IMPROVEMENT OF DOCUMENTATION OF WHEAT RELATIVES FOR MORE EFFICIENT USE IN BREEDING

Zaharieva M.[1], Dreisigacker S.[1], Hernandez E.[1], Rodriguez F.[1], Payne T.[1] and M. Warburton[1]

[1]International Maize and Wheat Improvement Center (CIMMYT), Apdo Postal 6-641, 06600 Mexico, D.F., Mexico.

In order to breed crop plants required for the future, an efficient use of genetic resources is essential. During the last decades thousands of *Triticum* and *Aegilops* accessions have been collected and are stored in various genetic resources centers. The success in the use of these genetic resources in breeding is however dependent upon the quality of descriptive information of the conserved germplasm. Documentation is, therefore, one of the most critical functions concerned with genetic resources.

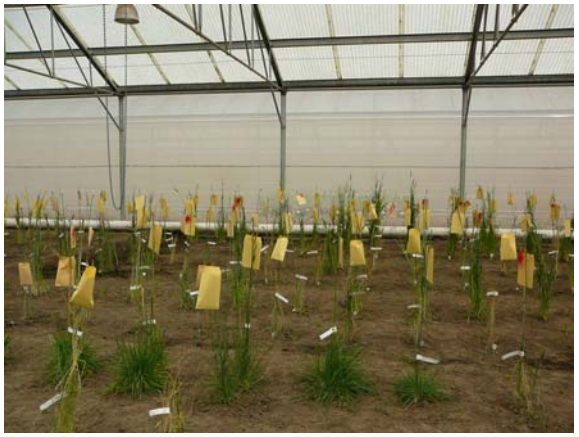

Figure 1. Plants in screen house. Due to the long flowering and maturity period and the brittle rachis of wild species collecting is done daily.

Triticum monococcum L. subsp. *aegilopoides* (Link) Thell. Wild Einkorn

Triticum urartu Tumanian ex Gandilyan

Triticum turgidum L. subsp. *dicoccoides* (Korn. ex Asch. & Graebn.) Thell. Wild Emmer

Figure 4. Virtual herbarium of spike and spikelets specimens of wild *Triticum* species (Species nomenclature from van Slageren, 1994)

Figure 2. Morphological traits measurement (culm diameter)

Figure 3. Variation in precocity among accessions (in front, an early accession from *Triticum turgidum* L. subsp. *dicoccum* (Schrank ex Schubl.) Thell.

In the present study, 150 accessions of different wheat relatives held in the CIMMYT Germplasm Bank (and part of the wheat composite collection of the Generation Challenge Program) were grown in a screen house at CIMMYT (Fig. 1) and:

- **characterized for morphology and phenology**, including qualitative (i.e. leaf, node and glume pubescence; leaf waxiness; leaf, glume and awn color) and quantitative (i.e. number of days to heading; plant height; culm, leaf, spike, awns, glume and awn length; number of spikelets per spike, growth habit, and earliness) traits (Fig. 2 and 3). Observations and measurements were performed on three randomly selected plants from each accession.
- **assembled in an herbarium** of dried plant specimens and in a virtual (photographic) herbarium (Fig. 4 and 5) and submitted to taxonomic revision (according to a variety of diagnostic descriptors in particular those of the inflorescence and the spikelet) and validation of accession identity since accessions frequently arrive to genebanks with incorrect taxonomic description or accession identity.
- **complemented for passport data** (particularly information related to the geographical origin of accessions) collected by going back to donors databases.
- **genotyped** using 34 microsatellite loci distributed throughout the genome (Dreisigacker et al., 2006; Zaharieva et al., 2007)

Triticum monococcum L. subsp. *monococcum* Einkorn

Triticum turgidum L. subsp. *dicoccum* (Schrank ex Schubl.) Thell. Emmer

Triticum turgidum L. subsp. *polonicum* (L.) Thell. Polish Wheat

Triticum timopheevii (Zhuk.) Zhuk. subsp. *timopheevii* Rivet Wheat

Triticum aestivum L. subsp. *spelta* (L.) Thell Spelt Wheat.

Triticum aestivum L. subsp. *compactum* (Host) Mackey Club Wheat

Figure 5. Virtual herbarium of spike specimens of cultivated *Triticum* species (Species nomenclature from van Slageren, 1994)

This genotypic and morphological information guarantees a **quality control of important germplasm accession**.

The study allows the **analysis of genetic diversity** between and within species based on the morphological traits (Fig. 6) and molecular markers. Accessions can be grouped according to their growth habit, earliness and plant height, or any other trait.

Information is provided that permits the **optimization of experimental designs for further phenotyping**

Finally, this study can be used to initiate the development of a **database of wheat wild relatives** at CIMMYT, and a well-documented set of accessions to be further phenotyped, enabling plant breeders to make decisions regarding the material to be used in breeding programmes.

Figure 6. Variation in spike morphology within the Persian wheat *Triticum turgidum* L. subsp. *carthlicum* (Nevski) A. Love and D. Love

References

Dreisigacker S., Thachuk C., Crossa J., van Ginkel M., F. Balfourier F., Xueyong Z., Nachit M. and Warburton M. 2006. Genetic characterization of global wheat genetic resources and their wild species. Poster presented at the International Plant Breeding Symposium, August 20-25, 2006, Mexico City, Mexico

van Slageren, M. 1994. Wild wheats: a monograph of Aegilops L. and Amblyopyrum (Jaub. & Spach) Eig. Wageningen Agric. Univ. Pap. 1994

Zaharieva M., Dreisigacker S., Bedoya C., Kishii M., Mujeeb-Kazi A., Payne T, and Warnurton M. 2007. Exploiting untapped wild genetic diversity for CIMMYT wheat improvement. 18th EUCARPIA Genetic Resources Section Meeting, May 23-26, 2007, Piestany, Slovak Republic, submitted.