Wayne M. Porter and David H. Smith, Jr.
Beltsville Agricultural Research Center, ARS, USDA, Beltsville, MD

Computer-Assisted Management of the USDA Small Grain Collection

Wheat, barley, oats, rye, and triticale are among the most important food crops of the world, in terms of both production and place in the diet. Wheat and barley were the first plants we know were cultivated by man. The small grains have been an integral part of human culture since before written records existed. Their cultivation was crucial to the development of the early civilizations of western Asia and eventually Europe (1).

These crops often face a hostile and variable environment. They are particularly threatened by continually changing pests. To maintain their high yield levels, the crops must change to meet the new variants of their enemies. Plant breeders introduce new characteristics into their materials and recombine those already present to obtain new varieties of a crop that will resist these stresses. A germ plasm collection, such as the USDA Small Grain Collection with its enormous diversity (Fig. 1), is often the source of the new genes needed to produce a characteristic.

Improved varieties of some crops, such as wheat, have made rapid inroads into undeveloped areas that were previously centers of genetic diversity for those crops and have displaced the old land races found there. Such displacements have caused decreases in naturally occurring variability in those areas and have increased the importance of germ plasm collections, which may serve not only as readily available sources of particular genes but, increasingly, as the only source.

Contribution of Germplasm Resources Laboratory, Plant Genetics and Germplasm Institute, ARS, USDA.

In 1948 the USDA established the Small Grain Collection as an official working collection at Beltsville, Maryland. The nucleus of the collection was the 16,000 accessions (seed stocks) collected by the leaders of the wheat, barley, and oat research programs. There are now over 82,000 accessions; about 45% are *Triticum*; 28%, *Hordeum*; 24%, *Avena*; 2%, *Secale*; 1%, *Triticosecale*; and less than 1%, *Aegilops*. These accessions, which originated in 87 countries, are stored in a cold room (Fig. 2) to preserve their viability. New accessions are added each year. Seed are distributed at no charge to researchers. In a typical year we fill requests from 70 different countries.

The National Seed Storage Laboratory, located in Fort Collins, Colorado, maintains duplicate samples of all accessions. That laboratory serves as the center for long-term storage of all seed germ plasm. It distributes seed only in the event it is not available in a working collection.

Contributions of the Collection

The Small Grain Collection has contributed invaluable germ plasm to U.S. and international breeding programs. For example, Norin 10 was introduced into the collection in 1946 and then distributed to seven U.S. breeding programs. Personnel in the program in Pullman, Washington, crossed Norin 10 with Brevor. This cross produced selections used to produce the first domestic semidwarf wheat. Seed of the F_2 generation were used in the breeding program at the International Maize and Wheat Improvement Center (CIMMYT) to produce the semidwarf wheats that made a dramatic impact in many countries (3).

Plant pathologists and entomologists have determined the reactions of several thousand accessions to many of the important pests of wheat, barley, and oats and have identified accessions resistant or tolerant to most of those pests. Many examples of uses of the pest-resistant accessions are available (7).

The Small Grain Collection has been a source of resistance to many insect pests. For example, Omugi (CI 5144) provided the winter barley cultivar Kerr with resistance to greenbug. The Indiana wheat variety Knox 62 has resistance to Hessian fly race B from PI 94587, which came from Australia. The wheat variety Fuzz (Fig. 3) obtained resistance to cereal leaf beetle from CI 9321, which was collected in China.

Genes from many accessions now help to control the diseases that constantly threaten our cereal crops. The wheat PI 178383 has resistance to 4 races of stripe rust, 35 races of common bunt, and 10 races of dwarf bunt and tolerance to flag smut and snow mold. It was used extensively in programs in the Pacific Northwest and was a parent in both Crest and Moro (2). Arthur wheat has stem rust and powdery mildew resistance from CI 12633. PI 94407 supplied *Septoria* resistance to Oasis wheat. In oats, PI 174544 contributed crown rust resistance to Diana.

