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SLU

ICARDA

Science for resilient livelihoods in dry areas

Squeezing the good stuff out of the vaults:

fields, genomics, or genebankomics?

Filippo M Bassi

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M Sanchez-Garcia, A Visioni, Z Kehel, K H Kabbaj, M Zaim, AT Sall, Y Jabbour, A Gautam, El Hassouni, S Alahamad, AA Niane, M Nachit, L Hickey, I&J King, R Ortiz, M Bouhssini, M Baum, **A Amri**

icarda.org

International Center for Agricultural Research in the Dry Areas

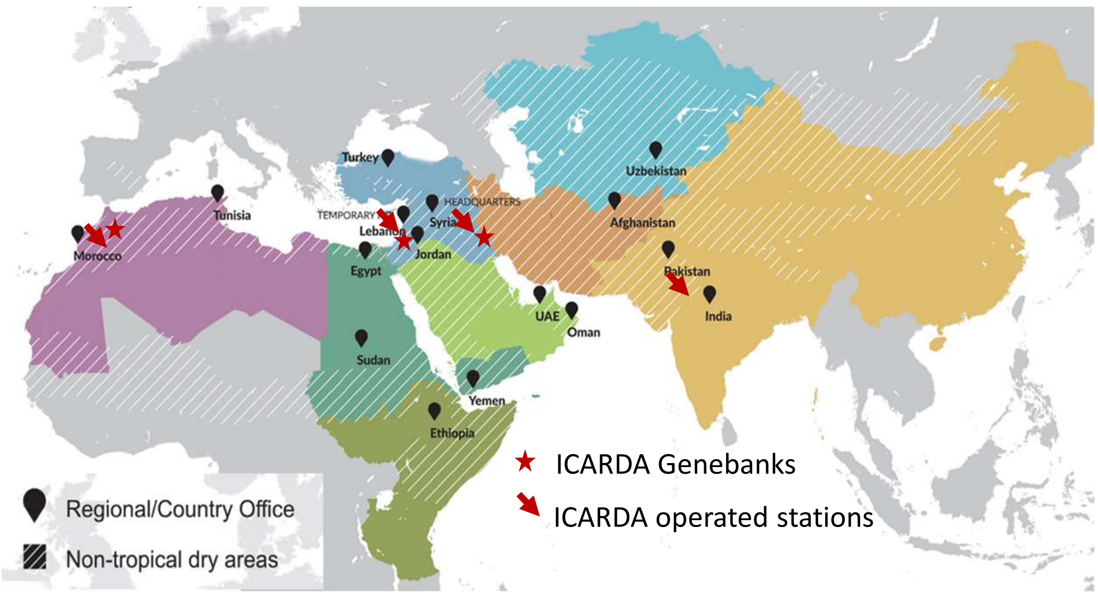
CGIAR RESEARCH PROGRAM ON Wheat

cgiar.org

A CGIAR Research Center

CGIAR

ICARDA: non tropical dryland agriculture



Marchouch (Morocco) ★

Terbol (Lebanon) ★

Amlaha (India)

Tel Hadya (Syria) ★

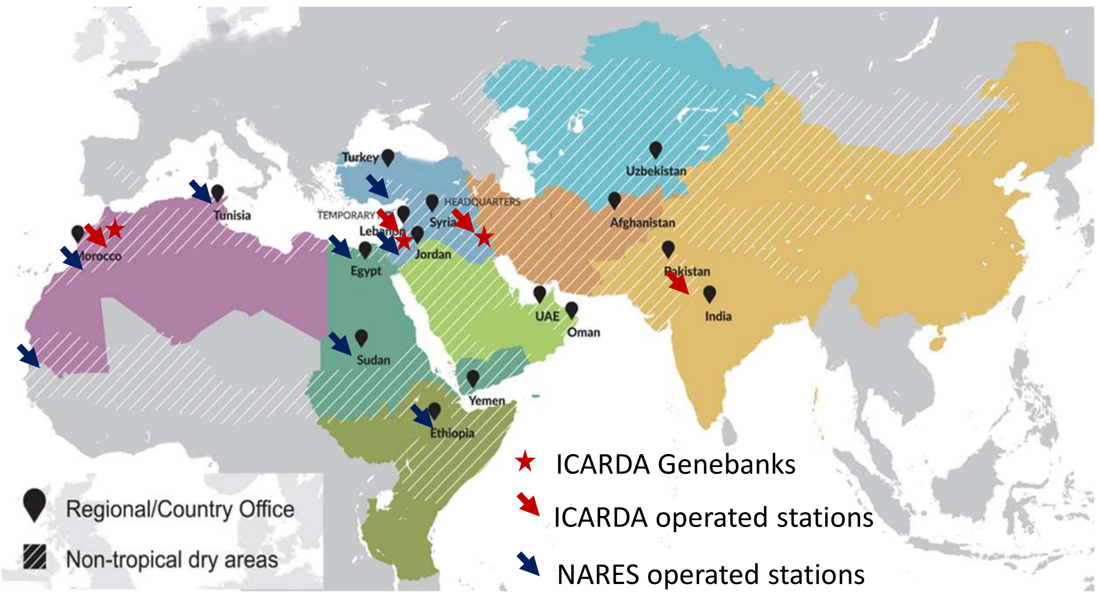
Over 1,200 agricultural innovations adopted globally

50 current projects in 33 countries

187 current partners

1600 total ISI publications

ICARDA: non tropical dryland agriculture



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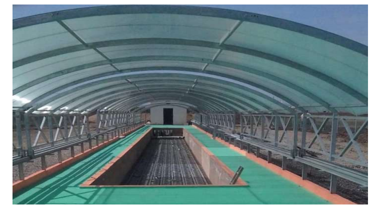


Sidi el Aydi (Morocco)

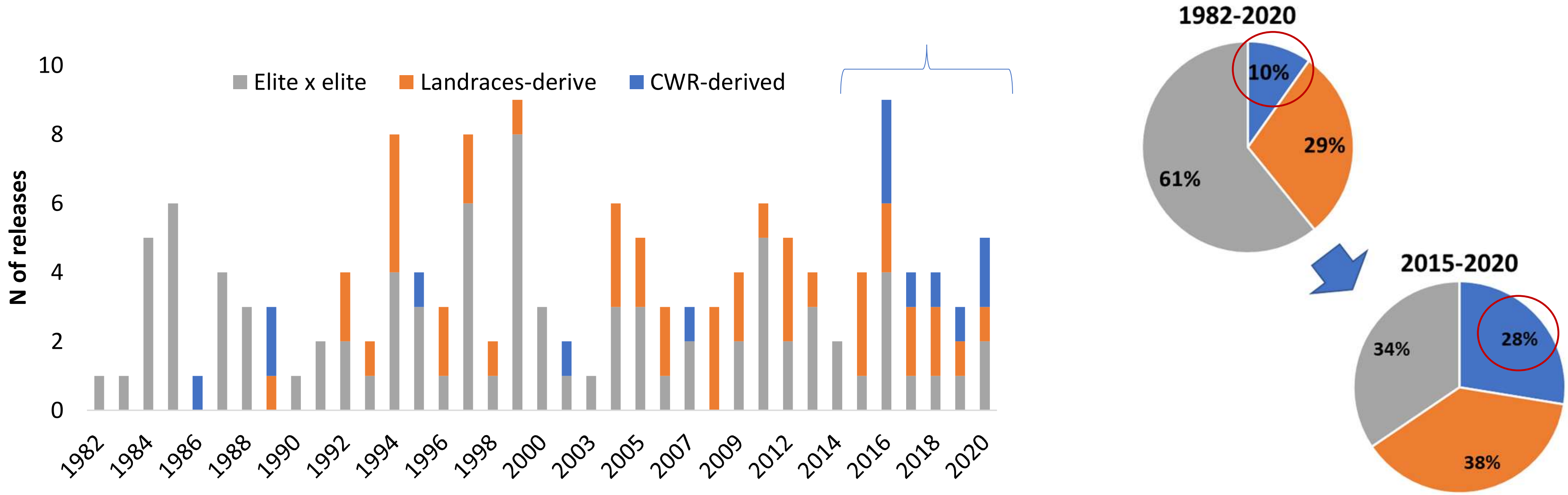
Izmir (Turkey)

Wad Medani (Sudan)

Fanaye (Senegal)

In « wide » we trust!

