UNIVERSIDAD NACIONAL DEL SUR

TESIS DE DOCTORADO EN AGRONOMIA

Variabilidad genética en germoplasma argentino de manzano silvestre (*Malus spp*)

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Resumen

El manzano (*Malus x domestica* Borkh.) es una de las especies frutícolas más importantes y Argentina es uno de los principales productores de manzanas del hemisferio sur.

Desde su origen, en el centro de Asia, ha experimentado una gran expansión y selección, producto de los objetivos de agricultores y programas de mejoramiento.

Las variedades con predominio a nivel mundial son muy pocas, consecuentemente la especie ha sufrido procesos de erosión genética en las últimas décadas. Con el fin de aumentar la variabilidad genética se ha propuesto incrementar el número de entradas de cultivares primitivos y tipos silvestres en los bancos de germoplasma, asegurando su disponibilidad para ser incorporados en programas de mejoramiento o para su cultivo directo.

El objetivo de este trabajo fue colectar y conservar manzanos silvestres en la región cordillerana, determinar la variabilidad genética de los materiales colectados mediante marcadores isoenzimáticos y moleculares y evaluar la distribución de la variabilidad genética en las poblaciones.

Se relevaron 68 poblaciones de manzanos silvestres en un área comprendida entre 38° 50'- 40°11' Latitud S y 70° 55'- 71° 40' Longitud O. En cada sitio se tomaron datos de posicionamiento geográfico y se realizó un censo poblacional. Se tomaron datos morfométricos de los árboles muestreados que fueron analizados a través de técnicas multivariantes.

Se colectaron yemas invernales de los árboles muestreados. Éstas fueron injertadas sobre portainjertos clonales mediante injertos de tipo "chip budding". Las plantas obtenidas de esta manera fueron conservadas en el Banco de Germoplasma de la EEA Alto Valle-INTA.

Se evaluó la diversidad genética de 105 de los individuos colectados en 23 poblaciones mediante sistemas isoenzimáticos, primers de secuencias amplificadas al azar (RAPD) y primers de repeticiones de secuencias simples (SSR). En general, los valores encontrados para las distintas medidas de variabilidad estudiadas resultaron menores a los reportados en otras poblaciones de manzanos silvestres.

Con respecto a la distancia genética entre los individuos, la misma no permitió establecer agrupamientos coincidentes con su población de origen. En concordancia con estos resultados, no se encontró correlación entre las distancias genéticas y las distancias geográficas de las poblaciones estudiadas. Las mismas mostraron diferenciación con respecto a las variedades cultivadas.

Se estudió la diversidad genética y su distribución en las distintas poblaciones a través de diferentes métodos e indicadores. Los diferentes abordajes metodológicos coincidieron en que la mayor parte de la variabilidad genética se encuentra dentro de las poblaciones. Esto se atribuyó al flujo génico durante el establecimiento de las poblaciones, principalmente a través de semilla. Sin embargo, la proporción de diversidad genética entre las distintas poblaciones no es despreciable y alertaría sobre un proceso incipiente de fragmentación.

La falta de una estructuración evidente en el agrupamiento de los individuos, la ausencia de correlación entre las distancias genéticas y geográficas, y la ubicación de los sitios relevados indicarían un fuerte factor antrópico en la dispersión de los manzanos en el área de estudio.

El germoplasma colectado y conservado puede considerarse representativo de las poblaciones silvestres cordilleranas y diferente al de las principales variedades cultivadas.

Abstract

Apple tree *(Malus x domestica* Borkh.) is one of the most important fruit species. Argentina is one of the leading apple producers of southern hemisphere.

Since its origin in central Asia, this species has undergone a major expansion and selection in response to the interests of farmers and breeding programs.

The main worldwide varieties are very few; consequently the species has experimented genetic erosion in recent decades. In order to increase genetic variability it has been proposed to increase the number of accessions of primitive cultivars and wild types in genebanks, ensuring their availability for their incorporation into breeding programs or for direct use.

The aim of this study was to collect and preserve wild apple trees from the Andean mountain region, determine the genetic variability of the materials collected through isozyme and molecular markers and assess the distribution of genetic variability in populations.

Sixty-eight populations of wild apple trees were surveyed in an area between 38° 50'- 40°11' S Latitude and 70° 55'- 71° 40' W Longitude. In each population geographical positioning data and a census of trees were taken. Morphometric data from the sampled trees were analyzed through multivariate techniques.

Winter buds were collected from sampled trees. These buds were grafted on clonal rootstock by "chip budding" grafting. The obtained plants were conserved in the Germplasm Bank of INTA EEA Alto Valle.

Genetic diversity of 105 individuals collected from 23 populations was assessed using isozyme systems, primers random amplified sequences (RAPD) and primers of simple sequence repeats (SSR). The values found for the different studied measurements of variability were lower than those reported in other populations of wild apple trees.

Respect to the genetic distance between individuals, this does not allow to establish groupings matching with its population of origin. Consistent with these results, no correlation was found between genetic distances and geographical distances. Wild populations showed differentiation from the cultivated varieties.

Genetic diversity and its distribution in different populations were studied through different methods and indicators. The different methodological approaches concurred in finding most of the genetic variability within populations. This may be due to the presence of gene flow during the establishment of populations, mainly through seeds. However, the proportion of genetic diversity among different populations is not negligible and aware about an incipient process of fragmentation.

The lack of a clear structure in the grouping of individuals, the absence of correlation between genetic distances and geographic location of the surveyed sites indicate a strong anthropic factor in the spread of apple trees in the study area.

The germplasm collected and stored can be considered representative of wild populations and different from the germplasm present in the main cultivated varieties.

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