

## Formal collaboration between John Innes Pisum Collection and USDA-ARS Collection over *Pisum* genetic stocks

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The importance of reference collections of genetic stocks encompassing the known variation in a crop are of high strategic importance to the international research and breeding communities. Since the John Innes Centre took over the formal responsibility for the international *Pisum* genetic stock collection from Stig Blixt of the Nordic Gene Bank in 1993, the collection has continued to grow and a web searchable gene list has been developed (1). This collection is maintained on behalf of the Pisum Genetics Association and forms an integral part of the larger John Innes Pisum collection. In addition to stock curation, there are ongoing genetic studies and further mutation resources are being developed that are incorporated into the main collection over time. The collection is further promoted through the growing out of an annual demonstration of a subset of mutants in cultivated *P. sativum* forms offering visitors the opportunity to look over a range of mutations that cover plant habit, foliage, flowers, pods and a host of other phenotypic traits. The demonstration is updated each year to include new mutations or combinations thought worth promoting. The wider understanding and appreciation of these stocks and the variation they represent, is only possible through regular contact with the growing plants exhibiting the traits as in many instances they exhibit variable penetrance and expressivity.

The USDA genetic stock collection is incomplete, only 101 genes (mutations) are represented with no alleles from another 246 published pea genes represented in the collection. The USDA pea genetic stock collection is primarily the life work of the pea geneticist Dr. Gerald A. Marx ([www.ars-grin.gov/cgi-bin/npgs/html/listdsc.pl?PEA-GENSTOCKS](http://www.ars-grin.gov/cgi-bin/npgs/html/listdsc.pl?PEA-GENSTOCKS)). In his lifetime, he endeavored to cross all known pea mutations into a common background in complex mutation combinations (2). Dr. Marx referred to this as a dynamic crossing program. The strength of this collection is that the interaction of pea mutations can be studied to explore epistatic and pleiotropic interactions. The weakness of the Marx pea collection is that the lines were received into the NPGS as still segregating populations. Scientists using the collection understand the limitations and several researchers have assisted in fixing some traits in the Marx lines (N.F. Weeden, D.A. DeMason). However, there is an increasing demand by USA researchers for the rest of the published pea genes not in the USDA collection. This germplasm is desired for pea breeding programs for crop improvement through fundamental studies on pea genetic processes (functional genetics/genomics).

A formal collaboration has been initiated between the John Innes Pisum Collection and the USDA-ARS where a mirror of the mutation collection will be incorporated into the National Plant Germplasm System where it will be curated on behalf of the U.S. Government and will be available to all qualified scientists/organizations, domestic and foreign under the Standard Material Transfer Agreement set up by the International Treaty on Plant Genetic Resources for Food and Agriculture ([www.fao.org/ag/cgrfa](http://www.fao.org/ag/cgrfa)). Funding enabled Clare Coyne to visit the John Innes Centre during the summer of 2008 to observe stocks growing in both glasshouse and field and for both curators to work together on the range of mutations. The exchange was expanded to include a demonstration set of lines selected by JIC to cover the widest possible range of variation represented in the John Innes Pisum Collection. In addition to the seed stocks, the visit afforded the opportunity to work with some of the associated bibliographic and image resources held at the JIC and a significant body of duplicate reprints will be sent to the USDA collection along with the stocks themselves. This project will increase the number of downloadable digital images available of specific allelic variation.

1. Pisum Genetics Association Gene List. Pgene, <http://www.jic.ac.uk/GERMPLAS/pisum/Zgc4g.htm>
2. Marx GA (1985) The pea genome: a source of immense variation. In: Eds Hebblethwaite PD, Heath MC, Dawkins TCK. The pea crop: A basis for improvement. Butterworths. London.486 p.