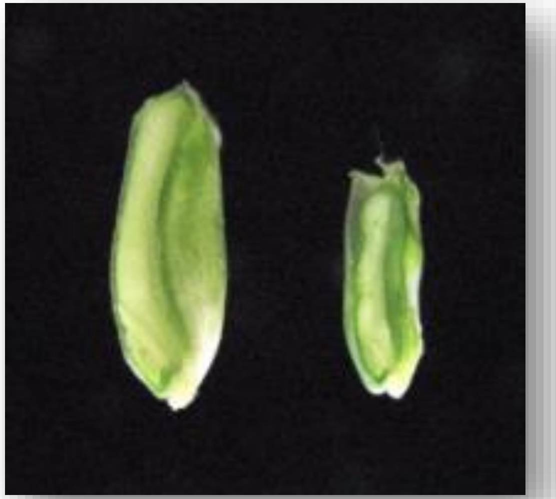
There will be a growing set of challenges and opportunities for which the current, adapted varieties are unable to provide the necessary traits.

- ✓ What are the prospects and the processes for making genetic improvement when the genes for the desired traits are not readily available?
- ✓ What are the alternatives?
- ✓ Where will the genes come from to meet these needs?

In cases like this you may think about…

PRE-BREEDING

- It is conducted to serve particular purposes and depends on various differing circumstances. **It is not an academic exercise.**
  - ✓ in the context of the final purpose that may be served
  - ✓ in the context of pre-conditions and circumstances
  - ✓ in the context of alternative options
  - ✓ in the context of practical implications



Thinking of our final objective…

- Broadening the genetic base of a crop to reduce vulnerability in biotic, abiotic factors (e.g., leaf rust resistance from *Ae. umbellulata* to wheat, salinity tolerance from *Thinopyrum bessarabicum, etc.*)
- Broadening the genetic base of a crop for novel traits (e.g., perennial wheat)
- Serve specific purposes (e.g. transfer of cytoplasmic male sterility for hybrid production)

Transfer of leaf rust resistance from *Aegilops umbellulata* to wheat (Sears, 1956)

Preconditions and Circumstances

- Successful pre-breeding depends on a range of pre-conditions and circumstances.
  - ✓ There is a reasonable possibility that the target trait or traits can be incorporated into farmer-accepted varieties and expressed at an appreciable level.
  - ✓ A well-managed genebank exists, with broad diversity, evaluated for the traits of interest.
  - ✓ Appropriate facilities exist (e.g., plastic houses, growth chambers, equipped laboratory (for embryo-rescue, chromosome doubling, chromosome mapping, etc.))
  - ✓ A comprehensive, capable and well-funded breeding program is operational.
  - ✓ The program can count on a supportive system of funding with a long-term perspective.

F1 interspecific wheat hybrids, after embryo-rescue
Photo: ICARDA

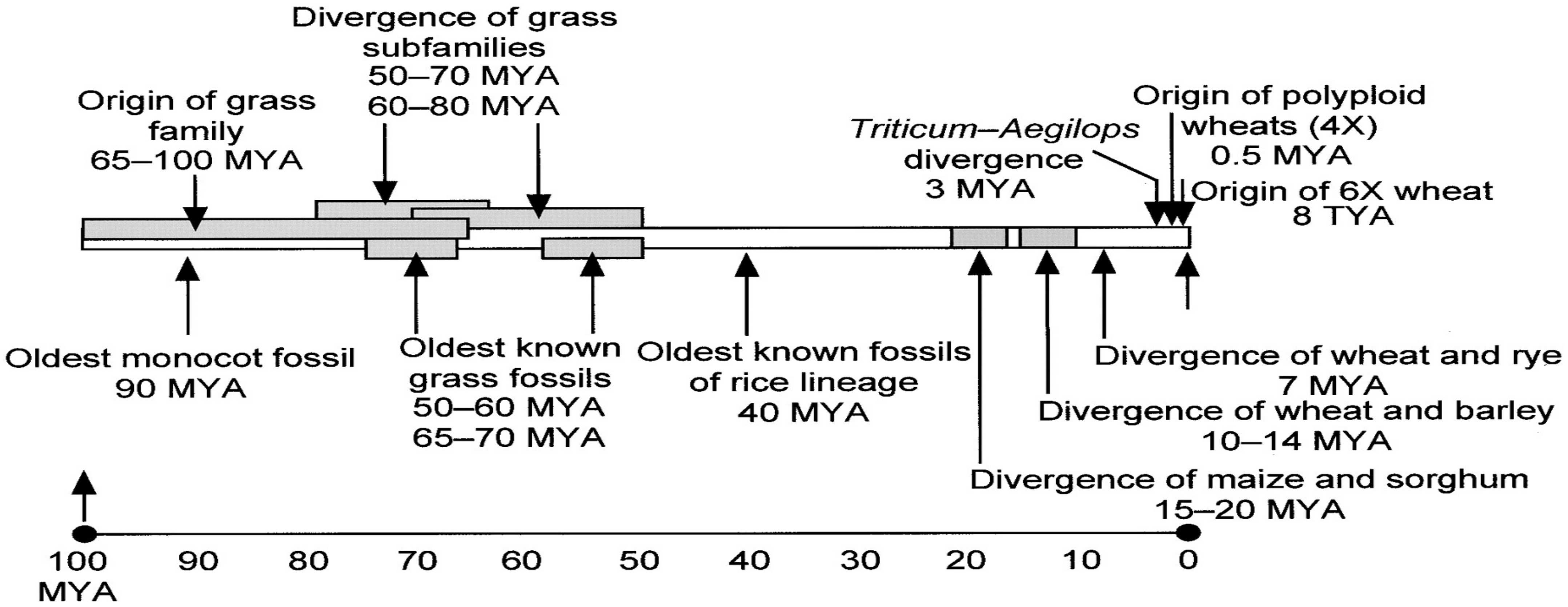
Chromosome doubling with colchicine
Photo courtesy: Dr Masanori Inagaki