Fig. 1. Wheat accessions from the USDA Small Grain Collection in the increase nursery at Mesa, Arizona.

Fig. 2. Cold-room storage of USDA Small Grain Collection in Beltsville, Maryland.

The aphid-transmitted barley yellow dwarf virus caused extensive losses in the California barley crop. The subsequently developed varieties CM 67 and CM 72 obtained resistance to this disease from CI 2776 and CI 1237, respectively. These accessions came from Ethiopia. CI 967 (Jet), another Ethiopian barley introduction, was an important source of resistance to loose smut. The Canadian variety Conquest has this resistance and was an important variety for several years.

Using Data Processing to Manage the Collection

Although the collection has been an invaluable source of genes for disease resistance, its size made efficient management difficult. One problem was the amount of routine paperwork required to maintain and distribute the accessions. Another was the difficulty in identifying the accessions best suited to the needs of a specific research program. The implementation of a computer-assisted documentation system has increased the efficiency and usefulness of the collection.

We distribute more than 100,000 packets of seed a year. Much of the work of labeling and record keeping is now automated. When scientists request seed with certain characteristics, such as resistance to cereal leaf beetle and spring growth habit, the computer selects the accessions with these characteristics, prints a list of the accession numbers for use in preparing seed for shipment, and prints the accession numbers and other information directly on custom-made, pin-fed seed envelopes. This saves time and increases accuracy.

In addition to helping with the preparation of the seed, the computer produces a list with such registry information as accession name, origin, species, and plant growth habit. Manual preparation of this list would be an overwhelming task, and yet it is imperative to distribute accurate information with the seed. The entire automated procedure from production of seed list through the final list of information decreases the chance of error, such as transposing digits in an accession number.

The computer can produce three types of catalog for each crop onto microfiche: one by accession number, another alphabetically by accession name, and the other first by species, then by plant growth habit, and finally by country of origin. All three types contain the basic registry information. These three catalogs allow quick access to the information available and identification of needed accessions without querying the computer. A researcher might need *Triticum dicoccum* having winter growth habit and originating in Ethiopia. The catalog shows that four accessions meet these criteria.

A microfiche can contain 269 pages of information. All the catalogs that previously required several bookshelves for storage in printed form fit easily into one loose-leaf notebook. Copies of the microfiche cost only 15¢. This medium permits distribution of information to large numbers of users, which was not economically possible before.

Storing Data on Reactions to Diseases and Insects

The registry information and a few morphological descriptors have been in a computer file for 13 years. The characteristics most important to breeding programs, however, are frequently those of reactions to stresses. Because this type of data could not be handled adequately by the registry file, new files compatible with the old one were developed for the wheat collection. We will extend this to the oat and barley collections.

Data for reactions of plants to stresses, particularly the biotic ones, such as pathogens and insect pests, pose several problems. One is that these reactions depend on the pathogenic strain (physiological race) of the pathogen or insect used for the test and on the environmental conditions of the test. Because two evaluations of an accession's reaction to a pest could give completely different, although valid, results, details of each evaluation must be readily available, the pathogenic strain must be specified when known, and the capability of storing multiple observations for any descriptor must exist.

Another problem is that people use different evaluation criteria to take data for reactions to pests. Machine searches using these original data would be extremely cumbersome and prone to error (4). Therefore, we express all reactions to pests on a 0 to 9 scale, with 0 being the desirable extreme from the breeder's viewpoint. Values of 0 to 3 are of interest to the breeder; those of 4 to 6, of possible use; and those of 7 to 9, undesirable. Data not in this form are converted, but the original expressions are maintained so the computer can associate them with the scaled value.

New pests or pathogenic strains of pests that need to be controlled confront germ plasm users. A pest that existed previously may become a problem, as did the cereal leaf beetle in 1962, or new pathogenic strains may develop. The computer files must easily accommodate data of new descriptors.

