

GENETIC IMPACT OF THE PEA SEEDBORNE MOSAIC VIRUS ERADICATION PROGRAM ON THE U.S.A. NATIONAL PISUM COLLECTION

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Pea seedborne mosaic virus (PSbMV) was first described in 1968 and since then has been found to occur not only in production fields but also in genetic resource collections across the world (3). PSbMV has been a chronic problem in the collection maintained by the Northeast Regional Plant Introduction Station (NERPIS) for the past two decades (2). In collaboration with three USDA-ARS scientists located in Washington and Oregon, an intensive program was initiated to: 1) eradicate PSbMV from the collection and, 2) increase seed of the virus-free accessions. The PSbMV eradication phase included obtaining a seed stock source for each plant introduction (PI) with the minimum potential of PSbMV infection, growing 20-30 plants per PI under aphid-free, greenhouse conditions, and roguing individual plants showing symptoms visually or through an enzyme linked immunosorbent assay (ELISA). Seed harvested from the PSbMV-free plants was bulked to form the increase and serve as a sanitized stock for future increase and distribution. An earlier study utilizing a limited number of PI accessions and genetic markers had suggested the selection pressure introduced by roguing infected plants during the virus eradication process might cause a potential reduction in genetic diversity (1). Collaborators in the eradication program attempted to minimize the genetic impact of their activities. Nevertheless, we felt it would be instructive to conduct a detailed follow-up study assessing the degree of genetic shifts incurred in a broad range of morphological and biochemical markers during an actual virus eradication program.

Fifty PI accessions comprising heterogeneous landraces and cultivars representing diverse geographic origins and which had undergone the virus eradication program were selected for study. Seed for each individual PI accession came from two sources: 1) stock from either the National Seed Storage Laboratory of the NERPIS collections, referred to as "source stock" and 2) stock increased from its source stock in the PSbMV eradication program, referred to as "sanitized stock". Thus, each PI accession was represented by a pair of stocks, one having undergone one generation of selection during the virus eradication program and one unselected and therefore presumably retaining the original genetic diversity of the PI. Forty plants for each stock of each entry were grown in the greenhouse and analysed for 12 biochemical and 20 morphological markers. In addition, all plants were tested for the presence of PSbMV 21 days after germination using the ELISA.

Based on these 32 characters, F-similarity coefficients (Genstat 5 Statistical Program, Oxford University Press) have been calculated for 20 of the 50 pea accessions. Preliminary results suggest that genetic shifts occurred between the source and sanitized stocks within all accessions. Quantitative characters exhibited the least amount of shift while qualitative and isozymic markers were highly affected by the eradication and regeneration processes. Additional statistical analyses are being employed to determine which specific characters were most affected. Nei's diversity index was calculated for all isozyme data and pooled across all

accessions (5). Two loci, Aat-3 and Pgd-1, showed a high degree of diversity with no observable shifts occurring between source and sanitized stocks. Gpi-2, Idh-1, and Lap-1 were monomorphic for both source and sanitized populations. However, in five isozyme loci under investigation (Aat-2, Dia-3, Pgd-2, Pgm-1, and Pgm-2) genetic shifts were observed. Furthermore, allelic diversity at two loci (Lap-1 and Mdh-2) was completely eliminated by the eradication and regeneration processes. For 10 morphological characters, the Shannon-Weaver index was calculated for each pair of stocks within an accession and averaged across all accessions (4). Within the populations studied, diversity was generally greatest among flower- and seed-related traits and lowest among pod-related traits. Frequency shifts occurred among all 10 qualitative morphological characters.

These preliminary observations suggest the critical need for caution in undertaking large-scale disease eradication and seed regeneration programs, particularly when maintenance of broad genetic and phenotypic diversity is paramount. Changes in genetic diversity might be minimized by alternate types of eradication strategies, for example therapy, rather than roguing of infected materials. However, genebank managers ultimately must consider the cost of disease eradication programs from both financial and genetic perspectives.

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