Evaluation of Genetic Resources, Identification of Diversity and Priorities of Its Exploitation for Wheat Improvement

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ABSTRACT

The primary objective of *ex situ* crop germplasm collections is to provide crop breeders germplasm to satisfy particular production constraints. Often plant breeders find appropriate germplasm variation that can be utilized through conventional breeding procedures. However, when these sources are exhausted, plant breeders turn to crop collections for sources of desired genetic characters or, if they are not found there, to more exotic sources within related genera through intergeneric and interspecific hybridization.

A problem with most *ex situ* crop collections is their massive size. Globally, *ex situ* genebanks conserve about 0.5 milion *Triticum* accessions posing a major logistical evaluation problem for the researcher. Several methods have been proposed to structure collections to enhance the researcher's chances of finding the desired germplasm. We are suggesting that novelty in one genetic character (such as glutenin variability) may be associated with novelty in other characters, especially if, from a genomic point of view, the characters are in close proximity and genetically linked.

To test the hypothesis of novelty in one genetic character as a predictor of novelty for other characters, we have evaluated 50 entries for glutenin types and are projecting screening for resistance to *Helminthosporium sativum*, Kernel bunt, and tolerance to Al+++ as part of breeding emphasis for wheat improvement.

INTRODUCTION

For plant genetic resource collections to be effective in plant improvement, curators of crop collections must be able to identify likely sources of useful germplasm. Currently, the *ex situ Triticum* genebank resource exceeds 0.5 million accessions (Adham and Van Sloten 1990) and by virtue of its size represents a major obstacle to full evaluation.

To enhance evaluation of crop collections, either the size of the global collection must be rationalized to fewer accessions, or some sort of systematic sampling strategy needs to be developed. In the latter case, the International Plant Genetic Resources Institute (formerly the International Board for Plant Genetic Resources) is promoting the concept of a "core collection" with barley as an example (Van Hintum 1992). With this strategy, the core collection is a physical subset of the global *ex situ* genebank resource, where individual accessions are chosen to represent with minimum repetitiveness, the genetic diversity of a crop and its relatives. The core collection is not designed to replace the global collection but is believed that with such a subset, genebank accessions will become more accessible. From a conceptual point of view, the core collection with its stratified sampling of the species, genetic diversity appears feasible. However, plant breeders usually turn to genebanks for new genetic variation only when their usual sources of germplasm are exhausted, and as such are looking for the rare or unusual genetic combinations. Therefore, the practicality of identifying realistic strata to include the rare and unusual genetic combinations appears remote. The problem also remains of the massive size and innerent duplication within the global genebank resource.

The rationalizing of the global genebank resource to fewer accessions has been proposed (Cross 1992, Cross et al. 1992), and by virtue of a smaller number but significant pools of germplasm, plant researchers and breeders would be encouraged to make full evaluation of the resource. Selected strata would include the traditional partitions of geographical origin and particular ecological niches such as disease "hot spots", and accessions within each of these strata rationalized to fewer individuals based on phenotypic dissimilarity.

Further evaluated (Cross and Guo 1992) were a diverse pre-1935 world bread wheat collection for

glutenin variation. In this survey of 1889 accessions, these authors identified 19 novel glutenin types among 148 accessions, thereby almost doubling the number of published alleles found within the hexaploid genome (Payne and Lawrence 1983).

To test the usefulness of landrace varieties in comparison to their more modern counterparts, we are evaluating the pre-1935 bread wheat landrace varieties used earlier (Cross and Guo 1992) for some resistances of current importance to the CIMMYT wheat breeding effort. If any resistance(s) are found, besides the obvious advantage of identifying useful germplasm, the experiment will lend by practical example toward the strategy of rationalizing *ex situ* world genebank collections. In this paper we review the materials under test, by consolidating the novel glutenin variation and project, and evaluation cycle of 50 lines for biotic and abiotic stresses; positive results of which shall be agglomerated with elite lines with novel glutenin ands and desirable bread-making.