Relational data base concepts have allowed the incorporation of all these features. Martin (5) explains these concepts in detail. The basic approach is that all data are expressed as two-dimensional tables. Data from one table may be related to that in another by using common descriptors from each. Users can visualize data expressed this way more easily than with a hierarchical or other alternative method.

The simple data base we use stores the scaled value, used for developing subsets, and the original value. It can store unlimited observations for the same descriptor. Race, biotype, pathogenic strain, or culture of an insect or pathogen can be specified when known. The details of the evaluation are maintained in the data base. These features give great flexibility and power to accessing information in the data files.

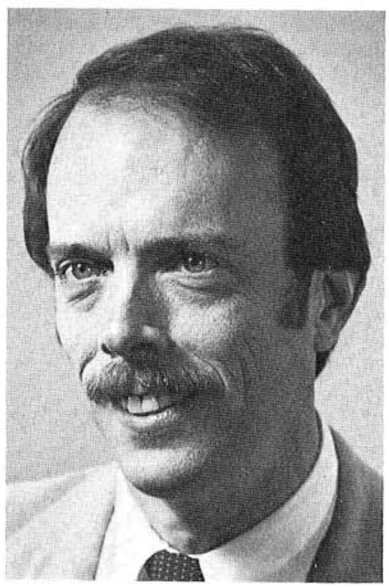
Using Insect and Disease Data

The computer produces a catalog on microfiche using the information from these files (Fig. 4). This catalog contains registry information and all available evaluation data. Over 130 wheat research workers in the United States periodically receive a set of microfiche, which is a convenient reference when information about a specific accession is needed.

The new files are useful chiefly as a tool for identifying accessions that fill specific needs in breeding programs. This is accomplished through computer queries of the data base. We can easily identify which of the 36,000 wheat accessions was classified as resistant or tolerant to a single disease or insect or to a particular pathogenic strain of that pest. Multiple pest resistance is often needed, however, so it is more important that we can identify those accessions with resistance or tolerance to specific combinations of pests. This would be an almost impossible task without the computer, since there are at present an average of 10 observations for each wheat accession in our computer files. These were made by many cooperators over a period of 30 years.

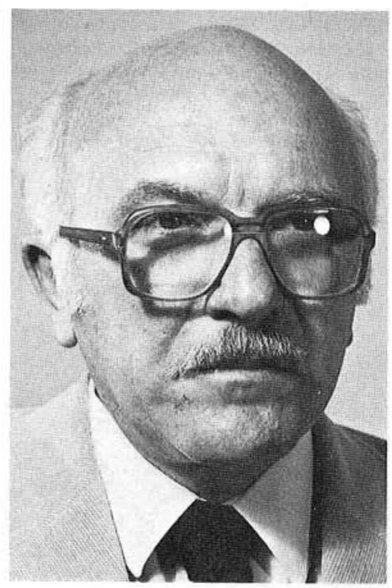
One goal of a germ plasm collection is to promote the broadening of the genetic base of cultivated crops. Often, a single accession is the only source of a characteristic for almost all breeding programs. This promotes a near monoculture for that particular locus and can

Fig. 3. Wheat variety Fuzz (left) is resistant to cereal leaf beetle; Genesee (right) is susceptible. (Courtesy James A. Webster)



Wayne M. Porter

Dr. Porter is a research agronomist in the Germplasm Resources Laboratory at Beltsville, Maryland. He obtained a B.A. in biology at Western Maryland College and a Ph.D. in plant breeding and genetics at Purdue University. He worked for 2 years with the cowpea germ plasm collection as a postdoctoral fellow at the International Institute of Tropical Agriculture in Ibadan, Nigeria. After 2 years as coordinator of a bean research program in Guatemala, he began his present work with the Small Grain Collection.



David H. Smith, Jr.