Pre-breeding Activities at ICARDA

- Pre-breeding using wild progenitors started in 1994-1995
  - Durum wheat derivatives developed from crosses with:
    - *Aegilops speltoides*
    - *Triticum urartu*
    - *Triticum monococcum* subsp. *boeoticum*
    - *Triticum dicoccoides*
  - Synthetic hexaploids developed from crosses with *Aegilops tauschii* *(AABB x DD) → AABBDD (Synthetic hexaploid wheat)*

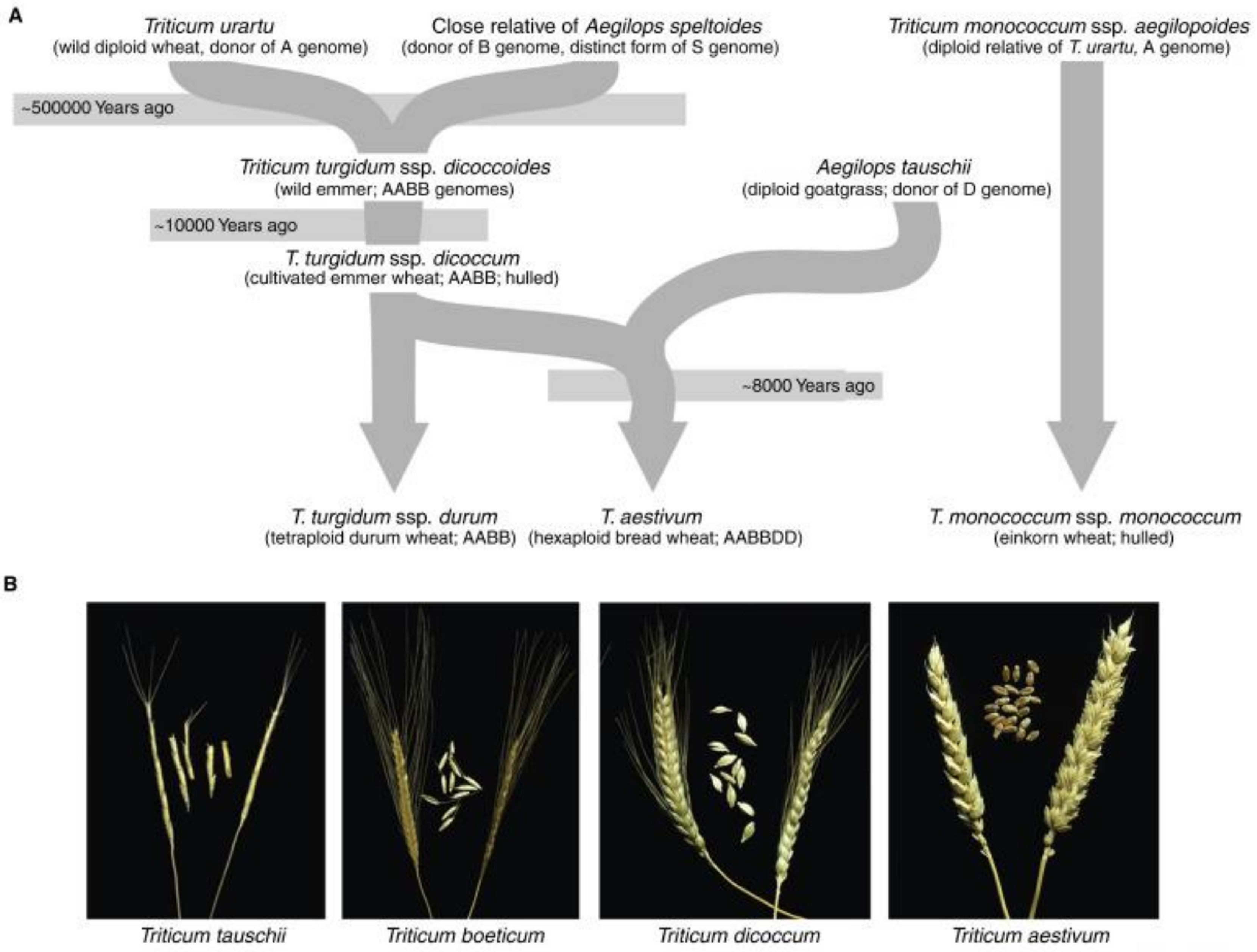
Synthetic hexaploidy wheat (middle) between Jennah Khaifa (durum wheat, left) and *Ae.tauschii* (IG48677, right)
Photo courtesy: Dr Masanori Inagaki

