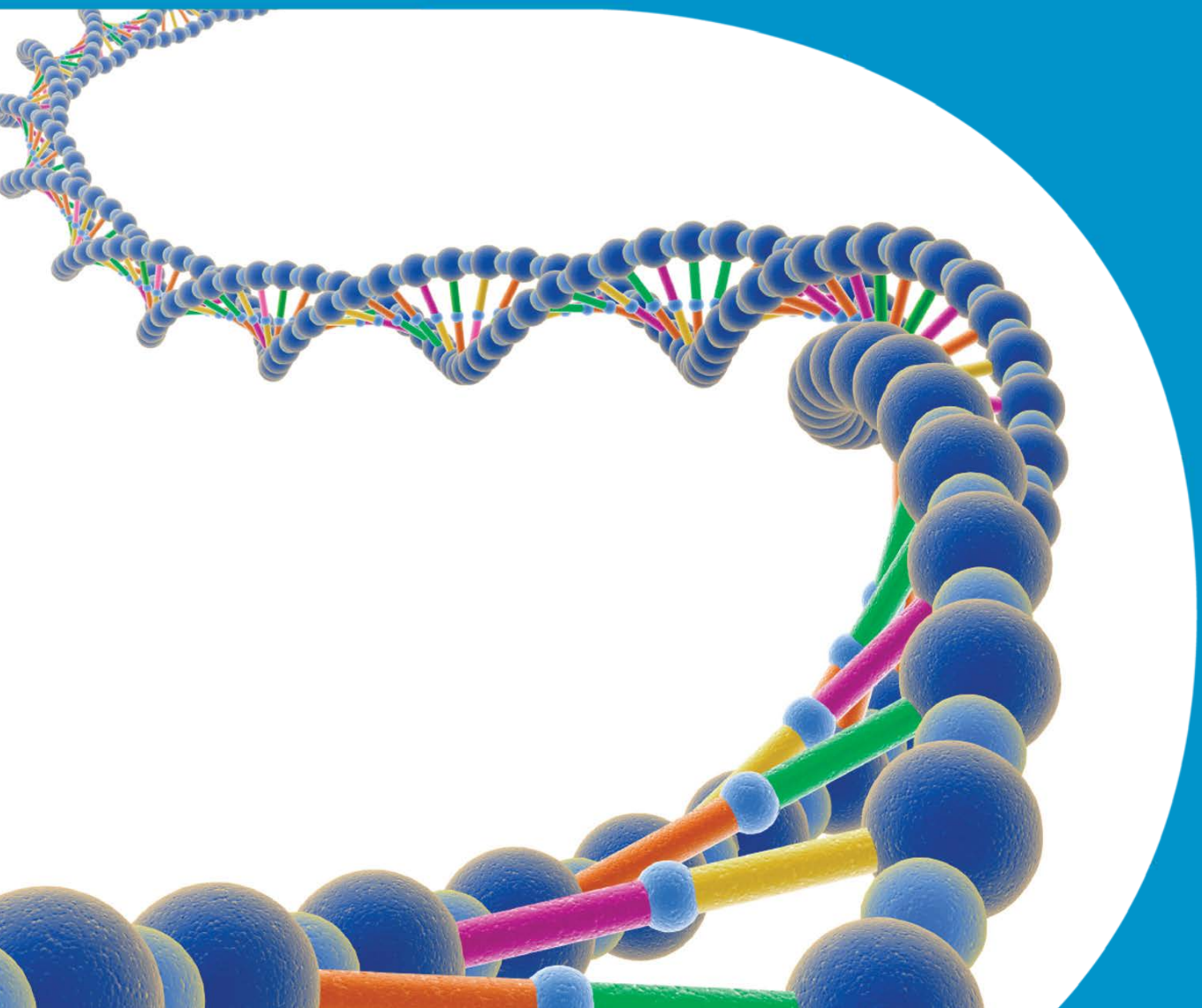
High Impact Paper of the Month
November 2014

*Ca*DMR1 cosegregates with QTL Pc5.1 for resistance to *Phytophthora capsici* in pepper (*Capsicum annuum*).