After receiving a B.S. in biology from Hamline University, Dr. Smith completed the M.S. degree in plant pathology at the University of Minnesota. He majored in plant breeding and genetics at Michigan State University, where he joined the Crop and Soil Science Department as an assistant professor after obtaining his Ph.D. In 1965 he became a research geneticist with USDA/ARS, working on host plant resistance to the cereal leaf beetle in cereal crops at Michigan State University. He is currently serving as the curator of the USDA Small Grain Collection in Beltsville, Maryland.

result in disaster. Such was the case with the oat crop of the Midwest in the 1940s, when most of the varieties contained the gene for crown rust resistance derived from the variety Victoria. Associated with that gene, however, was susceptibility to Victoria blight (*Helminthosporium victoriae*). Wide distribution of this single gene resulted in a severe epidemic in 1946 (6). The Norin 10 gene for semidwarfness is another example of a widely distributed gene from a single source. Although there have been no severe problems yet, the wide use of this single genetic source does increase the vulnerability of large portions of the world's wheat crop.

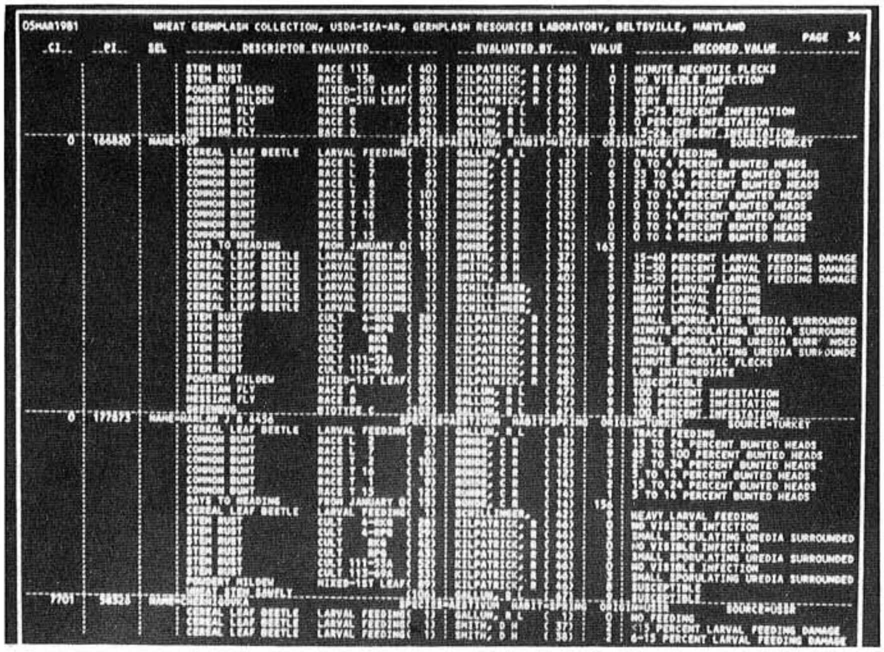


Fig. 4. A page from a microfiche containing information on reactions to pathogens and insects reproduced on the screen of a microfiche reader.

We shall try to increase the use of diverse germ plasm by better distribution of information about the accessions. If users are aware of the alternative sources of a trait, they might use a greater diversity of genes controlling the expression of that characteristic. We recently distributed a microfiche with evaluation data for 261 wheat accessions selected because they had 12 or more evaluations with scaled values in the range of 0 to 3. Some of these, such as CI 4013 (Khapli), have contributed genes for resistance to stem rust to many breeding programs. Hopefully, others will prove to be useful. We will make more specific queries and distribute the results to interested groups.

Ultimately, with the aid of the computer we will identify crosses with a high probability of producing segregants with desired traits. This should increase diversity even more, since the computer is capable of considering more combinations than a person could manually. In some cases, the most obvious choice for a cross may not be the best.

Plant breeding teams have excelled in supplying adapted, resistant varieties. Epidemics are remarkable for their infrequency, not their frequency. Use of the computer will permit us to look more extensively at the collection for any given characteristic. This comprehensive view may tip the balance of diversity in our favor. We hope that with this new tool we can increase the flow of diverse, useful materials into the world's breeding programs.

Acknowledgments

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