- Among **143** varieties released in 22 countries, **10%** from CWR, and **29%** from landraces
- Last 5 years: **28%** from CWR, and **38%** from landraces



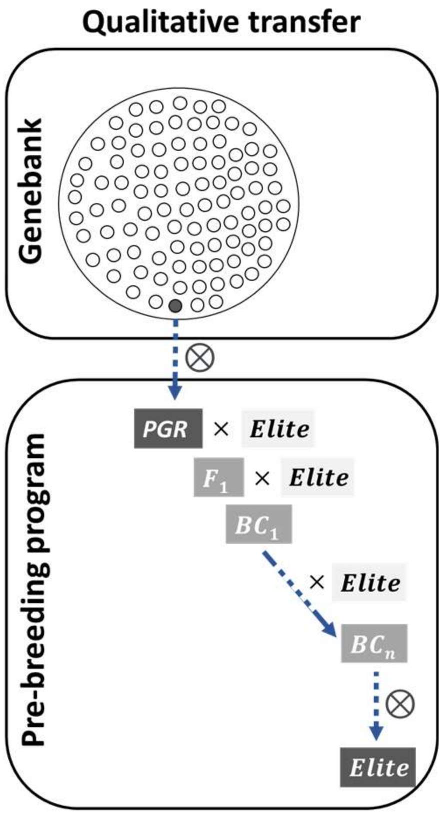
Three players to "score" change

Genebank(er)

Breeder

Pre-breeder

Qualitative transfer



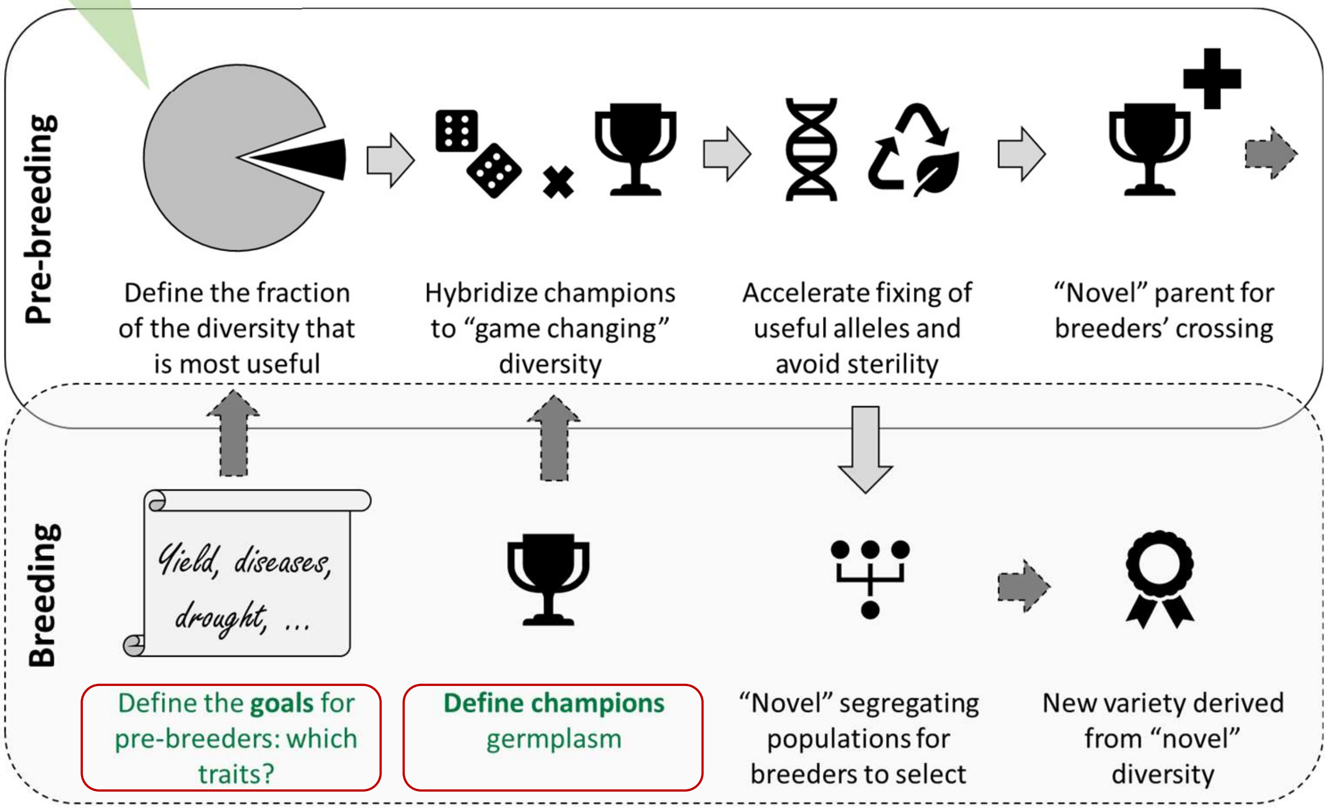
Albert W. Schulthess, *IPK*

- Breeders want **ONE trait** and "nothing else"
- The germplasm collection is screened first
  - **Phenotyping of PGR** needs to be possible
- Back-crossing (PGR/A//A/3/A) vs top-crossing (PGR/A//B)
  - MAS is a good option, but it requires investments
- When the elite parent(s) are good> **direct release**
  - *i.e. adding a useful trait to an already great elite*

"the fear" of the pre-breeders

Shivali et al. submitted. Introducing beneficial alleles from plant genetic resources into the wheat germplasm

The (Pre-)breeding pipeline continuum



Langdon set (NDSU, Fargo)

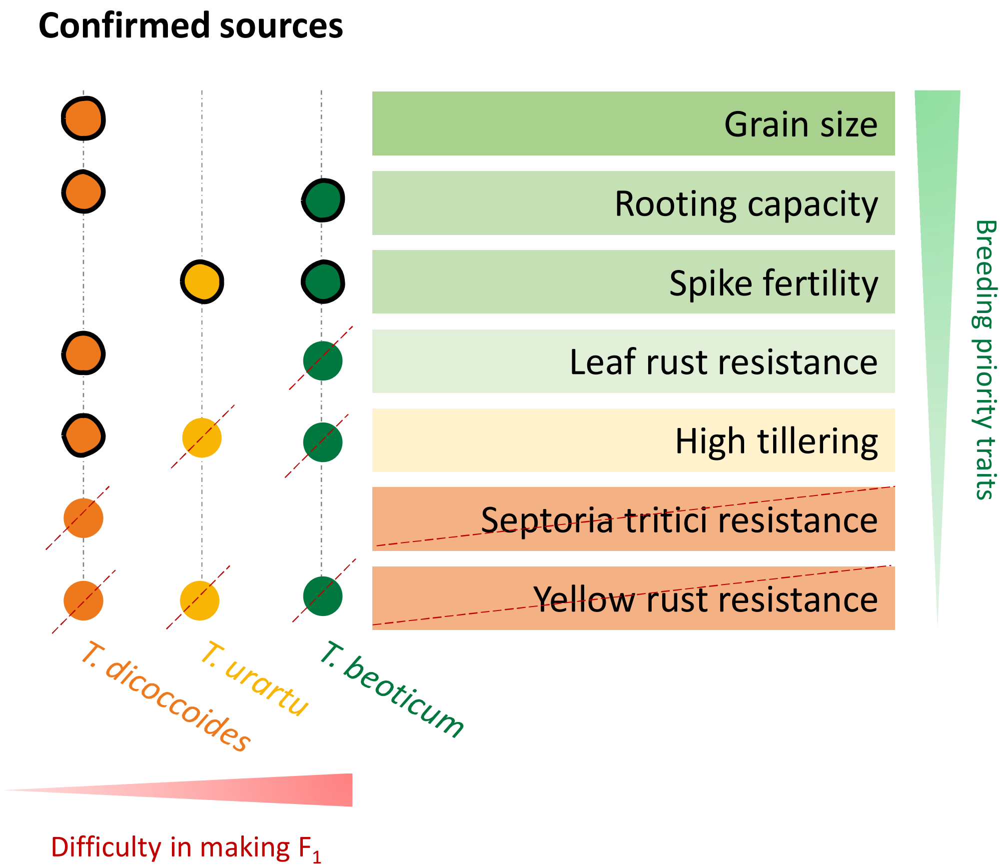
Shivali et al. submitted. Introducing beneficial alleles from plant genetic resources into the wheat germplasm

Seeking the ONE trait: « *alone* »

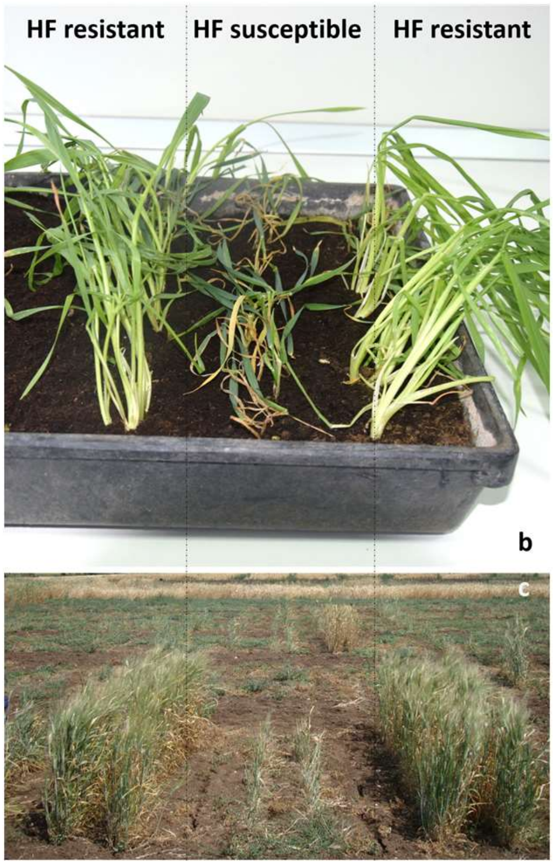
Confirmed sources

Trait	*T. dicoccoides*	*T. urartu*	*T. beoticum*
Grain size	●		
Rooting capacity	●		●
Spike fertility		●	●
Leaf rust resistance	●		●
High tillering	●	●	●
Septoria tritici resistance	●		
Yellow rust resistance	●	●	●

