## The tetraploid wheat collection system

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#### The tetraploid wheat collection system

- In the frame of the *«Wheat Initiative Expert Working* Group on durum wheat» two panels for germplasm analysis have been developed.
- GLOBAL TETRAPLOID wheat COLLECTION (GTC): a germplasm collection developed in the frame of the work on the durum wheat genome sequencing, mainly focussed on wild relatives (emmer), landraces and tetraploid subspecies (size: 1,856 accessions).
- GLOBAL DURUM PANEL (GDP): a breeding dedicated tool, mainly focussed on modern varieties (size: 1,056) and landraces. About 300 accessions are in common between the GDP and the GTC.

### Origin of the GDP

In 2015, about 2,500 accessions of durum wheat were proposed by breeders and geneticists to represent the genetic diversity currently exploited by durum wheat globally (including parents of RILs, ILs, GWAS panels and accessions with special traits).

#### The initial GDP was:

- Genotyped with 94 Kasp<sup>®</sup> markers for genome-wide distributed loci (including *RhtB*, *Vrn1*, *Ppd-2A*)
- Phenotypic data for phenology were collected in 2015-2016 in Terbol, Lebanon (c/o F. Bassi, ICARDA)
- Analysed with STRUCTURE «linkage» model (haplotype informed)

### Preliminary genotyping

- 96 Kasp<sup>®</sup> SNP markers, including markers for *Rht-B1b* and *Vrn-5A*
- Genotypic data filtered for:
  - Accessions with more than 50% missing data (10 lines, unreliable estimate of relationships)
  - Monomorphic markers (two markers)
  - Markers detecting multiple loci (loci calls with heterozygous calls at high frequency, two markers).

- 2,503 accessions x 88 markers, average MAF ~ 0.20.
- The informative Kasp SNPs were integrated on the durum 90K SNP consensus map (Maccaferri et al. 2015).
- STRUCTURE analysis run with the «linkage» model (haplotype informed).

Preliminary genotyping with 94 Kasp<sup>®</sup> markers for genome-wide distributed loci and phenology data were achieved in 2015-2016 (c/o F. Bassi, ICARDA). The main STRUCTURE subpopulations for the GDP were determined (k = 3-5).





#### Accessions collected in 2015 to develop the GDP

Tetraploid species	Total
T. durum	1,955
T. dicoccum	216
T. dicoccoides	88
Evo-INRA collection	175
T. turanicum	20
T. polonicum	19
T. turgidum	19
T. carthlicum	13
T. ethiopicum	10

# A GDP final set with 1,056 accessions was selected based on genotypic and phenological data.

DWRC Sub-Panels	Accessions	Main features		
T DICOCCOIDES + TETRAPLOID	1 PLATE (96)	Objective: maximization of diversity	_	
RELATIVES				Gene discoverv
T. DICOCCUM	1 PLATE (96)	Objective: maximization of diversity		• • • • • • •
DURUM LANDRACES	2 PLATES (192)	Objective: maximization of diversity		Allele-mining
(TALL, GENET DIVERSE)				Pre-breeding
INRA	1 PLATE (96)	Objective: maximization of diversity		
NON-SEMIDWARF DURUM VARIETIES	1 PLATE (96)	TALL MATERIALS		
(TALL)		(CANADIAN, MIXED ORIGINS)		
ELITE SEMI-DWARF DURUM PHOTOP-	1 PLATE (96)	PPD/VRN SENSITIVE MATERIALS		Phonomics
SENSITIVE/VRN SENSITIVE		(FRENCH, ITALIAN, CENTRAL EUROPE, MIXED)		Fileholinics
ELITE DURUM FOR MEDIT-LIKE ENVS.		1/3 CIMMYT MATERIALS		GWAS
(semi-dwarf, vernalization	4 PLATES (288)	1/3 ICARDA MATERIALS		Prooding
insensitive)		1/3 MEDITERRANEAN (ITALY, SPAIN,		breeding
		NORTH AFRICA, DESERT DURUM, ETC)		

GDP is being multiplied (c/o ICARDA) and genotyped with the Illumina 90K SNP aeeay. Seeds (and genotypic data) will be distributed for phenotyping to the durum wheat community.

## Global Durum Panel characterization (2015-16) c/o Filippo Bassi, durum breeder at ICARDA







Science for Better Livelihoods in Dry Areas

#### **Phenotypic variation**



 Flowering: 111 to 155 days (+/- 44 days)

 Weight:
 0.1 to 1,700 gr per plot

 PLH:
 60 to 185 cm

 DtM:
 165 to 195 days





### Next steps to implement the GDP project

- 1. Multiply and distribute the seed (ICARDA)
- 2. Genotyping
  - SNP array platforms
  - Population analyses (in progress)
- 3. Seed multiplication and distribution (ICARDA)
- 4. Phenotyping in partners' nurseries
- 5. GWAS analysis

#### Annual meeting of the EWG on durum wheat 14 November 2017, Bologna



#### The durum wheat diversity collections

#### A global tetraploid wheat resource

#### DW Expert working group Durum wheat breeders world-wide





Svevo Genome Sequencing Consortium

<u>Global Tetraploid Collection (GTC)</u>



### Steps for the assembly of the GTC (2016-2017)

#### Collecting the accessions

- 1. 2,515 tetraploids (all subspecies) previously genotyped (Illumina 90K array) by contributors.
- Collection completed with ~ 500 tetraploids sampling all known subspecies/domestication areas.
- 3. SSD increased at CREA (E. Mazzucotelli) and UNIBO (M. Maccaferri + 90K array at USDA-ARS, (S. Xu).
- 4. Centralized genotype call @ AGRIBIO, Melbourne (c/o M. Hayden).
- 5. Genotype and passport data carefully inspected.

### Steps for the assembly of the GTC (2016-2017)

#### Wheat 90K SNP data analysis

- 1,856 unique GTC accessions with 14,676 single locus
   90K SNPs anchored on the Svevo genome.
- 7. Population structure analysed with ADMIXTURE, DAPC, SNMF, fineSTRUCTURE, software.
- 8. The "non-durum modern" accessions are being increased by CREA and UNIBO to complement the GDP and accessions deposited at ICARDA and USDA-ARS.
- 9. All results are reported in the Svevo genome sequencing manuscript (Maccaferri et al., in review).

#### **GTC Phylogeny and population structure: PCA plot**



#### LD decay rate in the tetraploid diversity panel



Distance between SNP pairs (Mb)

LD decay over physical distance within main germplasm groups. With an LD threshold value of  $r^2 = 0.2$ , the LD reached background level at:

WEW: 195 kb < DEW: 1.4 Mb < DWL: 1.6 Mb < DWC: 4.5 Mb

### **Conclusion and perspectives**

The tetraploid wheat genetic resources are a great reservoir of genetic diversity now accessible for genetic analysis based on the released wheat genomes.

A durum wheat pangenome study coupled with the use of the GDP and the GTC will provide a valuable bridge between wheat tetraploid ancestors and hexaploid wheat.

The joint analysis of the GDP and GTC based on detailed phenotyping has the potential to further speed and focus breeding activities.

#### **The Global Tetraploid Wheat Collection**



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