Cereals: A diversity traced back to millenniums

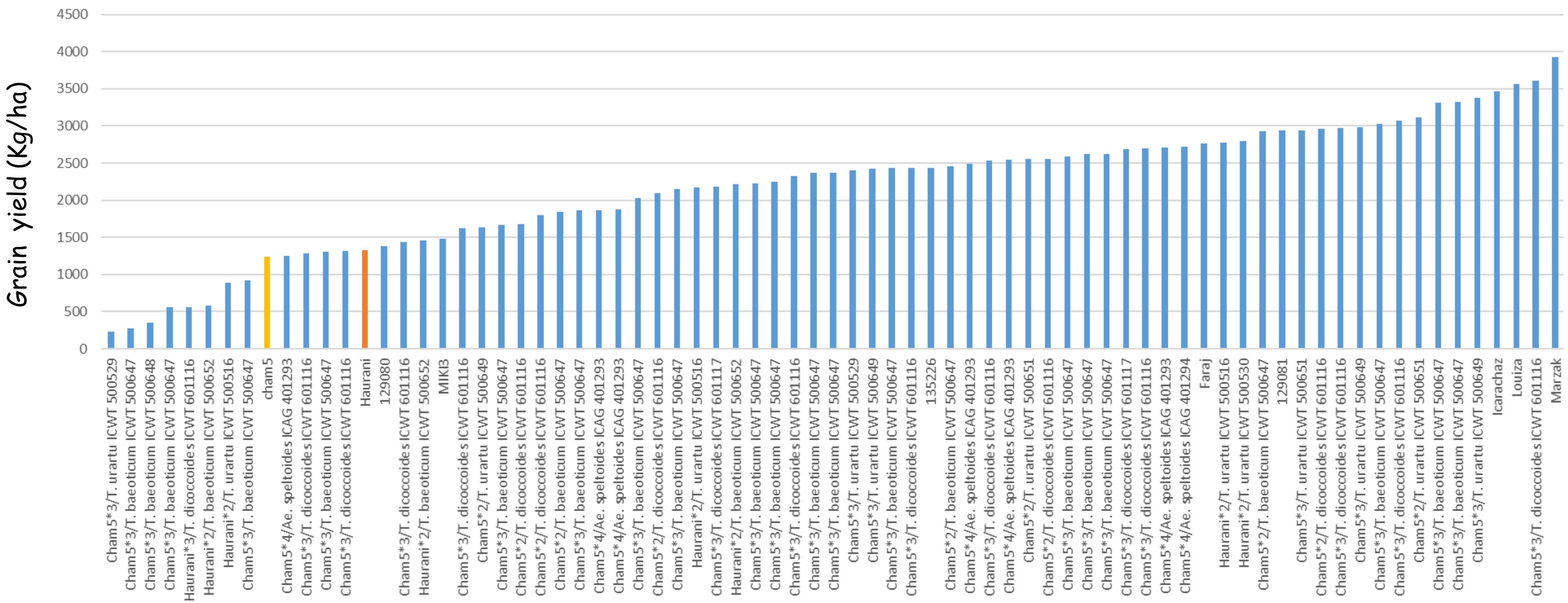


Raupp, 2004; Huang *et al.*, 2002

The Evolutionary Pathway of Wheat

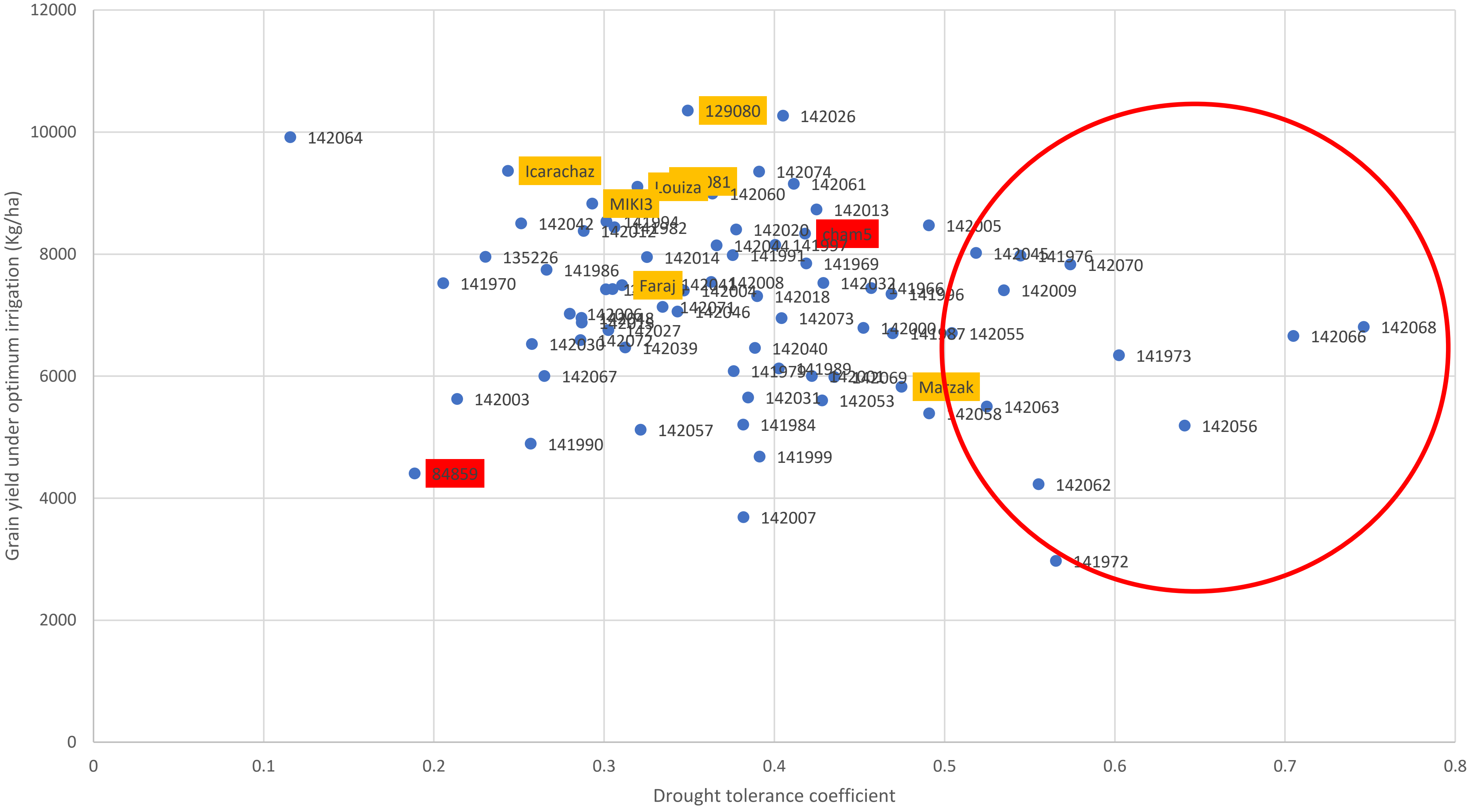


Pre-breeding Activities at ICARDA



Grain yield of durum wheat derivatives under heat stress in Sudan (2016-2017) (Aberkane H., 2021)

Pre-breeding Activities at ICARDA



Tessaout, Morocco 2016-2017 (Aberkane H., 2021)

Evaluation of Hordeum spontaneum accessions to diseases

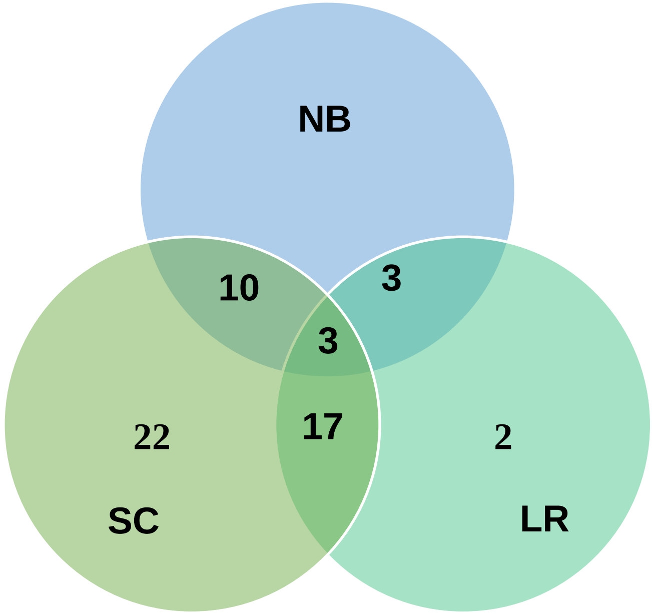
Screening of barley accessions with Spot blotch, Net blotch, LR

		# of Resistant accessions		
	# of accessions	*NB	*SB	¶LR
H. spontaneum	114	55	17	9
FIGS- Spot Blotch	48	3	6	-
FIGS- Scald	40	3	-	-
FIGS-Leaf Rust	75	-	-	2

* Seedling
¶ Adult plant

Novel disease resistance sources from *H. spontaneum*

Screening of 90 *H. spontaneum* accs. under field conditions, by artificial inoculation



Pre-breeding Activities at ICARDA


Breeding Science 61: 347–357 (2011)
doi:10.1270/jsbbs.61.347

Applicability of *Aegilops tauschii* drought tolerance traits to breeding of hexaploid wheat

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Few genes are available to develop drought-tolerant bread wheat (*Triticum aestivum* L.) cultivars. One way to enhance bread wheat's genetic diversity would be to take advantage of the diversity of wild species by creating synthetic hexaploid wheat (SW) with the genomic constitution of bread wheat. In this study, we compared the expression of traits encoded at different ploidy levels and evaluated the applicability of *Aegilops tauschii* drought-related traits using 33 *Ae. tauschii* accessions along with their corresponding SW lines