



**PHARMACEUTICALS EXPORT PROMOTION COUNCIL**  
(Set up by Ministry of Commerce & Industry, Govt., of India)

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Dated: 14<sup>th</sup> July, 2011

## Genome map: Better spuds on the way

An international team has mapped the potato genome, taking a big step closer to improving the world's most important non grain food crop.



Researchers were successful in identifying possible mechanisms by which inbreeding depression occurs. All told, the results could help potato breeders reduce the amount of time it takes to develop new varieties, which typically takes around 15 years. (Credit: [iStockphoto](#))

The Potato Genome Sequencing Consortium, an international team of 39 scientists from 14 countries, began work on the potato genome project in 2006. The complete sequence is estimated to be 840 million, about one-quarter the size of the human genome. The draft sequence, which covers 95 percent of potato genes, is available at [www.potatogenome.net](http://www.potatogenome.net).

The potato is a member of the Solanaceae, an economically important family that includes tomatoes, peppers, eggplants, petunia, and tobacco. Despite the importance of tubers, the evolutionary and developmental mechanisms of how they grow and reproduce remained elusive—until now, says



Robin Buell, Michigan State University plant biologist.

“This is the first plant with a tuber to be sequenced,” says Buell, who is part of the team that announced the findings in the current issue of the journal *Nature*. “It will still take researchers awhile to use the genome information to improve its agronomic traits, such as improved quality, yield, drought tolerance, and disease resistance. But our most-recent research will accelerate efforts on improving potato varieties and help close the gap in bringing a better potato to the farmer.”

Even though potatoes have flourished on every continent except Antarctica, they are susceptible to pests, pathogens and inbreeding depression (passing on undesirable traits that lead to weaker offspring). Ireland’s 19th-century potato famine is one illustration of how the collapse of such an important crop can affect a large population.

In 2009, the research team was able to identify the potato’s genetic blueprint. During the last two years, the team has worked to determine which genes are expressed in specific tissues, such as the tuber versus the flowers, to better understand the growth and development of the plant’s tuber. The team focused on two types of potatoes, which provided data on a wide spectrum of the potato’s genomic diversity.

“Since our initial release of the sequence in 2009, we have improved the quality, identified and analyzed the genes and analyzed the genetic basis for biology of the potato and its tuber,” Buell says.

“Our analysis revealed that the potato genome contains 39,000 protein coding genes, of which, 90



percent of the chromosomal positions are now known.”

Additionally, researchers were successful in identifying possible mechanisms by which inbreeding depression occurs. All told, the results could help potato breeders reduce the amount of time it takes to develop new varieties, which typically takes around 15 years.

Buell is looking to continue her research to address these evolutionary inadequacies as well as expand to include more varieties of potatoes as well as other members of the Solanaceae family.

Buell’s research is supported by the U.S. Department of Agriculture, the National Science Foundation, and MSU Ag BioResearch.

Source: Futurity