

Potato genome sequenced

July 10 2011



Since potatoes do not self-pollinate, Virginia Tech Horticulture Professor Richard Veilleux engineered inbred lines from immature pollen extracted from flower buds by using plant tissue culture. Credit: Virginia Tech Photo

The Potato Genome Sequencing Consortium (PGSC), a team of scientists from institutions worldwide, including Virginia Tech, has published its findings in the Sunday July 10 online issue of the journal *Nature*.

The successful sequencing of the genome of the world's third most important crop began when Richard Veilleux, who is the Julian and Margaret Gary Professor of Horticulture in the College of Agriculture and Life Sciences at Virginia Tech, wondered if the then new applications of plant tissue culture could be used to develop parent lines for hybrid potatoes. The concept was developed from his doctoral

research, completed in 1981 at the University of Minnesota.

Most modern crop varieties are hybrids because hybrids are usually more vigorous than either parent. For example, with corn, a variety with desirable characteristics is self-pollinated for many generations, and the resulting seed is grown and crossbred with another similarly developed line with a different genetic background.

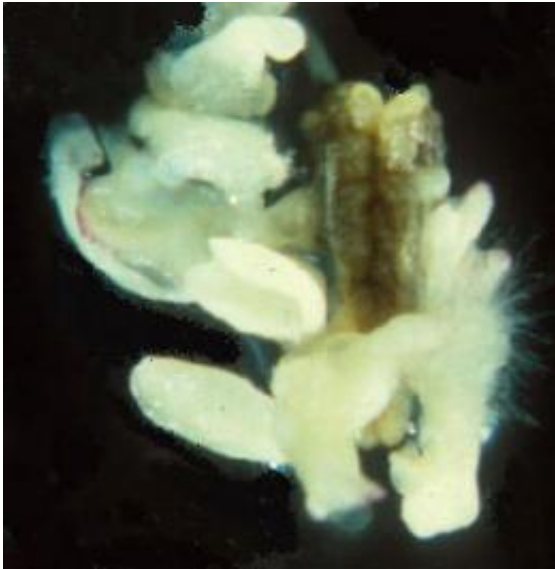
Since potatoes do not self-pollinate, Veilleux engineered inbred lines from immature pollen extracted from flower buds by using plant tissue culture. The result, potato plants with half the chromosomes of the parent, was completely sterile. "Their chromosomes have to be doubled, up to 24, which results in plants with completely identical pairs of chromosomes – a homozygous inbred line," said Veilleux. "In one cycle, you have accomplished what it takes five generations to do to create a maize inbred line the old-fashioned way."

Since that initial success, he has conducted years of basic research to improve these lines as building blocks for hybrid potato seed, supported by the U.S. Department of Agriculture through Hatch grants, among other funding. Over the years, he reported at international meetings on his progress toward developing a vigorous homozygous inbred line with desirable traits for hybrid parenthood.

By 2006, when an international team formed the Potato Genome Sequencing Consortium to attempt to sequence the genome of the potato, Veilleux's simple little spuds were poised for fame as the first potato to have its genome sequenced.

But first, the consortium, made up of groups at institutions from 14 countries, wanted to sequence a more popular and productive tuber, more resembling what is found on dinner tables worldwide. The consortium was working with a diploid variety that, like Veilleux's

potato, has only 24 chromosomes. However, the pairs of chromosomes of the selected line are not identical; they carry variations of similar genes, resulting in thousands of differences in the base pairs – or rungs on the DNA ladder-- between chromosome pairs.



These embryos from anther culture of potato grow into plants with half the chromosomes of the parent. This spring, students in Richard Veilleux's graduate class in advanced plant genetics crossed commercial varieties and hybrids from his inbred lines. Credit: Virginia Tech Photo

Modern sequencing technology is a time saver, spitting out 50-base pair sequences millions at a time. But the well-regarded modern potato has 840 million base pairs. The variation between pairs of chromosomes essentially doubled that. Assembling the puzzle was becoming overwhelming.

Then scientists within the consortium remembered Veilleux's presentations at international meetings about a simple little potato he was

developing with hopes of it someday parenting a new hybrid.

Sanwen Huang with the Chinese Academy of Agricultural Science, and Robin Buell of Michigan State University, both members of the consortium steering committee, each approached Veilleux for permission to use his simpler homozygous diploid potatoes for sequencing.

"I said, 'sure', and was invited to become a member of the consortium," said Veilleux.

Veilleux sent his plant material directly to Buell, whereas Huang obtained DNA of the same potato from Peru, where Veilleux had sent cultures years before for breeding studies by Meredith Bonierbale of the International Potato Center (CIP). DNA tests were done to make sure that the potatoes Buell and Huang obtained were the same – which they were.

According to the consortium news release, "Analysis of the genome sequence data has revealed that the potato genome contains approximately 39,000 protein coding genes. For over 90 percent of the genes the location on one of the 12 chromosomes is now known. The analysis also reveals that the potato genome has undergone extensive genome duplication through evolution... The data also show clear evidence for how expansion of particular gene families has contributed to the evolution of the potato tuber – the edible storage organ that is the most striking feature of this important and fascinating plant. "

"We can thank many Hokies, who have been paid as undergraduate hourly employees for decades on the project to maintain the potato collection in tissue culture," said Veilleux. "Research specialist Suzanne Piovano trained them to conduct routine subcultures to fresh medium every few weeks and to keep the confusing potato identities straight. The

many potato crops required for the project have been grown under the vigilance of the horticulture department's capable greenhouse manager, Jeff Burr."

Veilleux's original potatoes actually came from South America – a diploid species called phureja that produces potatoes of many colors, textures, and tastes.

Now, the sequence of Veilleux's little potato will be used as a draft against which the genome sequences of more complicated tubers will be compared. "Sequencing technology is getting better, and now that we have sequenced this one potato, it is kind of easy," he said. "There are all kinds of spinoff studies that can be done, such as looking at the DNA sequence variation in the genomes of different kinds of potatoes.

"These sequences will allow scientists to locate genes for desired traits and develop new varieties. All potatoes have essentially the same genes but the forms of the genes vary so that similar genes found in Idaho Russets or Red Norlands on the supermarket shelves can be compared to those in the sequenced line to determine how differences in the genetic code affect traits that make up the quality of commercial potatoes," Veilleux said.

What about using inbred lines to produce hybrid varieties? That may never happen, but Veilleux said he will keep trying. Just this spring, students in his graduate class in advanced plant genetics were working in Virginia Tech's greenhouses, crossing commercial varieties and hybrids from his inbred lines. Maybe the next crop of hybrids will find their way onto tables eventually.

The project is also resulting in new collaborations. "Dr. Huang wants to work with me to find out what genetic material was left behind in the process of creating the inbred lines," said Veilleux.

More information: [www.nature.com/nature/journal/...
ull/nature10158.html](http://www.nature.com/nature/journal/full/nature10158.html)

Provided by Virginia Tech

Citation: Potato genome sequenced (2011, July 10) retrieved 25 April 2024 from
<https://phys.org/news/2011-07-potato-genome-sequenced.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.