under well-watered and drought conditions. We found wide variation in *Ae. tauschii*, and even wider variation in the SW lines. Some SW lines were more drought-tolerant than the standard cultivar Cham 6. *Aegilops tauschii* from some regions gave better performing SW lines. The traits of *Ae. tauschii* were not significantly correlated with their corresponding SW lines, indicating that the traits expressed in wild diploid relatives of wheat may not predict the traits that will be expressed in SW lines derived from them. We suggest that, regardless of the adaptability and performance of the *Ae. tauschii* under drought, production of SW could probably result in genotypes with enhanced trait expression due to gene interactions, and that the traits of the synthetic should be evaluated in hexaploid level.

Key Words: wheat, *Aegilops tauschii*, synthetic hexaploid wheat, wild relatives of wheat.

Introduction

Feeding the world's growing population is becoming a huge challenge. Food prices, food shortages, and malnutrition are increasing (Webb 2010). Climate change is expected to worsen the current situation through its effects on global agricultural systems (Battisti and Naylor 2009, Bloem *et al.* 2010). Severe scenarios such as significant drying in some regions, leading to an increased frequency and severity of extreme droughts, are expected (Allen *et al.* 2010, Camicer *et al.* 2010, Soussana *et al.* 2010). Bread wheat (*Triticum aestivum* L.) is affected by periodic drought in around 50% of its cultivated area (Rajaram 2001), and its productivity is often limited because there is insufficient water to maximize biomass and complete grain-filling (Aprile *et al.* 2009).