Seeking the ONE trait: « *together* »



Hessian Fly resistant variety

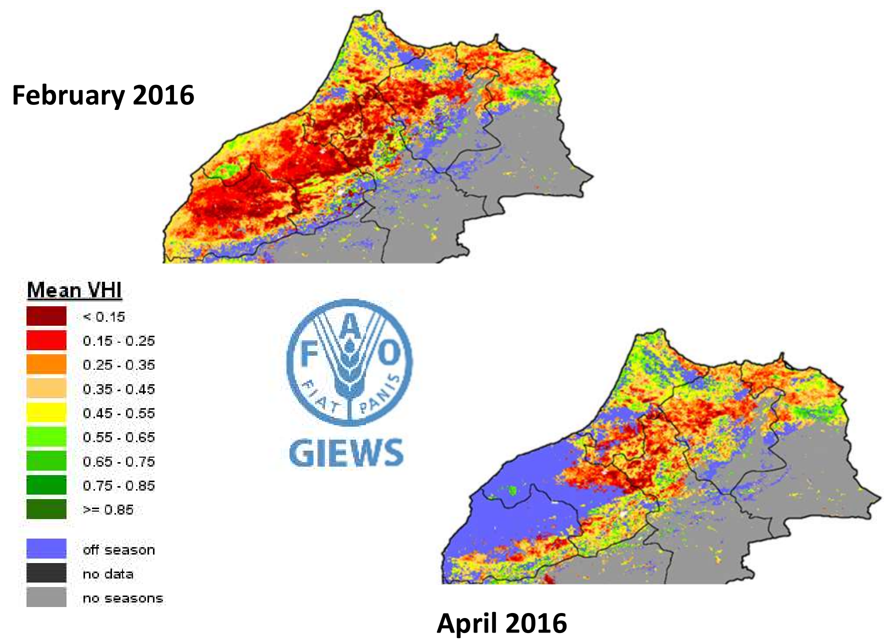


In Morocco, this insect causes 32–36% yield losses

- **1989:** 4 accessions of *Triticum araraticum* were identified as resistant from Kansas State University Small Grain
- **2003** (+14 yrs) first release of HF resistant cultivars
- **2007** (+18 yrs) release of "**Faraj**" after **3 "top crosses"**: **T.ararticum**/2*Arthur71//Lahn/3/Blk2/Lahn/4/Quarmal

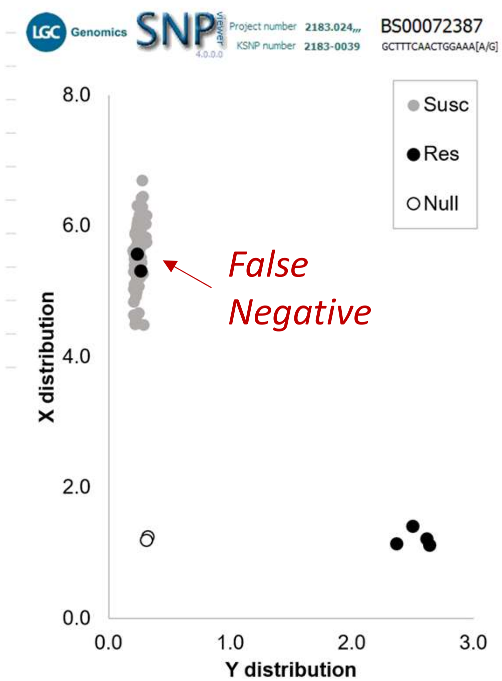
Bassi et al. 2019 Doi: 10.1007/s11032-019-0927-1

A difference in farmers fields



MAS for Hessian Fly resistance

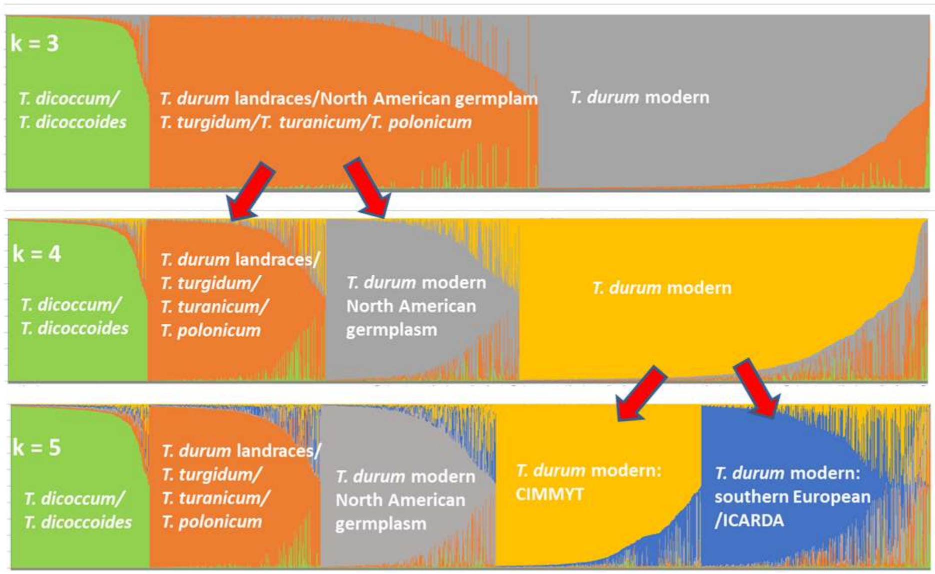
- **In 2019** (+30 years)**:** one marker validated for MAS > ready to scale in all germplasm



Allele	Type	HF response	N	Ratio
Suscept.	**TN**	**Susceptible**	**610**	**93%**
	FN	*Resistant*	*45*	*7%*
Resistant	FP	Susceptible	0	0%
	TP	**Resistant**	**32**	**100%**

Bassi et al. 2019 Doi: 10.1007/s11032-019-0927-1

The Global Durum Panel (GDP)



- Seeking the **help of the whole community**: it was derived from 3,700 entries (21 partners)
- It represents all the “exploited” diversity of durum wheat

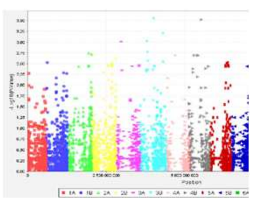
Mazzucotelli et al. 2021 Doi: 10.3389/fpls.2020.569905

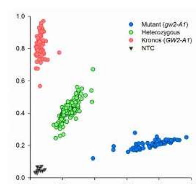
One global crossing block:

45 sets distributed

- Order the seeds at: http://indms.icarda.org/
- Get the 90K Illumina data from Gigwa

- Do your favorite phenotyping





- Run GWAS
- Validate for MAS

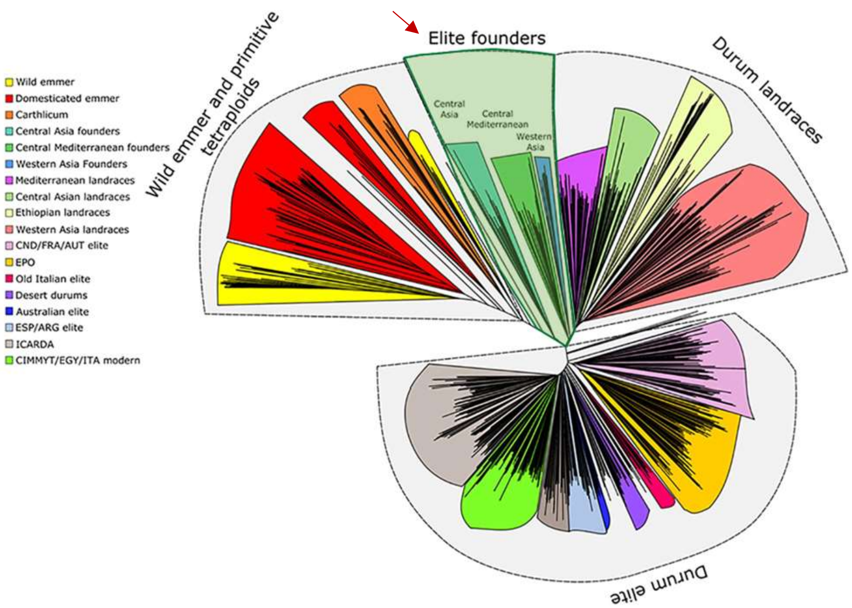
- Publish

- Tell the durum community

New alleles are rapidly exchanged to "save" durum from Climate Change

Diversity “pre se” vs “usable” diversity!