EXPERIMENTAL

The Crop and Food Research Institute (formerly the DSIR Crop Research) maintains as part of its genebanking activities a diverse pre-1935 world bread wheat collection. These 1889 landrace varieties were screened for the high molecular weight glutenin storage proteins at the Glu-A1, Glu-B1 and Glu-D1 loci using SDS-PAGE gel electrophoresis as previously described (Slack et al. 1985), and scored according to established nomenclature (Payne and Lawrence 1983). Selected lines comprising of novel glutenin alleles and/or unusual combinations of the less frequent but of known glutenin allelic types were re-evaluated and sown as part of the wider applied CIMMYT evaluation programme for resistance to *Helminthosporium sativum* (Poza Rica; field inoculation), Kernel bunt (Toluca, Mexico; field and laboratory inoculation), tolerance to aluminum (Al+++, Brazil; field tolerance) and seed increase for conducting bread-making tests.

RESULTS AND DISCUSSION

Novel forms of glutenin alleles

The novel forms of glutenin alleles at the Glu-A1, Glu-B1 and Glu-D1 loci found within the Crop and Food Research hexaploid wheat germplasm collection are detailed within Table 1. These results obtained by SDS-PAGE of 1889 hexaploid wheat pre-1935 landrace varieties of worldwide origin demonstrate the potential value of such collections toward the identification of new and novel forms of genetic variation. Glutenin has been implicated in having a particular influence in breadmaking quality (Payne et al. 1984) and the almost doubling of published allelic types (Payne and Lawrence 1983) provides researchers with a wider range of allelic contrasts when investigating the relative breadmaking potential of the various glutenin alleles (Goldsbrough et al. 1988).

Table 1. Novel high molecular weight glutenin alleles (Cross and Guo 1992) using SDS-PAGE within a diverse pre-1935 world hexaploid wheat collection.

	Glu-A1	Glu-B1	Glu-D1
New bands	fast 1	7*slow8	2+fast12
	fast 2*	fast6+slow8	3+fast12
	slow6+8	slow2+10	
	fast7+8	slow2+fast12	
Nullls		8+null	2+null
			10+null
			12+null
			fast12+null
New band pair combinations		6+9	5 + 12
		8+20	
		20+21	

Table 2. Entry code, varietal name, origin, year of accession to the Crop and Food genebank collection and allelic glutenin description of 50 lines under additional testing for biotic and abiotic stresses.

code	variety name	Origin	Year	Glu-A1	Glu-B1	Glu-D1
1. Novel band on Glu-A1						
8-14	Poland #5	POL	1935	fast1	7+8	5+10
13-7	Greece #15	GRC	1929	fast2*	7+8	2+12
13-17	Salonica #5	GRC	1929	fast2*	20	3+12
19-116	Salamanca #7	ESP	1930	fast1	13+16	2+12
2. Novel band on Glu-B1						
11-11	Secureni	ROM	1930	null	22+fast9	2+12
11-15	B2	ROM	1930	null	22+fast9	3+12
13-18	Salonica #7	GRC	1929	fast2*	20	3+12
13-19	Salonica #7 selr.	GRC	1929	fast2*	20	3+12
15-53	Belgrade #4	JUG	1929	2*	8+null	5+10
19-29	Navarre #23	ESP	1929	1	17+18	2+12
19-38	Navarre #46	ESP	1929	null	16+8	2+12
19-78	Valencia #10	ESP	1929	2*	17+18	2+12
19-79	Valencia #11	ESP	1929	2*	17+18	2+12
21-41	Morocco #47	MAR	1929	2*	23+24	2+12
21-46	Morocco #49	MAR	1929	2*	23+24	2+12
25-8	Rushmore Supresa	KEN	1961	2*	23+24	2+12
3. Novel bands on Glu-D1						
1-10	*T. vavilovi*	GBR	1948	null	7+8	3+fast12
7-402	*T. vulg. erythros.*	RUS	1940	2*	7+8	slow2+10
7-406	*T. vulgare graecum*	RUS	1940	null	7+8	slow2+10
7-501	*T. vulg. erythros.*	RUS	1940	null	7+8	slow2+10
7-502	*T. vulg. erythros.*	RUS	1940	null	7+8	slow2+10
13-20	Salonica #7	GRC	1929	2*	7+8	5+12
15-8	Sarajevo #3	JUG	1929	null	7+9	5+12
15-12	Sarajevo #5	JUG	1929	1	7+8	5+12
15-14	Sarajevo #9	JUG	1929	1	7+9	2+null
19-32	Navarre #26	ESP	1929	2*	6+8	2+fast12
20-6	Portugal #5	PRT	1929	2*	13+16	12+null
20-57	Trigo Galego	PRT	1929	2*	13+16	12+null
20-104	Barbaro	PRT	1939	2*	7	2+fast12
23-104	Sinai #7	EGY	1929	2*	20	5+12
4. Unusual combinations of known glutenin bands						
13-5	Greece #4	GRC	1929	1	17+18	4+12
13-10	Greece #18	GRC	1929	2*	7+8	5+10
20-202	Canary Islands #3	PRT	1929	2*	20	2+12
21-1	Morocco #2	MAR	1929	2*	20	4+12
21-8	Morocco #10	MAR	1929	2*	20	2+12
21-10	Morocco #12	MAR	1929	null	6+8	2+12
21-11	Morocco #14	MAR	1929	2*	6+8	2+12
21-18	Morocco #21	MAR	1929	2*	6+8	2+12
21-23	Morocco #28	MAR	1929	2*	20	5+10
21-25	Morocco #29	MAR	1929	null	20	2+12
21-29	Morocco #31	MAR	1929	1	7+8	5+10
21-57	Morocco #57	MAR	1929	1	7+8	5+10
22-1	Tunisia #1	TUN	1929	2*	20	2+12
22-3	Tunisia #2	TUN	1929	2*	20	2+12
22-5	Tunisia #9	TUN	1929	2*	7+8	2+12
22-6	Tunisia #10	TUN	1929	2*	20	2+12
22-8	Tunisia #11	TUN	1929	2*	20	3+12
22-10	Tunisia #24	TUN	1929	2*	20	2+12
23-3	Sudan #10	SDN	1964	null		2+12