Few genes have been identified in bread wheat that can be used to develop drought-tolerant cultivars. Millions of years ago, a natural hybridization may have occurred between the wild diploid wheat *Triticum urartu* (genome AA) and the wild grass *Aegilops speltoides* (SS), resulting in the AABB tetraploid emmer wheat, *Triticum dicoccoides* (Mujeeb-Kazi *et al.* 1996). Later, the domestication of emmer wheat led to the evolution of durum wheat, *Triticum durum* ($2n = 28$, AABB), which was in turn hybridized with the diploid wild goat grass *Aegilops tauschii* (genome DD) to produce hexaploid bread wheat, *Triticum aestivum* (AABBDD) about 8000 to 10 000 years ago (Feldman 2001, Helbaek 1959, Kihara 1944, Mujeeb-Kazi *et al.* 1996). Although considerable genetic diversity was preserved in the land races grown by farmers since ancient times, before the spread of modern cultivars with a narrow genetic base, modern wheat breeders have increasingly narrowed this genetic diversity by emphasizing pure-line cultivars. As increasing emphasis was placed on pure lines with higher yields during the Green Revolution, considerable genetic diversity was lost.

Improving wheat drought tolerance through selection and breeding requires a reasonably high level of heritable variation among wheat genotypes or the incorporation of variation from wild relatives, which may serve as a rich source of appropriate genetic variation (Ashraf 2010). As a widely adaptable direct ancestor of bread wheat, *Ae. tauschii* appears to be the most desirable species for wheat improvement among the more than 300 wild species in the tribe

Communicated by M. Iwanaga
Received July 4, 2011. Accepted August 5, 2011.
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However…

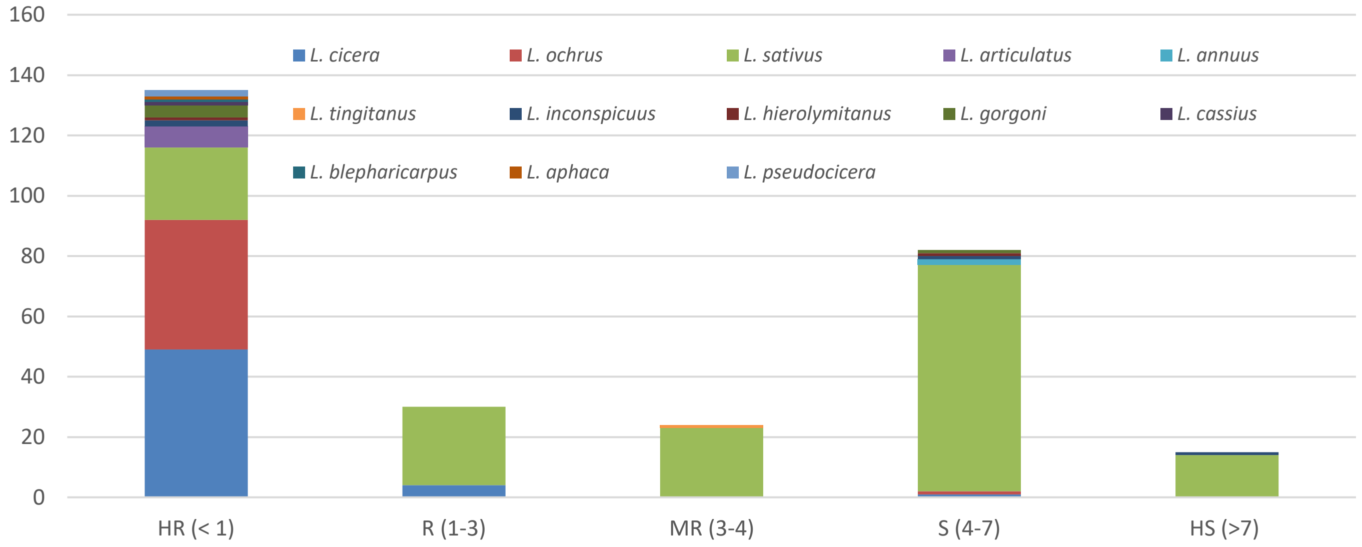
The traits of *Ae. tauschii* were not significantly correlated with their corresponding SW lines, indicating that the traits expressed in wild diploid relatives of wheat may not predict the traits that will be expressed in SW lines derived from them..

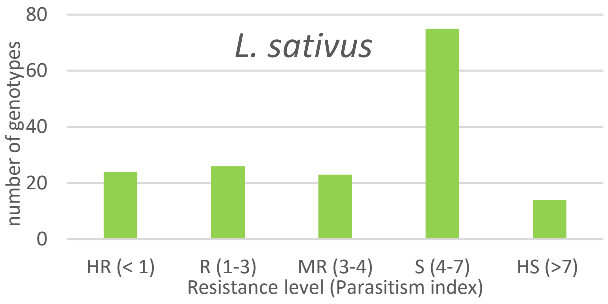
Sohail et al. (2011)

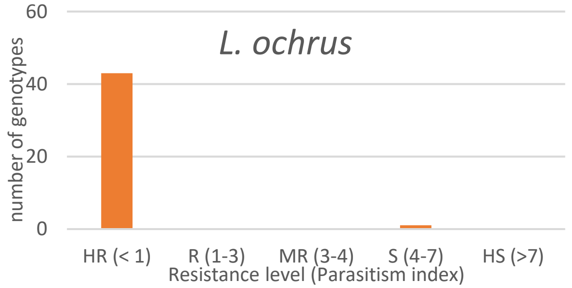
Screening for resistance to *Orobanche* spp. in grass pea

