



Potato Genome Sequence released by international group of scientists

The Potato Genome Sequencing Consortium (PGSC), an international team of scientists including researchers at SCRI and the University of Dundee has announced that it has released the first draft sequence of the potato genome.

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 food crop and the most important vegetable. Potato, a highly adaptive crop, is becoming increasingly important in Africa and many parts of Asia, giving it an important potential role in world food security.

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 started work on the project three years ago. 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.

SCRI, Scotland's world-renowned crop research institute and the University of Dundee are the only UK members of the consortium.

Dr Glenn Bryan at SCRI said, "This genome sequence is a major step forward in understanding potato biology. It will greatly accelerate the breeding of new varieties.

"Genetic-based selection methods are very promising and technology to exploit the genome sequence immediately is already being prepared in the UK and elsewhere.

"An understanding of the genetic blueprint for potato provides us with the option of genetically modifying the crop to engineer specific properties into existing varieties, such as enhanced pest and disease resistance and improved tuber quality characteristics."

Dr David Martin, of the Division of Biological Chemistry and Drug Discovery at the University of Dundee, said, "Piecing together the exact DNA sequence of the genome has been a technically demanding task, requiring the expertise of all our collaborators worldwide. We can see for the first time the secrets of the potato genome, and now begins the challenge of analysing them over the coming months and years".

The research in UK was funded by the BBSRC, the Potato Council, DEFRA (Department for Food, Environment and Rural Affairs) and the Scottish Government Rural Environment Research and Analysis Directorate (RERAD). The BBSRC-funded work also involves Dr Gerard Bishop at Imperial College London.

This first draft potato 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

Notes to editors

The potato genome

Every organism has a genome, a chemical 'instruction book' or 'blueprint' that describes how all the genes should be put together. This is written down as a DNA sequence, a long sentence made up of the chemical letters A, C, T and G. This sequence contains many tens

of thousands of genes which can be thought of as 'words' in the sentence. Each gene controls different aspects of how the organism grows and develops. Slight changes in these instructions give rise to different varieties - each individual has a slightly different version of the DNA sequence for the species.

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

Each copy of the potato genome consists of 12 chromosomes and has a length of approximately 840 million base pairs, making it a medium-sized plant genome.

A high quality, well-annotated genome sequence of potato will provide a valuable foundation which can be combined with existing knowledge of potato genetics and the continuing advances in analysing which genes are switched on or off and which chemicals are produced when and where. Observing how these changes are affected by changes in the genome will allow scientists to identify different variants of genes which are responsible for important quantitative traits in potato.

The Potato Genome Sequencing Consortium (PGSC) seeks to provide such a resource to the potato research and breeding community in the near future, allowing the full potential of biotechnology-based improvement of this important crop plant to be realised.

The Potato Genome Sequencing Consortium aims to deduce the complete genome sequence for potato by the year 2010.

About potato

Potato is a member of the *Solanaceae*, a plant family that includes several other economically important species, such as tomato, eggplant (aubergine), petunia, tobacco and pepper. Potato is an important global food source. After wheat and rice, potato is the third most important food crop, with a world-wide production of 309 million tons in 2007. By 2020 it is estimated that more than two billion people worldwide will depend on potato for food, feed, or income. Improving potato varieties so that they can better cope with environmental challenges such as drought, and pests or diseases are key objectives of global potato breeding programmes.

The potato has one of the broadest genetic diversities of any cultivated plant. Wild species of potato are very widely distributed in the Americas, from the South Western USA to Southern Chile and Argentina and from sea level to the highlands of the Andes Mountains. Many wild species can interbreed directly with the common potato and possess a wide range of valuable traits such as resistance to pests and diseases or tolerance to frost and drought, making them a useful resource for breeding new varieties.

Worldwide, an economic loss on the potato crop of about £3 billion per year is estimated from diseases such as late blight. These diseases are still largely controlled by frequent application of fungicides. It is expected that one of the first benefits of knowing the potato genome sequence will be a major breakthrough in our ability to characterise and select genes involved in disease resistance.

However, potato, unlike man, has four, slightly different, copies of the genome (it is polyploid). It gets two copies of its genome sequence from the mother plant, and a separate and slightly different set of two out of four from the father. This makes analysis rather complicated. Therefore we are working with a potato which, like human, has two copies of the genome. It gets one copy of the genome from one parent, and one copy from the other parent. These are slightly different, and different combinations of these differences are responsible for the differences we see between potato varieties, just as people differ from one another and from their parents.

This makes studying potato genetics complicated and many important traits are poorly understood. Yet, an understanding of its genetic composition is a basic requirement for developing more efficient breeding methods. The potato genome sequence will provide a major boost to gaining a better understanding of how potato traits are linked to genes, underpinning 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 reducing the cost.

Potato Genome Sequencing Consortium

The international Potato Genome Sequencing Consortium (PGSC) is a collaboration between 16 research groups in 14 countries; Argentina, Brazil, China, Chile, India, Ireland, Italy, The Netherlands, New Zealand, Peru, Poland, Russia, the United Kingdom and the United States. The PGSC has its basis in long-standing research on the

molecular genetics of potato within the partner organisations, and includes partners with world-leading expertise in genome sequencing and computational analysis.

Each partner raises the funding needed to contribute to the project independently, mostly through grants from government research agencies and industry bodies.

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More information from:

Lorraine Wakefield, Information Officer, SCRI, Invergowrie, Dundee, DD2 5DA.

Tel: 01382 560047 (direct line) or 01382 562731 (switchboard). Email:

Lorraine.Wakefield@scri.ac.uk or

Roddy Isles, Head of Press, University of Dundee, Nethergate, Dundee DD1 4HN.

Tel: 01382 384910 (direct line) or 07800 581902 (out of hours). Email:

r.isles@dundee.ac.uk