THE GENEVA COLLECTION OF PISUM GENETIC STOCKS: MOVING TOWARD COMPUTER ACCESSIBILITY

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The collection of genetic stocks of peas maintained in the Department of Horticultural Sciences at Cornell University's Experiment Station in Geneva has been growing steadily since it was started in 1959. Comprehensive and diverse, the collection contains lines from various other collections, e.g. the Weibullsholm and USDA Plant Introduction collections, and from individual workers throughout the world. It also contains wild and primitive forms, some varieties, breeding lines, and material from other miscellaneous sources. But by far the largest part of the collection comprises lines derived from over 5,000 crosses made over the last 25 years or more. Some 75,000 seed packets are now on hand. Included are multi-marker and multi-resistant stocks, isolines, groups of linked genes, etc. Over the years, many hundreds of seed samples have been distributed to serve the varied needs of users from many countries. This collection, hereinafter referred to as the Geneva collection, is separate and distinct from the collection of USDA Plant Introduction (P.I.) accessions, maintained nearby at the Northeast Regional Plant Introduction Station, Geneva, New York.

The importance of and need for maintaining the Geneva collection is generally recognized, but the difficulty of organizing the collection to make it readily accessible is not well appreciated. The Geneva collection is a working collection as opposed to a museum collection. It is therefore dynamic, with new lines being added regularly as a result of crosses made among lines already present and with new lines from outside sources. This dynamicism complicates record keeping and data retrieval. All data have been assiduously collected and manually recorded in books over a 25-year period. It is essential of course to link the identifying number of a given lino with the appropriate genetic and descriptive data for that line. Since, alter a cross is made, the identifying number for each progeny which descends from a given cross changes with each succeeding generation, and since the data collected in each generation may be slightly different from the generation before (until the line is genetically fixed), each new cross generates a wealth of information which must be evaluated and collated.

Heretofore, all record keeping was done manually. For example, each generation (3 per year) requires a new planting plan. Recorded in that plan, in addition to the current Identification number, is all the information pertaining to the history ofeach entry, i.e. previous identification number, cross number, identity of parents, pedigree, and relevant genetic or descriptive data. To trace specific lineages a whole series of data books had to be individually consulted for the identification numbers used in successively earlier generations. Moreover, it was only possible to trace backward from a given point, not forward. A particular cross may produce dozens, even hundreds, of entries after many generations. Searching for genetic or descriptive data was still more difficult.

Although gratifying progress has been made, much more work is required before the collection can be considered to be organized and ready for routine use. Considerably more data need to be entered into the computer. When a core collection of the most useful entries has been established, a continuing effort must be made to add to or refine the information already at hand. Stocks must be propagated to maintain their viability and, as each accession is grown for that purpose, genetic and descriptive data not previously noted will be added. A catalog of available Pisum stocks in the collection is not presently available. Such a catalog is needed if we and others are to benefit fully from the resources which have been diligently and systematically developed over nearly three decades.

Since October, 1983, the USDA-ARS has provided critical financial support for organizing and maintaining the Geneva collection, and the task is now underway. The collection has become a part of the National Plant Germplasm System (NPGS), but control and direction remain with the curator (GAM). Our goal is to develop a cross-indexed, multi-referenced "core" collection of stocks consisting of 4000 to 5000 genetically defined lines. To this end, more than thirty computer programs have been written to accomplish various retrieval objectives.

THE PISUM CULTIVAR DATABASE; A RESOURCE

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The purpose of this note is to advertise the existence of a database of pea cultivars and its associated software.

The Pisum Cultivar Database was created as an aid to cultivar registration work in the United Kingdom. The database primarily holds morphological and physiological data on 1350 cultivars and breeding lines, including all those cultivars on the European (EEC) Common Catalogue, those on the United Kingdom National List, and those entered for registration or the awarding of Plant Breeders' Rights. Registered material and material with Plant Breeders' Rights account for approximately 750 of the 1350 lines. We also hold approximately 1380 seed accessions in our seed reference collection.

The database has approximately 70 morphological and physiological descriptors plus passport information for each cultivar along with further details concerning each seed accession. As far as possible, the morphological characters describe the plant genotype. The descriptions are based mainly on observations made over two years, 1983 and 1984. We plan to grow the entire collection again in 1985 to fill gaps in the database and to improve the quality of the data we have collected.

The database software is written in dBase II, a popular commercial database package which runs on a wide range of micro-computers. We are using a Cromemco System II. The database and its associated software occupy 1.9 MB (megabytes) of disc space. The software allows data to be added, deleted, or interrogated in a variety of ways. Cultivar descriptions can be generated. The software can also be used to identify or classify cultivars in any specified way.