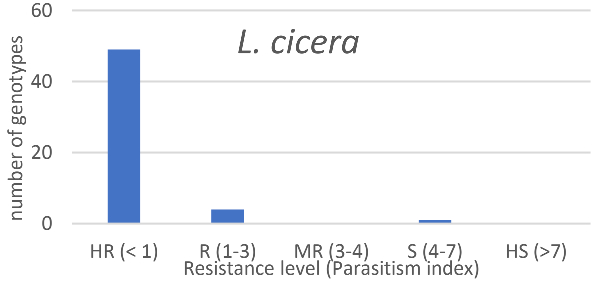
13 *Lathyrus* species, 286 genotypes

- *O. crenata* resistance: Douiyet and Marchouch, Morocco
- *O. foetida* resistance: Beja, Tunisia









Crossing program 2018

	♀ L. sativus (GP90111)
♂ L. ochrus (IG_65373)	x
♂ L. gorgoni (IG_65330)	x
♂ L. articulatus (IG_64786)	x
♂ L. cicera (IG_64862)	x
♂ L. sativus (IG_64782)	x
♂ L. sativus (IG_117496)	x

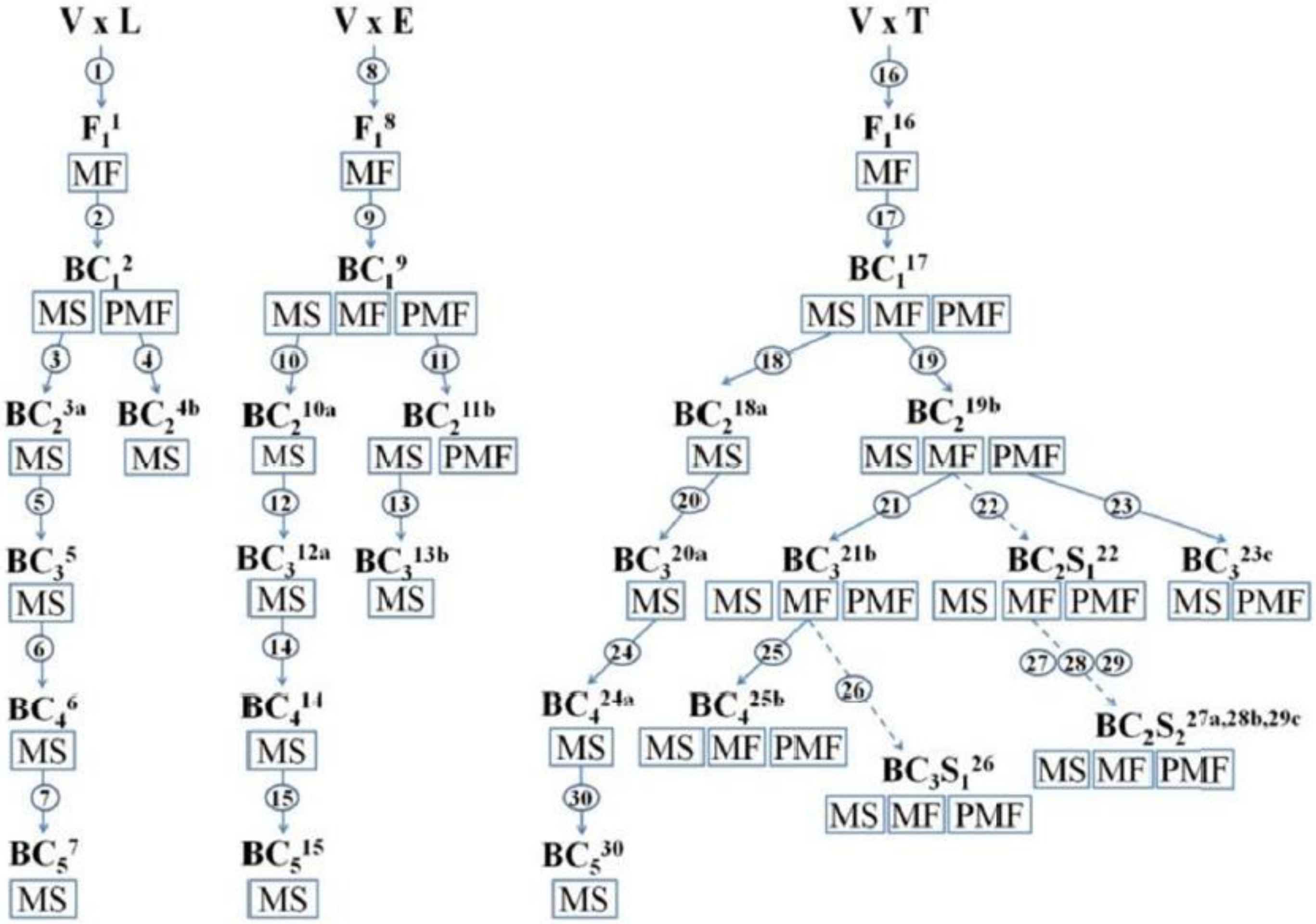
	♂ L. sativus (GP90111)
♀ L. ochrus (IG_65373)	x
♀ L. gorgoni (IG_65330)	x
♀ L. articulatus (IG_64786)	x
♀ L. cicera (IG_64862)	x
♀ L. sativus (IG_64782)	x
♀ L. sativus (IG_117496)	x