Rehrig, W. Z., Ashrafi, H., Hill, T., Prince, J., Van Deynze, A., 2014. The Plant Genome.



Value statement

CaDMR1 cosegregates with QTL *Pc5.1* for resistance to *Phytophthora capsici* in pepper (*Capsicum annuum*).

Pepper is a highly valued plant globally, having increased in consumption 40-fold since the 1980s. The root rot disease caused by *Phytophthora capsici* (Pc) in pepper (*Capsicum annuum*) is a major problem for crop growers that can reduce yields, and costs the industry large sums of money each year. This study from the University of California, Davis, successfully identifies quantitative trait loci (QTLs) in a collection of root rot resistant lines of pepper from multiple growing regions, in an effort to understand the genetic basis for the resistance and lead the way to improving crop yields.

The study identified two disease resistance loci - one on chromosome 5 which was common to multiple isolates, and one on chromosome 1 that provided a more modest resistance phenotype. From these QTLs, 12 SNPs were developed for validation using KASP genotyping assays. Two SNPs, CA_011264 and CA_004482, located in the gene *C. annuum* downy mildew resistant 1 (*CaDMR1***),** correlated highly with Pc resistance, identifying *CaDMR1* as a strong candidate for a Pc resistance gene in the root rot resistant pepper lines studied.

Rehrig, W. Z., Ashrafi, H., Hill, T., Prince, J., Van Deynze, A., 2014. CaDMR1 cosegregates with QTL Pc5.1 for resistance to Phytophthora capsici in pepper (Capsicum annuum). The Plant Genome 7(2) [online] DOI: 10.3835/plantgenome2014.03.0011.

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Paper commentary

Author bio

The corresponding author for this paper, Allen Van Deynze (avandeynze@ucdavis.edu) is director of research at University of California, Davis' Seed Biotechnology Center - a leading light for modern plant breeding that bridges the academic and commercial plant breeding communities. UC Davis is the number one school in the world for agriculture and food studies and is the most cited for scientific publications. The Seed Biotechnology Center's research team carries studies the genomics of many agricultural species to enhance breeding of crops such as carrots, cotton, lettuce, melons, peppers, and spinach, partnering with many of the crops' key breeders.

Background

The chilli pepper market is worth tens of billions of US dollars and consumption has been increasing for several decades, largely led by an increase in demand for hot chili types. It is therefore clear that pepper is economically important and taking steps to reduce the attrition of crops by pest and pathogens is essential. The pathogen *Phytophthora capsici* (*Pc*) affects a number of commercial crops, including cucumber, tomato and beans in addition to chilli pepper, causing blight and fruit rot, and understanding the genetic components of resistance to this blight could direct the development of disease management strategies in other crops as well as in pepper.

Currently, the 'Criollo de Morelos-334' (CM334) *C. annuum* landrace is known to be resistant to multiple races of Pc. Previous studies had indicated regions of the genome that may confer resistance, but the genes responsible not identified. This study provides insights into the individual and combined effects of specific SNPs important for the successful development of *Phytophthora capsici* (*Pc*)-resistant pepper lines.

Study aim

- To identify the genetic loci that afford resistance to Pc in pepper.

Methods and results

- **Quantitative Trait Loci (QTL) studies:** to identify regions of the genome that confer phenotypes. Biomarkers associated with such QTL then allow selection of the desirable trait. *Pc* resistance was evaluated using 20 different Pc isolates, with a variety of virulence levels, collected from different pepper growing regions.

- **Generate linkage map:** 66 recombinant inbred lines (RIL) of pepper were analysed, derived from crossing Pc-susceptible Jalapeño and *Pc*-resistant CM334, for resistance to these 20 *Pc* isolates.

- **Linkage Analysis:** To reveal QTL linked to *Pc* resistance. This then led to the identification of a locus on chromosome 5, which had been previously been implicated in resistance, as well as one locus on chromosome 1. The locus on chromosome 5 correlated with resistance in five out of seven of the most virulent isolates of *Pc* which that on chromosome 1 associated with intermediate resistance.

