

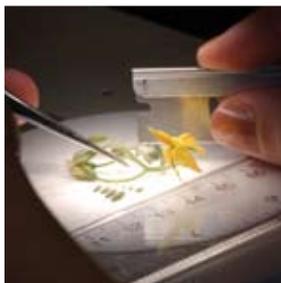
Increasing the Efficiency of Marker-Assisted Selection through in Silico and Experimental Discovery of Single Nucleotide Polymorphisms

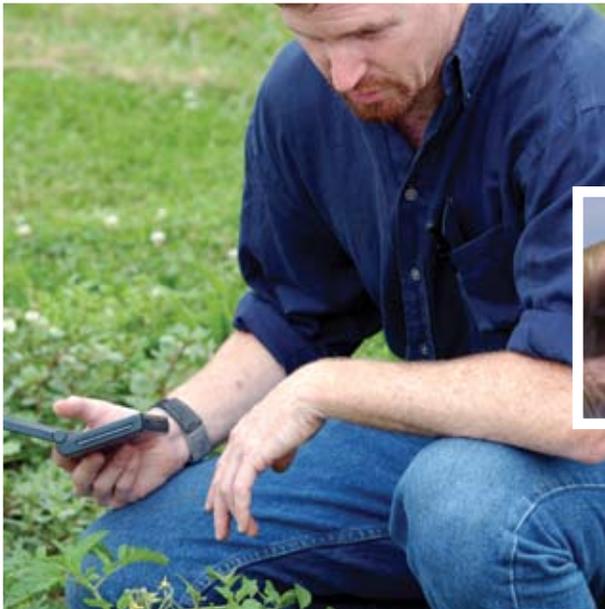
David M. Francis, Horticulture and Crop Science

■ This study developed data-mining techniques and identified more than 400 molecular markers for tomato breeding applications that are expected to yield new disease-resistant varieties for Ohio growers.

Ohio ranks third in the United States for the farm value of both fresh-market and processing tomatoes, with a combined farm value that exceeds \$85 million. The research supported by this grant was intended to bridge a gap in the availability of DNA-based markers for genetic analysis within breeding populations of tomato. The lack of genetic markers that detect differences between elite breeding lines has prevented detailed study of traits of agricultural importance.

Most academic studies in tomato have used wide crosses between weedy relatives and cultivated varieties. This approach maximizes genetic variation and has led to the discovery of new genes, but it has also left a void in our knowledge of and ability to manipulate many traits of agricultural importance. For this reason, the application of marker-assisted selection (MAS) to tomato improvement is primarily for the introduction of traits from poorly adapted plant material and has not been utilized to more fully compliment traditional plant breeding.





The aim of this study was to develop data-mining techniques that target variable portions of genes and then exploit these regions of variation for genetic mapping of traits important to Ohio growers and processors. The approach leveraged emerging data from genome sequencing projects, laboratory techniques, such as those used in forensics for DNA fingerprinting, and created a database to facilitate tomato breeding.

This project, and subsequent work funded by USDA's National Research Initiative (NRI) in the amount of \$157,895, identified more than 400 molecular markers for tomato breeding applications. Some 180 of these are currently available in our on-line database at <http://tomatomap.net>. These markers have been applied to the development of new disease-resistant varieties, and we are currently trying to improve color and color uniformity.

This scientist is currently pursuing even more efficient approaches for the discovery of new genetic markers, genes of agricultural value, and integrating technologies. One such approach uses a gene chip to identify genetic differences. The integration of genetic data and selected trait data is being accomplished in complex populations that are expected to yield new tomato varieties for Ohio growers.



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