Pre-breeding for Specific Purposes

- Transfer of CMS in eggplant (*Solanum melongena*) for hybrid production
  - ✓ Need for cost effective hybrid production in eggplant
  - ✓ A number of wild species can serve as cytoplasm donors in the development of eggplant CMS lines (*S. gilo*, *S. violaceum*, *S. virginianum*, *S. kurzii*, *S. integrifolium*, *S. anguivi* and *S. grandifolium*)
  - ✓ But… the development of reliable CMS systems accompanied by genes that restore fertility (Rf-genes)
  - ✓ In the NAGREF, Greece a CMS system accompanied by Rf-gene for fertility restoration has been developed by using the cytoplasm of *Solanum violaceum*

Pre-breeding for specific purposes (Transfer of CMS in eggplant)

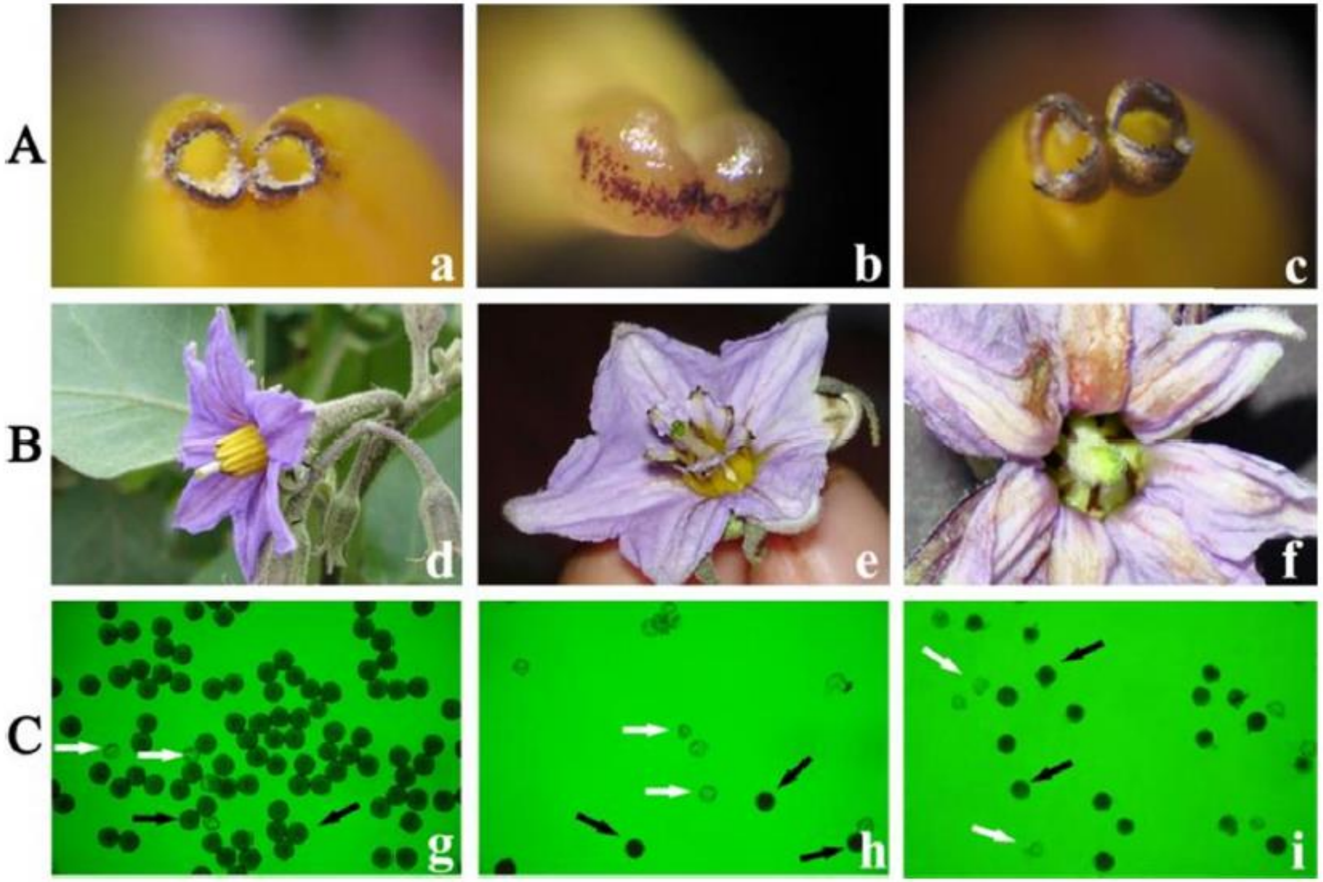
- Flowchart for the development of SMC lines



Krommydas et al. (2016), J. Agric. Sci. 8(2): 10-26

Pre-breeding for specific purposes (Transfer of CMS in eggplant)