- Breeders have captured more diversity than what we give them credit for
- Diversity “per se”: is it really “useful”?

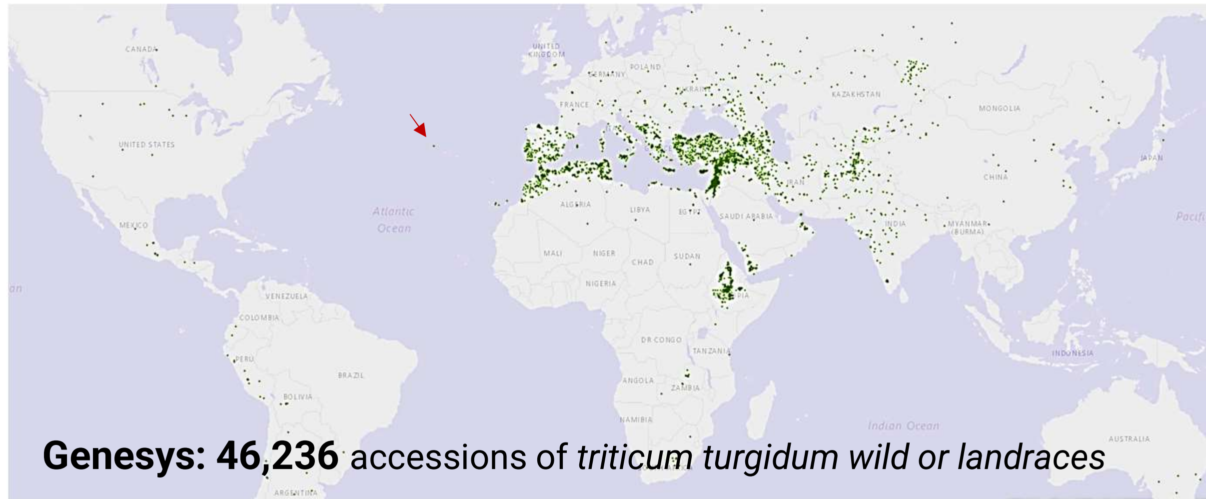


Cluster ID	N	MAF (%)	
		Common	Rare
1. Middle East	11	0.13	0.00
2. *T. abyssinicum*	18	0.42	0.01
3. Mediterranean	26	0.65	0.06
4. C. and S. Asia	27	<u>0.84</u>	<u>0.62</u>
5. ‘Om Rabi’	13	0.19	0.00
6. Italian	26	0.46	0.01
7. Exchange	58	0.58	0.04
8. Developed	30	0.43	0.01
9. ICARDA	119	0.51	0.03
10. CIMMY	42	0.44	0.21

Mazzucotelli et al. 2021 Doi: 10.3389/fpls.2020.569905

Kabbaj et al. 2017 Doi: 10.7717/peerj.281

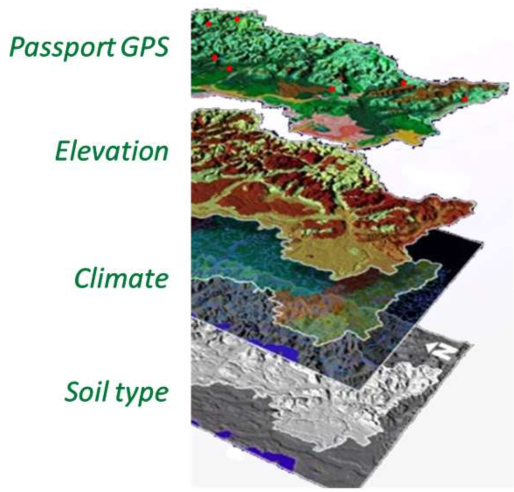
Immobilism by overabundance

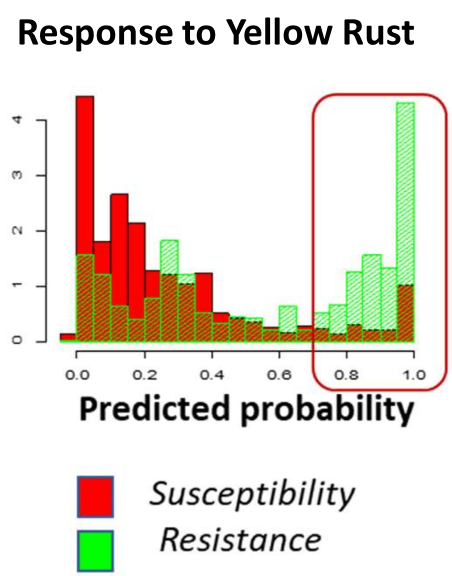


- It would take ICARDA program **50 years** to make a cross to each and bring it to inbreeding
- Many (pre-)breeders ask the question: **what should I use?**
- *.. and the answer is often more complex than one would imagine..*

Focus Identification of Germplasm Sources (FIGS)

- Using passport data (GPS) to sub-set the genebank collections
- It has proven very effective for many traits





FIGS subset		Confirmed	
Trait	**N**	**N**	**Ratio**
Net blotch	96	18	19%
Powdery mildew	352	98	28%
Leaf rust	84	45	54%
Yellow rust	*293*	*129*	*44%*
BYDV	100	27	27%

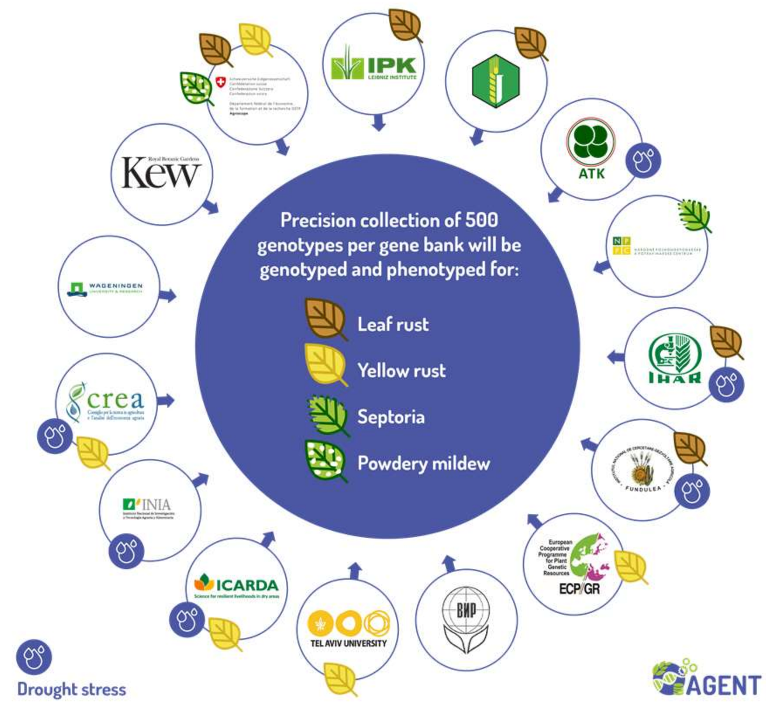
Activate GEnebank NeTwork

- Deploying genomic models to predict performances of landraces
- 15 Genebanks
- https://agent-project.eu/