Genebank management and wheat improvement

We suggest an alternative method to the management of global genebank collections is worthy of research. The "core collection" concept has promise but needs impartial scientific criticism and inspection of alternatives for the most appropriate management to be developed for this important world crop genetic resource. In the introduction, we reviewed earlier work (Cross 1992, Cross et al. 1992) where an alternative method to the management of global genebank crop genetic resources was proposed. In essence, current global collections are too large and because of that size, represents an impediment to research enquiry (Lyman 1984). We suggest evaluation would likely be encouraged by a comprehensive set of materials with minimum genetic duplication or redundancy. Such a collection would be based on eco-geographical strata, and rationalized to fewer accessions within each strata according to phenotypic dissimilarity. Earlier results (Cross and Guo 1992) highlight greater emphasis be taken of pre-1935 landrace varieties. Because a large proportion of the modern day wheat crop represents a reassortment and subsequent truncation of genetic diversity found within landrace varieties, then a refinement of the strategy of rationalizing the global *ex situ* genebank collection would be to apply the selection strata across the diversity present in landrace varieties. An additional strata would be necessary for those pools of germplasm naturally introgressed from alien sources such as the 1B/1R translocation from Petkus rye (Mujeeb-Kazi et al. 1992)

CIMMYT has fielded large screening programmers in the search for, amongst other characters, the currently narrow genetic range for resistance to *Helminthosporium sativum* and Kernel bunt. With a single survey of relatively few accessions (Cross and Guo 1992), (Table 1) it was demonstrated, at least with respect to SDS-PAGE glutenin variation, that varieties samples landraces from worldwide origin contain a surprising and significant range of genetic variation. This prompted our enquiry as to what other useful genetic variation does this resource have. We are currently testing the Crop & Food Research collection for resistances/tolerances to these particular production constraints.. A profile of the 50 novel/unusual glutenin lines currently under test is given in Table 2. These results will become available at the end of the current crop cycle.

Improvement in bread-making quality may alone exploit the novel variation that we earlier identified (Cross and Guo 1992) and have here reconfirmed. However, a blend of other attributes positive for some biotic and abiotic stresses stand to complement and alleviate breeding constraints. For *H. sativum* and Kernel bunt variation in close wheat relatives is limited while that for Aluminum tolerance is adequate, but additional genes are always advantageous for pyramiding them in cultivars. We feel strongly that not only novelty for a character has practical significance but a pool of such descriptors first amongst closer related species with high genetic homoeology is essential for crop improvement. Our observations with glutenin variation is seen as a start in this multi-faceted direction of future and on-going research.

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