IDENTIFICATION OF POTATO CULTIVARS AND CLONAL VARIANTS BY RANDOM AMPLIFIED POLYMORPHIC DNA ANALYSIS

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Abstract

Random Amplified Polymorphic DNAs (RAPDs) were used to distinguish commercial potato cultivars and clonal variants of cultivars. Primer 131, one of four primers used, distinguished 30 of the 36 cultivars tested. All 36 commercial cultivars were distinguished using only two primers (131 and 184). The RAPD pattern of 20 unidentified potato cultivars was compared with known patterns of 36 cultivars. Each one of the 20 cultivars was correctly identified. Particular primers appear to produce greater numbers of both amplified DNA fragments and polymorphisms, and are therefore suited to RAPD identification of potato cultivars. Polymorphism was obtained between Russet Burbank Idaho D and Russet Burbank White Skin with primer 251 and between Viking and Purple Viking with primer 380. However, polymorphism was not observed between Norgold, Norland, Sebago and Superior clones using only 20 primers. The RAPD technique is much more likely to detect polymorphism, regardless of tissue or environmental factors, than isozyme analysis and is easier, less costly and faster than the RFLP procedure. Thus, RAPD analysis represents a highly useful method of distinguishing and identifying potato cultivars and clonal variants of cultivars.

Compendio

Se utilizaron DNAs Polimórficos Amplificados al Azar (RAPDs) para identificar cultivares comerciales de papa y variantes clonales de cultivares. El Imprimador 131, uno de cuatro imprimadores utilizados, identificó 30 de los 36 cultivares estudiados. Todos los 36 cultivares comerciales fueron identificados utilizando solamente dos imprimadores (131 y 184). El modelo RAPD de 20 cultivares no identificados fue comparado con modelos conocidos de 36 cultivares. Cada uno de los 20 cultivares fue correctamente identificado. Imprimadores específicos parecen producir números mayores tanto de fragmentos como de polimorfismos amplificados de DNA y son por lo tanto apropiados para la identificación de cultivares de papa utilizando...
Se obtuvo polimorfismo entre Russet Burbank Idaho D y Russet Burbank White Skin con el imprimador 251 y entre Viking y Purple Viking con el imprimador 380. Sin embargo, utilizando solamente 20 imprimadores, no se observaron polimorfismos entre los clones de Nor gold, Norland, Sebago y Superior. La técnica RAPD es más apropiada para detectar polismorfismos, independientemente del tejido o de los factores del ambiente, que el análisis de isoenzimas y es más fácil, menos costosa y más rápida que el procedimiento RFLP (polimorfismo de restricción de la longitud de los fragmentos). Por lo tanto, el análisis RAPD representa un método muy útil para distinguir e identificar cultivares de papa y variantes clonales de los mismos.

**Introduction**

Potato cultivars are most commonly distinguished by differences in morphological traits. However, only a limited number of traits are stable over all environments, and several months may be required to observe the distinguishing characteristics. This approach often makes discrimination amongst closely related genotypes and clonally selected variants of cultivars difficult. While isozyme analysis has been successfully used to identify potato cultivars (6, 8, 15), the ability of isozymes to discriminate between clonal variants of commercial cultivars is low, because of the small number of loci sampled by the technique. Restriction Fragment Length Polymorphisms (RFLPs) have also been used to characterize potato cultivars (7, 10, 11). Molecular markers such as RFLPs are not affected by environmental factors, the type of tissue used, or the age of the tissue. Four cDNA probes, which generated a large number of RFLPs, were able to identify 130 of 136 potato varieties using a denaturing polyacrylamide gel (11). Unfortunately, detection of RFLPs is time consuming, requires the development of suitable DNA probes, and usually involves the use of radioisotopes.

A recently developed alternative to RFLPs is Random Amplified Polymorphic DNA (RAPD) analysis, a technique that uses the Polymerase Chain Reaction (PCR) to amplify discrete fragments of genomic DNA with a single synthetic primer of arbitrary nucleotide sequence. Polymorphisms observed in RAPD analysis may result from point mutations, insertions, deletions and inversions (17). These may change the sequence of the primer binding site, alter the size of the amplified fragment or prevent the successful amplification of target DNA. RAPDs are usually dominant markers and are inherited in a simple Mendelian fashion. As with RFLP analysis, the RAPD procedure is independent of environmental influences and the tissue type. It is also less expensive, the results can be obtained within a day and uses extremely small amounts of DNA (e.g., 0.1 to 25.0 ng). These advantages, together with the relative ease of the technical procedure, have led to increased use of RAPDs in genetic mapping and genotype identification (3, 5, 16, 17). In this paper we describe the potential of RAPDs in