Accuracy of prediction for grain morphology in landraces

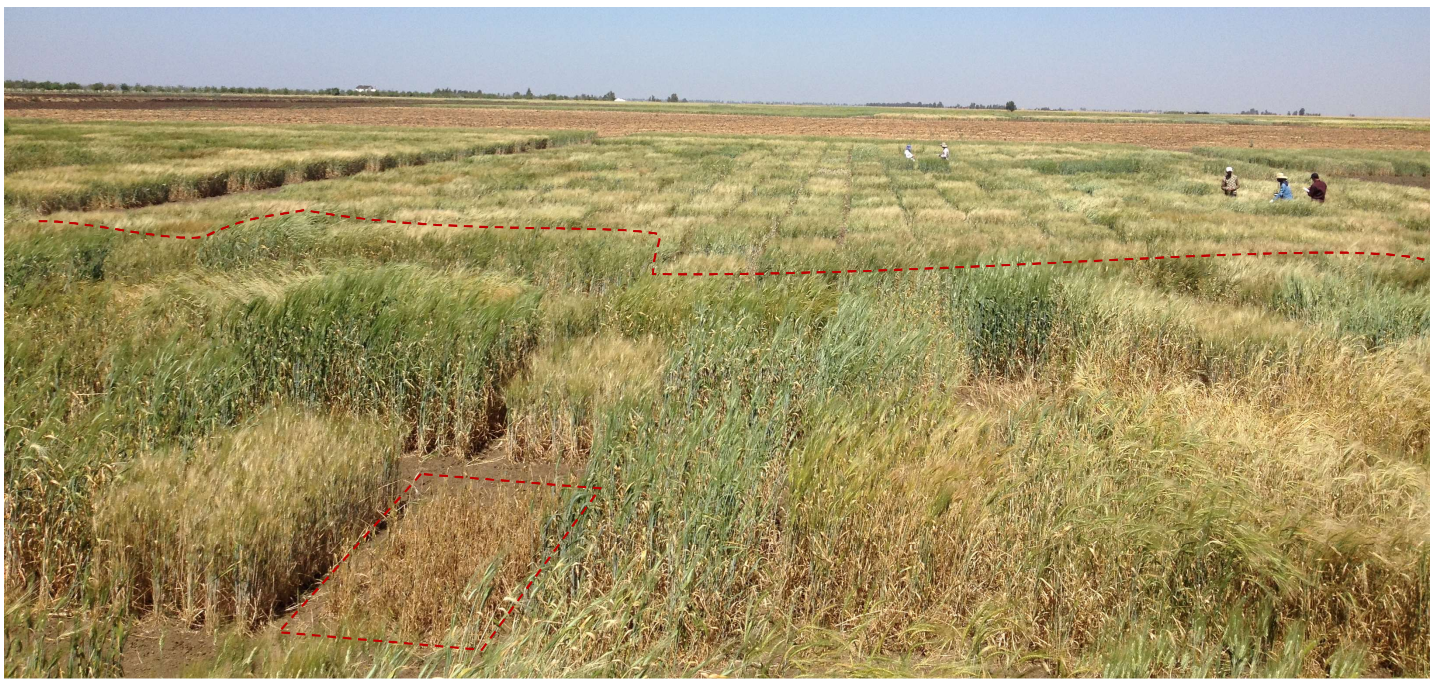
		Area	Perimeter	Length	Width
GEBV	Mean	0.70	0.64	0.66	0.74
	Maximum	0.76	0.73	0.74	0.80
	Minimum	0.64	0.55	0.57	0.67
FIGS+	Mean	0.75	0.70	0.70	0.78
	Maximum	0.78	0.75	0.77	0.81
	Minimum	0.66	0.59	0.59	0.69

Kehel et al. 2019 Doi: 10.3389/fevo.2020.00032

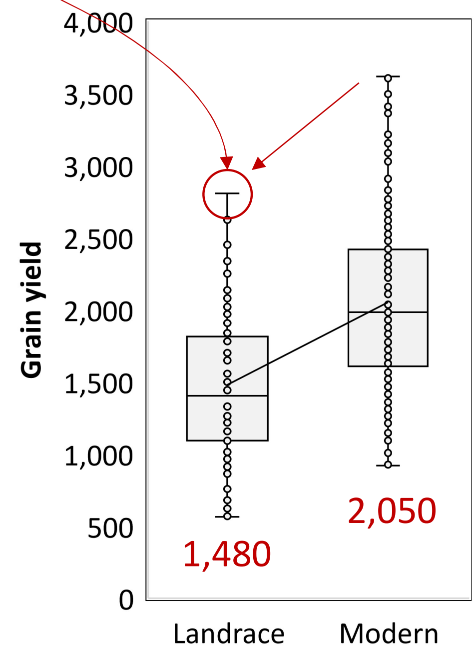


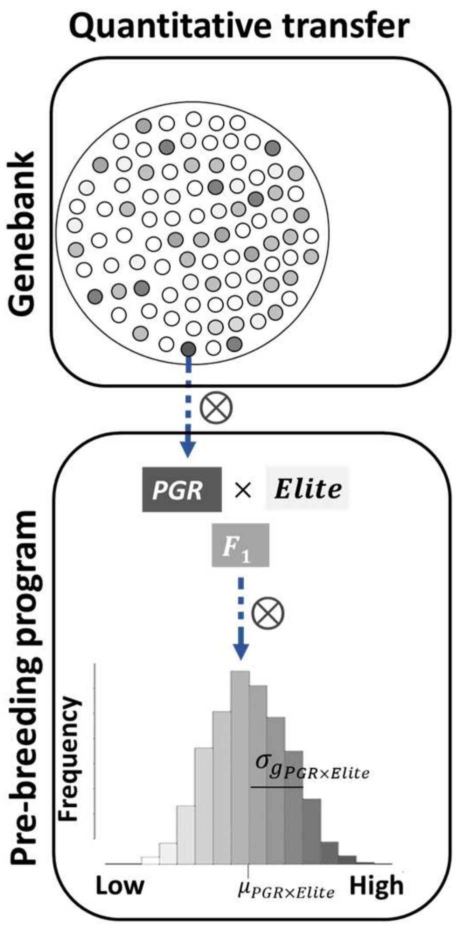
Quantitative traits: what role for PGR?

- **PGR:** are suitable to be characterized for traits with **low GxE effect**
- For complex quantitative traits, the comparison with modern germplasm creates bias for identification
  - i.e.: is a "*top yielding landrace*" useful for breeding?



Marchouch: dry year





Albert W. Schulthess, *IPK*

Quantitative transfer

- Breeders want **"Exploitable diversity"** for critical traits
- The germplasm collection *could be* screened first
  - **Phenotyping of PGR** can be very <u>challenging</u>
- 3- ways crosses are the preferred system
- Genomic predictions are an option, but hard to use:

all combinations of PGR x Elite crosses are extremely challenging to predict on the basis of the available genetic value of the two parents

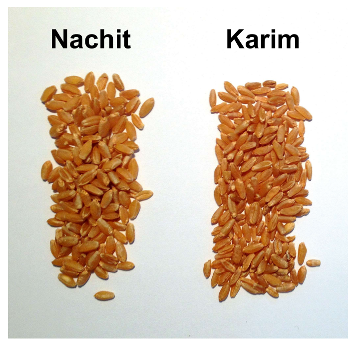
Shivali et al. submitted. Introducing beneficial alleles from plant genetic resources into the wheat germplasm

“Nachit” for drought tolerance

- Amedakul/**T. dicoccoides Syr**//Loukus

The cross was made by ICARDA GB without knowing the “actual value” of T. dicoccoides, the F_2 were given to breeders

- Released in **2017** by Dr Taghouti (INRA) as ‘**Nachit**’



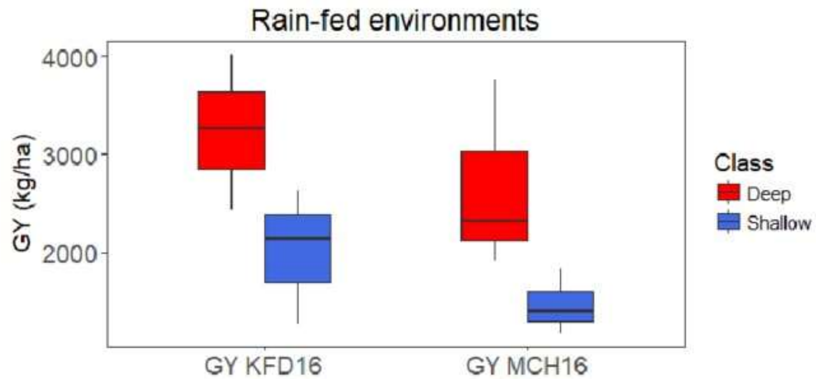
Zaim et al. 2017. **Field Crop Research**, 214:219-227.

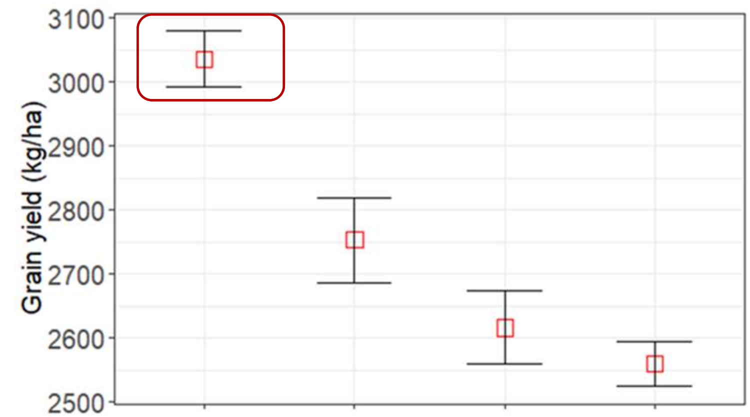
Beyond any reasonable doubts

- *Nobody thought of this use when making the cross* *for sure*
- Recycle drippers, 250-300 mm of water, and 150 Kg of Nitrogen:
  - **>13% protein , > 6 t ha^{-1} yield**


