



Potato Genome Sequence released by international group of scientists

Auckland, New Zealand. 23 September 2009...The Potato Genome Sequencing Consortium (PGSC), an international team of scientists including New Zealand's Plant & Food Research, has announced that it has released the first draft sequence of the potato genome. The PGSC started work on the project three years ago. The resulting 'blueprint' of how the potato works could revolutionise breeding programs.

Potato, a key member of the Solanaceae family, is a close relative of tomato, pepper and eggplant. It is the world's third most important crop and the most important vegetable crop. Access to the potato genome sequence, the "genetic blueprint" of how a potato plant grows and reproduces, is anticipated to assist potato scientists in improving yield, quality, nutritional value and disease resistance of potato varieties. More importantly, the potato genome sequence will permit potato breeders to reduce the 10-12 years currently needed to breed new varieties.

The PGSC was initiated in January 2006 by the Plant Breeding Department of Wageningen University & Research in the Netherlands and has developed into a global consortium of research groups from 14 countries.

New Zealand's Plant & Food Research is an original partner in the PGSC and leader of the work is Dr Jeanne Jacobs who is also a member of the PGSC steering committee. Dr Jacobs says New Zealand will benefit from the genome sequencing as scientists gain insights into the genetic control of important attributes including disease resistance, nutritional value, colour and flavour.

"If you know exactly which part of the chromosome holds the genes for a particular trait, then you can precisely target crop improvements using molecular markers and so speed up breeding," she says. "The research is also yielding genetic information important to the improvement of other crops that share some of their DNA sequences with potatoes," says Dr Jacobs.

The potato genome has 12 chromosomes and is estimated to be 840 million base pairs. At the onset of the project, the PGSC employed an approach in which the work was allocated to each consortium member based on chromosomes and was focused on the diploid line RH89-039-16 (RH) of cultivated potato, *Solanum tuberosum*. However, in the past two years, the advent of new sequencing technologies led to a significant change of approach within the PGSC and in 2008, the consortium initiated sequencing of the doubled monoploid DM1-3 516R44 (DM) potato derived from a diploid landrace of potato in order to simplify and complement the RH effort. In June 2009, PGSC members came together in Carlow, Ireland to plan the final phases of the project.

Currently, the PGSC is busy with finalising the sequence data for both RH and DM with an end goal of a high quality draft sequence of both of these potato lines by the end of 2009. Currently, genome coverage is greater than 70X using a combination of data generated by using three different sequencing platforms including two of the Next Generation Sequencing Platforms. The assembly, which covers 95% of the genes in potato, was possible due to a newly developed computer program by the Beijing Genomics Institute, a member of the PGSC from China.

This first draft genome assembly is now available in the public domain at www.potatogenome.net and updates will be made over the next six months as additional data is generated including annotation of the genes, analysis of when and where they are switched on and off, and analysis of specific suites of genes that are critical to potato production.

A complete listing as well as contact details for all PGSC members can be found at www.potatogenome.net

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Background

First for NZ

This is the first plant genome sequence to be published that scientists in New Zealand have been involved in. New Zealand's Plant & Food Research scientists are also involved in piecing together the large jigsaw puzzle or architecture that holds all the pieces in the genome together.

The potato genome

Every organism has a genome, or chemical 'instruction book' sometimes referred to as a 'blueprint', that describes how all the genes should be put together. This is a DNA sequence and each gene within it controls different aspects of how an organism grows and develops. Slight changes to that blueprint give rise to different varieties of the plant.

Understanding the complete genome sequence will help scientists develop a better understanding of how potato grows and develops, leading to improved crops worldwide.

Potato

Potato has one of the broadest genetic diversities of any cultivated plant. Studying potato genetics is complicated and many important traits are poorly understood. The potato genome sequence will provide a major boost to gaining a better understanding of how potato traits, or characteristics, are linked to genes and it will underpin future breeding efforts.

Currently, potato breeding takes about 10-12 years to develop a new variety. It is expected that being able to use the genome information will dramatically shorten the time taken to breed new varieties as well as reduce the cost.

Potato Genome Sequencing Consortium

The Consortium is a collaboration between 16 research groups in 14 countries: Argentina, Brazil, China, Chile, India, Irish Republic, Italy, The Netherlands, New Zealand, Peru, Poland, Russia, the United Kingdom and the United States. Each partner raises the funding needed to contribute to the project independently, mostly through grants from government research agencies and industry bodies.

Getting the potato sequence is just the beginning

Once the genome has been sequenced it is necessary to identify where all the genes for how the plant grows are located and what they do. Sophisticated computer programmes are used to predict this and scientists test it in the laboratory. Having the genome is just the start of being able to read the complete genetic instruction book for the potato.

Benefits of having the potato sequence

Knowing the genetics of the properties desired in a plant means they can be selected very early on in breeding programmes saving many years and reducing the resources needed to develop these new lines.