

Research Report
To
Oregon Processed Vegetable Commission
(for the year 1991)

Title: Genetic Mapping of Beans via Restriction Fragment Length Polymorphism of DNA.

Project Leaders: David Mok and Machteld Mok, Horticulture

Project Status: Continuing to 1992.

Project Funding for this Period: \$9,000

Funds were used to support a doctoral student working on the project. Other sources supporting the principal investigators include competitive grants from the National Science Foundation.

Objectives:

1. To utilize direct DNA mapping techniques to generate a linkage map of beans.
2. To associate particular DNA fragments with quantitative traits of economic importance in order to assist targeted selection in plant improvement.

Progress:

The long term objective of the project is to construct a genetic map (not available at present) of beans using DNA markers. This approach eliminates the effects of the environment (and other non-biological factors) on the expression of characters which interfere with classical gene mapping. Ultimately, the information will be used to correlate specific DNA markers with economically important traits to assist breeding. Some of the potential applications include identification of desirable individuals in early generations, and association of qualitative traits and disease resistance with specific DNA fragments. Methods of generating interspecific hybrids (between common beans and runner beans), extracting plant DNA and generating DNA probes that are polymorphic (different and can be distinguished between genotypes) have been described previously.

In the past year, 60 polymorphic probes have been identified. Over 170 F_2 progeny have been screened. A partial linkage map consisting of eight linkage groups has been generated. Additional markers are being added to the map continuously. In addition, DNA markers associated with maternal transmission have been identified. For example, a probe (395) has been identified as the histone gene which is transmitted only via the female parent in interspecific crosses. Therefore, the RFLP markers can also be utilized in gene cloning.

Future work will continue the mapping of markers into separate linkage groups (there are at least 11 linkage groups in beans, equal to the pairs of chromosomes), followed by determining the order and map distance of markers within each linkage group. When the genetic map is completed, breeding populations of the common bean will be examined and existing data on their performance will be correlated with the segregation of particular DNA markers.

Summary:

The construction of a genetic map based on DNA markers and correlating specific markers with performance will facilitate variety improvement by providing a means to directly assess the genetic composition of breeding lines and to predict their potentials.

Signatures:

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