Var. 'Nachit' in Melk Zehr, 2019

"Nachit": a deep rooted dicoccoides



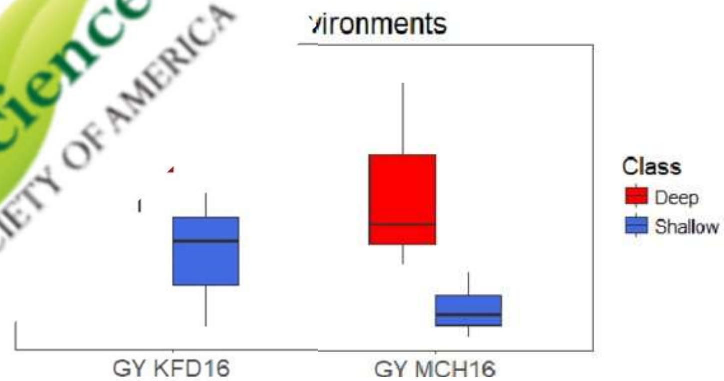


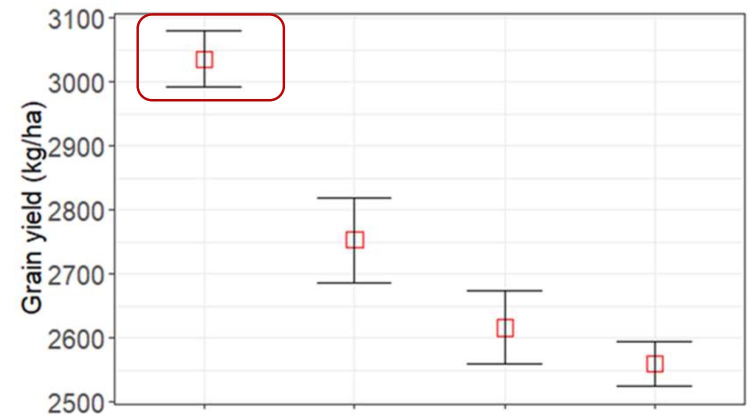
QTL.ICD.Root.01	+	+	-	-
QTL.ICD.Root.02	+	+	-	-
QTL.ICD.Root.04	+	-	+	-

- Deep roots under drought have a yield advantage of **+39%**
- Three QTLs controls root angel and together increase yield **+300 Kg ha^{-1}**

El Hassouni et al. 2018 Doi: 10.2135/cropsci2018.01.0076

“Nachit”: a deep rooted dicoccoides





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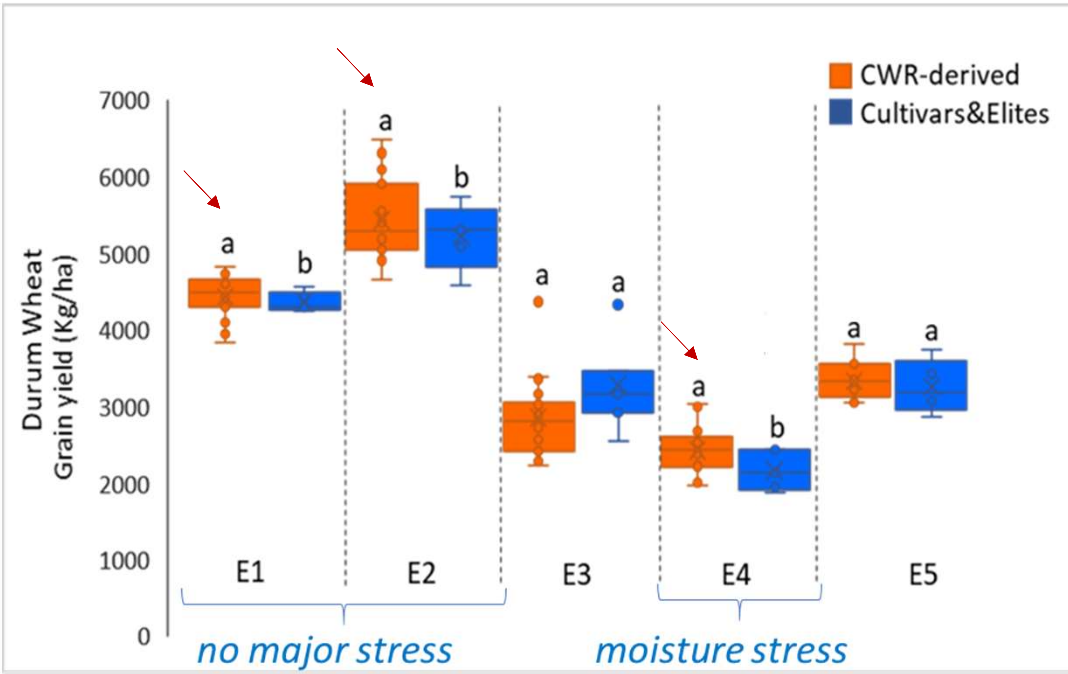
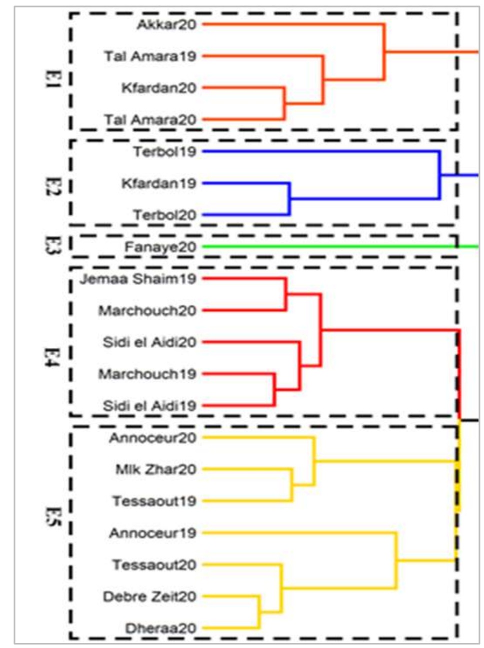
CWR-derived across more env.





Testing in 20 environments in Morocco, Lebanon, Ethiopia, and Senegal

- Again CWR-derived showed top yield performances

CWR-derived off station

DIIVA-PR: participatory farmers research

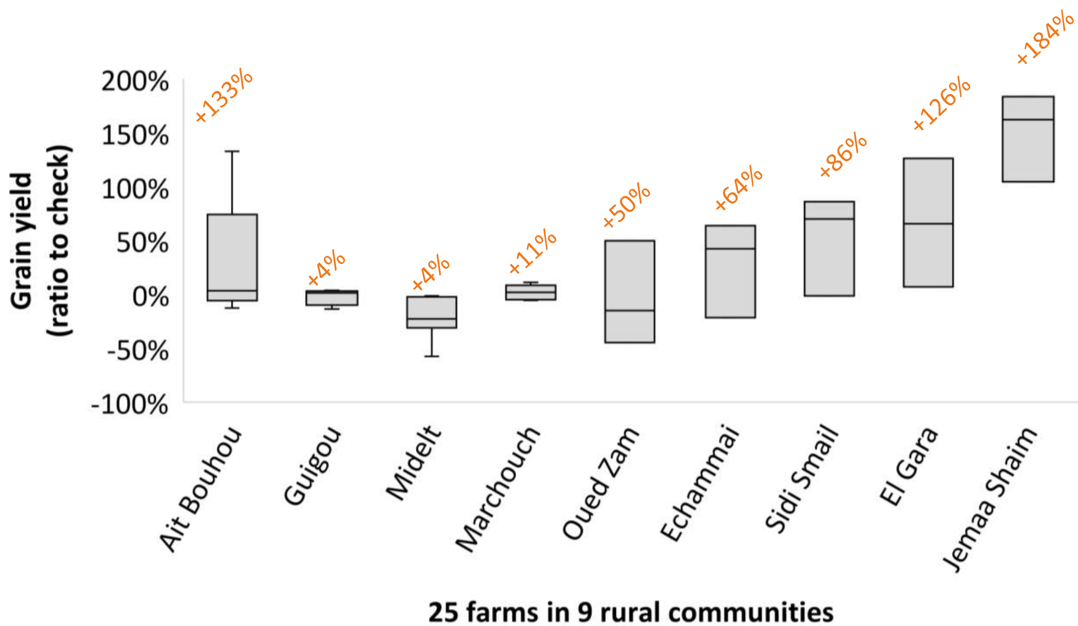
- Incorporate farmers preference
- Include the whole value chain

https://mel.cgiar.org/projects/divapr

DIIVA PR

Dissemination of Interspecific ICARDA VArieties and elites through Participatory Research

Participatory variety selection (PVS)