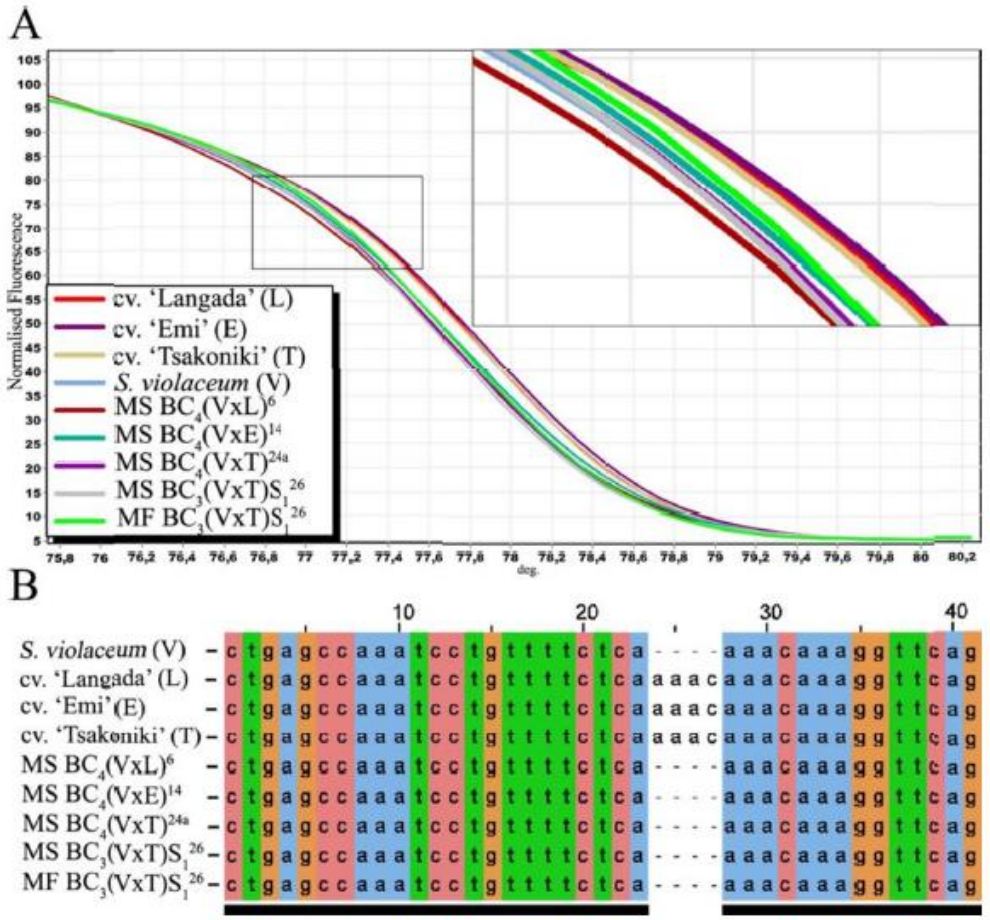
- Anther dehisence (A), anther morphology (B) and pollen viability (C) in MS and MF plants carrying the *S. violaceum* cytoplasm



Krommydas et al. (2016), J. Agric. Sci. 8(2): 10-26

Pre-breeding for specific purposes (Transfer of CMS in eggplant)

- Chloroplast DNA anasysis in three eggplant cultivars, the *S. violaceum* accession and MS plants carrying the *S. violaceum* cytoplasm



Krommydas et al. (2016), J. Agric. Sci. 8(2): 10-26

Alternative Options

- If a target trait is common in unadapted genebank accessions, it could probably be found in some adapted varieties as well, and pre-breeding should not be necessary.
  - ✓ Screen larger number of individuals within adapted germplasm
  - ✓ Employ "novel" cultural techniques/practices (e.g. grafting)

Thinking of the Practical Implications

Pre-breeding is generally a strategy for practical, applied results.

- However…
  - ✓ Sometimes the results may be more theoretical than applied…. Literature full of references for potentially useful traits among cultivated and wild relatives.
  - ✓ Little discussion about cost, time, or facilities required to move the genes of interest into suitable varieties.
  - ✓ Rare comparisons to other means of achieving the same level of expression of a trait.

Photo courtesy: Dr Masanori Inagaki

Questions to be answered ahead of time…

- Is the same trait available in better-adapted material?
- Are there lower-cost or more effective options than genetic manipulation?
- How long will it take and how much will it cost to move the genes in question into commercial varieties?

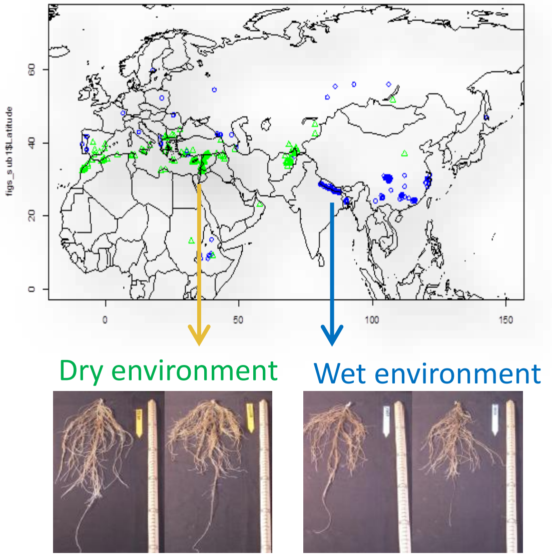
The challenge is to find useful genes in material that is reasonably easy for the pre-breeder to work with to develop new sources for the breeder.

Transfer resistance to Hessian Fly from *Triticum araraticum*

Exploit wild wheat germplasm through pre-breeding to solve Hessian fly problem of wheat in Morocco and beyond

↓

Five Hessian fly resistant durum wheat and four bred wheat varieties are released in Morocco, all derived from interspecific crosses



THANK YOU FOR YOUR KIND ATTENTION!

PRE-BREEDING

All the activities designed to identify desirable characteristics (and/or genes) from unadapted germplasm, and to transfer these traits to an intermediate set of materials that breeders can manipulate further in producing new varieties for farmers.