- **Validation:** 11 SNP markers out of 12 developed were successfully validated in these loci. 682 KASP genotyping assays (http://www.lgcgroup.com/products/kasp-genotyping-chemistry/) were performed on 62 of the RIL; two SNPs, CA_011264 and CA_004482, on chromosome 5, were found to highly associate with *Pc* resistance and verified in three other populations.

- **Functional Studies:** Comparison to a number of other plant species identified a resistance gene candidate that was orthologous to *DOWNY MILDEW RESISTANT 1* (*DMR1*) in *A. thaliana* and tomato (*SlDMR1*). This homoserine kinase, the alteration of which in several species confers pathogen resistance, was therefore assigned the name *CaDMR1*. Here it was found to contain a nonsynonymous A to G mutation, leading to a threonine to isoleucine substitution at position 28 of the putative translation product.

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Discussion and applications

This study identifies the *CaDMR1* gene as a critical component in the resistance to several of the most virulent isolates of *Pc* in pepper, but also highlights the complex nature of the genetic resistance. For example, in addition to *CaDMR1*, other alleles have been reported to confer moderate resistance in some pepper accessions, but may have been overshadowed in the CM334 accession used in this study. It is also reported that some pepper accessions containing SNPs which have been found to confer moderate resistance are shared with others which exhibit extreme susceptibility to *Pc*.

This paper describes significant insights into controlling Pc resistance and showcases the complement of genomic methods used. Studies like this provide a template for other groups looking to improve crop quality and production, particularly with regards to biotic stress, using the most up-to-date genomics tools and breeding techniques.

KASP genotyping

LGC's KASP genotyping assays are used widely to genotype polymorphisms (namely SNPs and Insertion/deletions) in a comprehensive variety of organisms. KASP genotyping offers high-resolution, flexible and cost-efficient assays either to run in your own laboratory or as a service out of our own, world-class laboratories located in the UK, Germany and the US.

Why this paper was chosen

This is an example of how the best modern genomic tools, techniques and understanding can be applied to enhance and accelerate improved breeding of the world's key crops.

Pressures on food production mean new and innovative techniques are required to optimise crop productivity across the globe. This article, written by a plant sciences expert and published by the Crop Science Society of America, provides a demonstration of how agrigenomics can be used to improve crops in response to biotic stress.

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Other articles you may be interested in

Genetic structure and domestication of carrot (*Daucus carota* subsp. *Sativus*) (*Apiaceae*).

Even though the domesticated carrot is an important vegetable that is consumed worldwide, the genetic structure, diversity and history of domestication are not well understood. This study aimed to generate data on the genetic structure of the carrot genome based on an analysis of the transcriptome from a collection of both wild and cultivated carrots from different regions of the world.

Sequence data from 84 specimens were used to detect SNPs and a total of 4000 primer pairs were designed for use in KASP genotyping assays. Of these, 3326 SNPs were found to be polymorphic and used for diversity analysis of the wild and domesticated carrot.

Phylogenetic comparison indicated that the closest genetic relatives to domesticated carrot were wild carrots from Central Asia while the origin of the orange colour of domesticated carrot was found to have been generated from selective breeding of wild carrot in Europe. Interestingly, unlike other domesticated crops, the analysis revealed that there has been no apparent reduction in genetic diversity in carrot since domestication. This was attributed to the introgression of genes from wild carrot through the traditionally used open-pollinated breeding system. With the wealth of data produced, this study provides a genetic framework on which to base future investigations as well as biomarkers that will be useful for tracking changes in diversity due to modern hybrid-based cultivation.

Iorizzo, M., Senalik, D. A., Ellison, S. L., Grzebelus, D., Cavagnaro, P.F., Allender, C., Brunet, J., Spooner, D.M., Van Deynze, A., Simon, P.W., 2013. Genetic structure and domestication of carrot (Daucus carota subsp. Sativus) (Apiaceae). Am J Botany, 100(5), pp. 930-938.

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