Testing on 25 farms in Morocco in 2018-19 and 2019-20

- Yield gains were always recorded for CWR-derived over checks

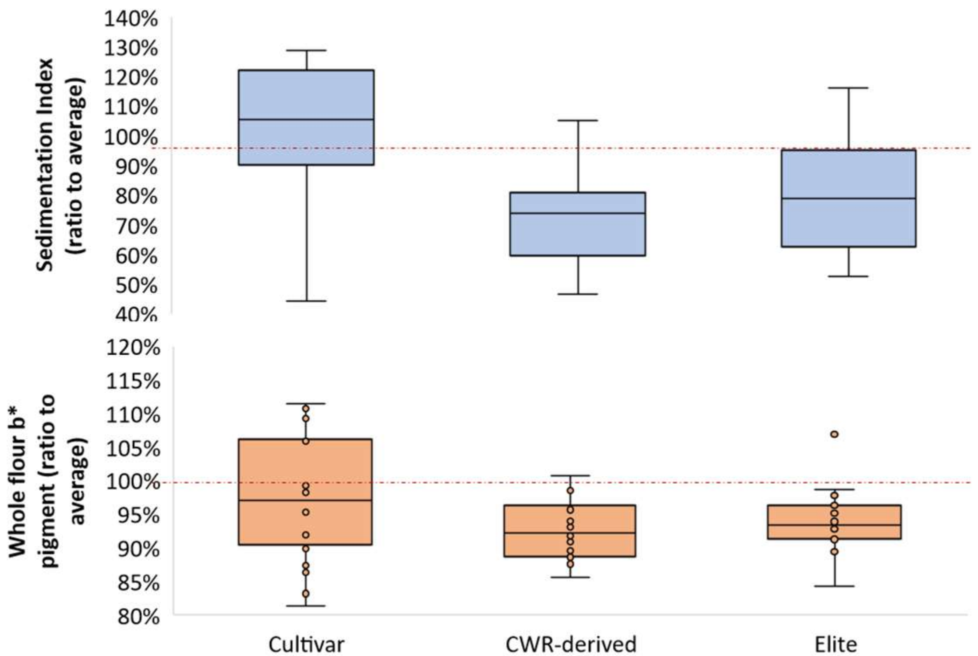
Norad CROP TRUST crop wild relatives

.. it does not only work in the developing world

- Multi-loc trials in Australia (2017)
- Several entries derived from landraces of CWR matched or outyielded the commercial varieties.

	North Star	Narrabri	Roseworthy	Kapunda	Kaniva
Mean yield (t/ha)	3.75	3.97	4.11	5.15	5.64
			CVE		
HYPERNO	0.26	0.05	0.42	0.50	1.15
DBA AURORA	-0.02	0.08	0.36	0.24	0.73
SAINTLY	-0.66	0.05	0.25	-0.09	0.61
JANDAROI	0.12	-0.04	-0.13	-0.02	-0.22
TJILKURI	-0.72	0.00	-0.16	-0.48	-0.47
Landrace	0.29	0.03	**0.42**	**0.56**	**1.28**
Landrace	**0.47**	**0.17**	**0.55**	0.49	0.80
Landrace	-0.08	**0.21**	**0.54**	0.14	0.52
T. dicoccoides	**0.49**	-0.15	-0.18	0.33	0.34
T. urartu	0.09	**0.19**	**0.48**	0.19	0.41
T. araraticum	**0.46**	**0.12**	**0.43**	0.44	0.68
A. speltoides	**0.36**	**0.15**	0.25	0.12	-0.15

CWR: finding the linkage drag?



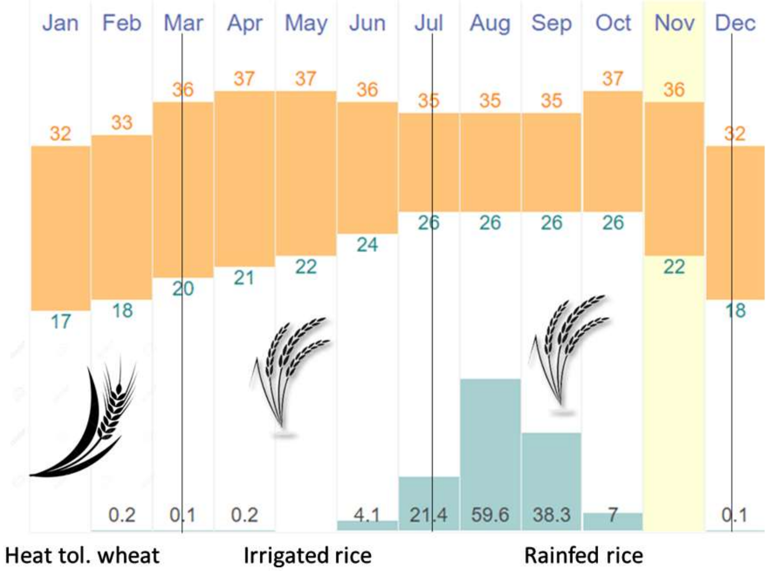
Trait	Type	Best		Worst		Average
Sedimentation Index	Cultivar	CDC Desire	129% a	Margherita2	44% a	101% a
	CWR-derived	DWAyT-0215	105% b	Icambel	47% a	72% b
	Elite	Mkilo	107% b	Secondroue	53% a	79% b
Yellow pigment (b*)	Cultivar	CDC Desire	111% b	Berghouata1	81% a	98% a
	CWR-derived	DWAyT-0215	99% c	DAWRyT-0308	86% a	93% b
	Elite	Moulsabil2	116% a	Kunmiki	84% a	94% ab

CWR-derived showed low scores for "quality"

- Did not do enough selection for rheological traits in PGR-derived germplasm
- CWR-derived with good quality are available now

El Haddad et al. 2020 Doi: 10.1002/csc2.20223

Heat tolerance along the Senegal River



Testing of durum wheat under **>32° C** throughout the season

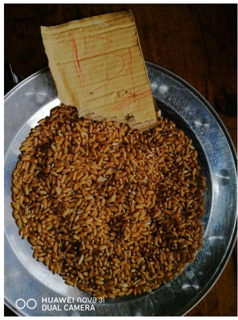
Durum Wheat Breeding: In the Heat of the Senegal River.
Sall et al. Agricolture, 2018, 8
Heat tolerance of durum wheat (Tritcum durum Desf.) elite germplasm tested along the Senegal River
Sall et al. J Ag Science, 2018, 10:2

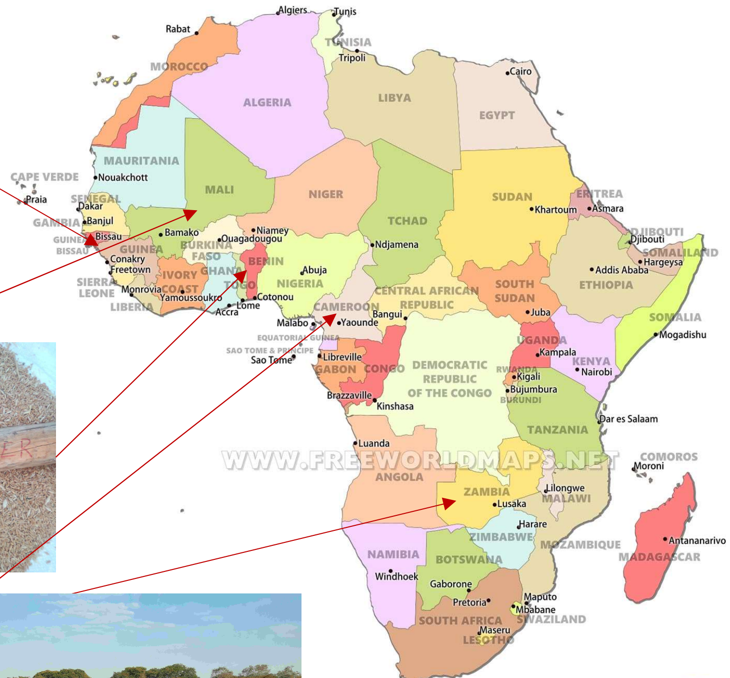
Var for the Senegal River

Haby: Mrb5/T. dicoccoides Aleppo Collection//Cham1


Amina: Korifla/Aegilopis Speltoides Syria//Loukos


Farmers trying varieties across Africa





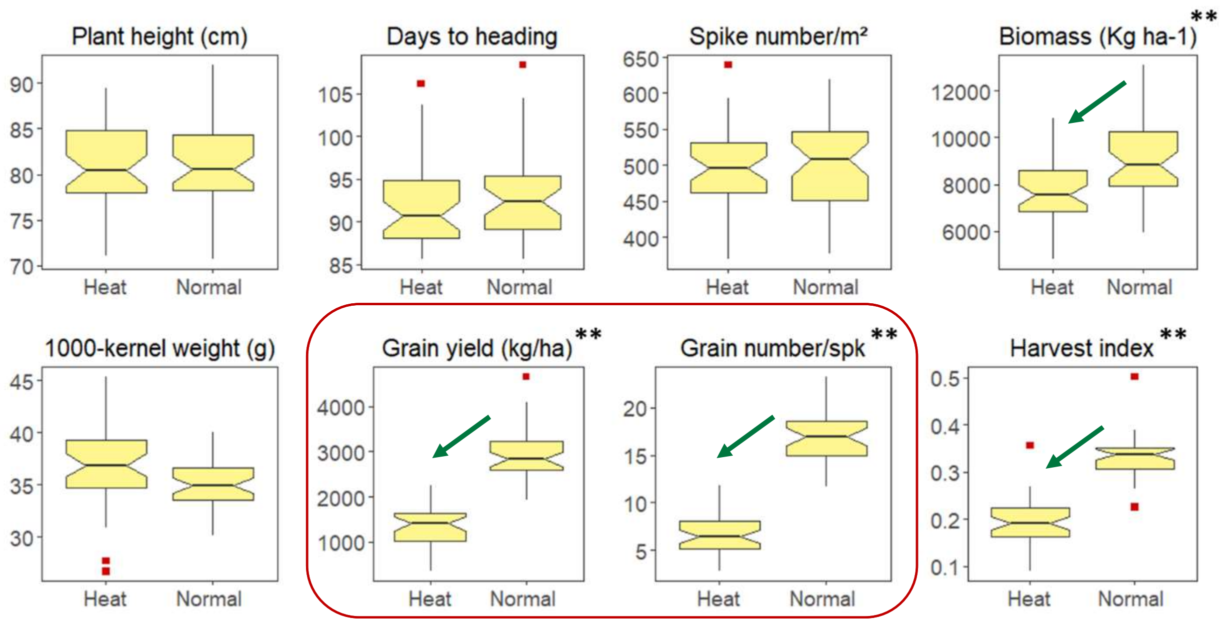
SSA countries testing them:

1. Senegal
2. Mauritania
3. Mali
4. Benin
5. Ivory Coast
6. Guinea
7. The Gambia
8. Togo
9. Nigeria
10. Cameroon
11. Tchad
12. Zambia

Olam PRIZE FOR INNOVATION IN FOOD SECURITY

Sall et al. 2019 Doi: 10.3390/agronomy9050263

Heat tolerance: spike fertility

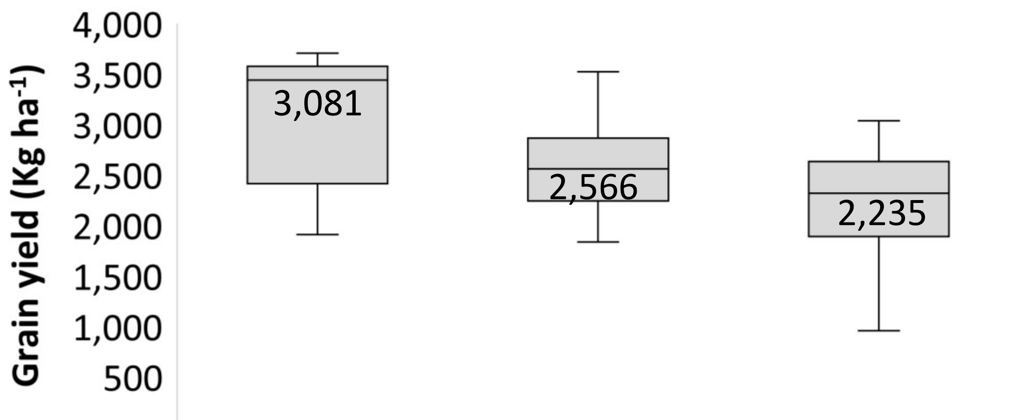


- Application of plastic tunnels at the time of flowering +**10 C**
- ***Grain number per spike*** (fertility) seems to be the most critical trait

El Hassouni et al. 2019 Doi: 10.3390/agronomy9080414

KASP marker validated for heat tol

- 2 QTLs from Speltoides for spike fertility
- GY across 3 heat stressed env:
  - +500 Kg ha^{-1} (20%) on average



Q.icd.HSI.07	+	-	-
Q.icd.heat.09	+	+	-

icarda.org

El Hassouni et al. 2019 Doi: 10.3390/agronomy9080414

Genebank-breeding partnership

GB and breeder design 20 CWR Top cross/year

GB produces viable F_1

GB plants fertile F_2

Breeder: 30 spikes from all

GB brings all to F_6

__GB__ screening for many traits

Best ones to be recrossed

Breeder conducts selection to F_6

__Breeder__ Stage 1 and 2 yield trials

**include quality testing*

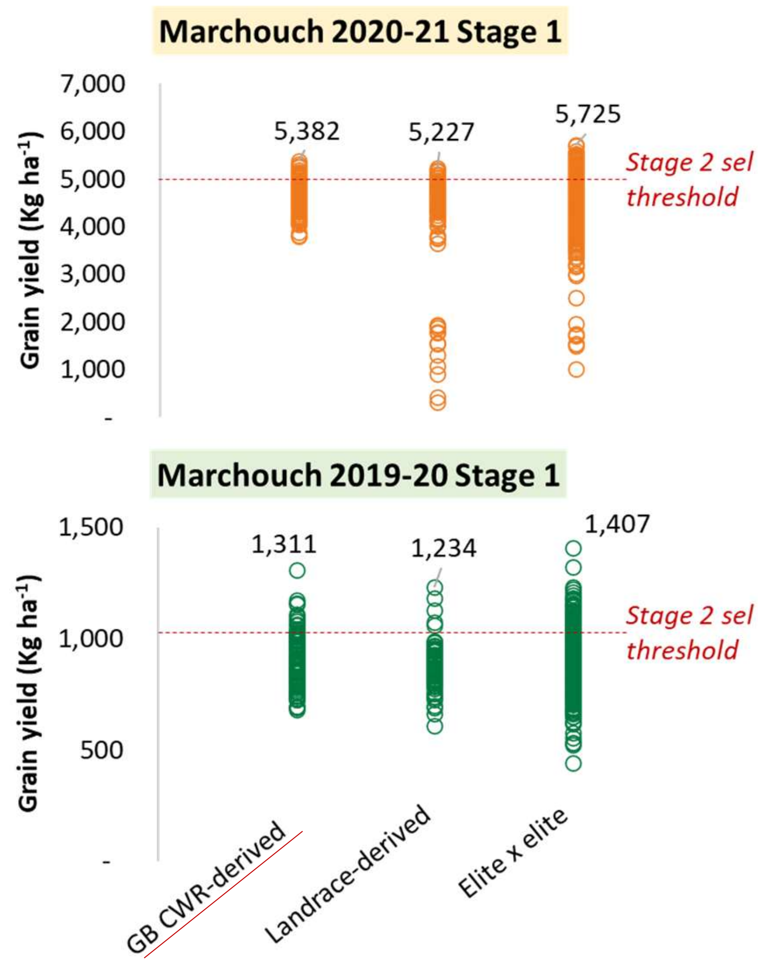
Follow normal variety pipeline

- Top-crosses to **landraces** are done as part of the breeding program
- The breeding selection takes care of height and phenology better than GB

Results from preliminary yield trials

	CWR-derived		Landrace-derived		Elite x elite	
	Progenies	Crosses	Progenies	Crosses	Progenies	Crosses
Stage 1	120	20	300	50	2,700	600
Stage 2	30	15	20	10	440	200
Success rate	**25%**	**75%**	7%	20%	16%	33%

- CWR crosses made by the Genebank have the highest success rate.. **but why?**



Genetic gain: where is the secret of CWR?

$$\boldsymbol{Genetic\ gain} = \frac{\boldsymbol{Intensity} * \boldsymbol{Accuracy} * \boldsymbol{Heritability}}{\boldsymbol{Years\ per\ cycle}}$$

Genetic gain: where is the secret of CWR?

Often we do not know the traits

$$Genetic\ gain = \frac{Intensity * Accuracy * Heritability}{Years\ per\ cycle}$$

Extra time for pre-breeding pipeline

Genetic gain: where is the secret of CWR?

Fewer crosses, but maybe more alleles segregating?

Often we do not know the traits

Same as for breeding, a bit easier to discard “craps”

$$Genetic\ gain = \frac{Intensity * Accuracy * Heritability}{Years\ per\ cycle}$$

Extra time for pre-breeding pipeline

Genebank of tomorrow?

- Guide breeders on what germplasm to use is critical
  - Characterize with genomic models (#AGENTproject)

How many disease resistance genes do we really need?

  - Time to work for the 'quantitative" traits!

MEX002	3,889
LBN002	1,244
USA029	924
USA1004	674
BRA015	302
NLD037	257
CZE122	40
BRA003	31
ROM002	9
AUT001	7

- GB need to **do the actual cross**, characterization is not enough

*7,300 CWR accessions = 10 genebanks * 20 crosses = 40 years*

  - But genebanks are NOT set up to do effective field selection
  - Let (pre-)breeders do the field selection

Breeders are NOT afraid of handling 20 "more crosses", if these arrive as ***F_2 from elite top crosses***

A wild MAGIC revolution ahead?

- **M**any crosses for elites each year.. Need to do the same for CWR crosses too
- **A**lleles are “unknown” in elites, why do we need to know them in CWR?
- **G**ene bank is the best partners, you can not do without
- **I**nsane and “it will never work” is the very reason we work in research, right?
- **C**rop breeding is in the field with simple principles, need to be applied here too

..it does work..

Thank you

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