

Potato genome set to revolutionise breeding and ensure food security

UK scientists, as part of an international consortium, have sequenced the genome of potato – the first major UK crop plant to be fully sequenced. This news holds great promise for speeding up the traditionally time-consuming process of developing new varieties (currently 10-12 years to breed a new variety); varieties that in many cases will help to ensure future food security due to improved yield, quality, nutritional value, and resistance to pests and diseases.

Potato is one of the top staple foods in the world and is the most important non-grain crop for human consumption. Consumption is expanding in developing countries, which now account for more than half of the global harvest and where the potato's ease of cultivation and high energy content have made it a valuable cash crop for millions of farmers. With the global population set to reach 9 billion by 2050 there will be many more mouths to feed and the genome sequence will allow scientists and breeders to increase the efficiency of potato production to help meet this challenge.

The UK component of the Potato Genome Sequencing Consortium (PGSC) is led by The James Hutton Institute in Scotland with the University of Dundee and Imperial College London. Funding for the UK-based research is from the Biotechnology and Biological Sciences Research Council (BBSRC), The Department for Environment Food and Rural Affairs, The Potato Council, and the Scottish Government.

Jim Paice, Minister for Agriculture, said "This is a great achievement by British scientists and is fantastic news for our farmers. If we're to feed the nine billion people projected to be living on the planet by 2050 then potato crops with improved water uptake and resistance to disease and drought will be an important development."

Dr Glenn Bryan from The James Hutton Institute, who led the UK team said "This genome sequence is a major step forward in understanding potato biology. It will lead to accelerated breeding of new potato varieties through use of the genome data to identify genes and genetic markers for important traits".

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

"In addition, an understanding of the genetic blueprint for potato gives us the option of introducing - through breeding programmes – desirable characteristics into existing varieties, such as enhanced pest and disease resistance and improved tuber quality characteristics."

Dr David Martin, who led the bioinformatics team 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".

Dr Gerard Bishop, Imperial College London said “The wider crop research community has been eagerly anticipating this news; the potato genome will also help our understanding of closely related crops such as tomato, which will be of enormous benefit.”

Potato is a member of the Solanaceae family, which also includes tomato, capsicum (the peppers we all buy in the supermarket), and aubergine. As a food it is becoming more and more popular, and is increasingly important in Africa and many parts of Asia, giving it an important potential role in global food security.

Professor Douglas Kell, Chief Executive, BBSRC said “This is wonderful news – the potato genome will enable scientists to do research now to underpin the developments we will come to rely on in 30-40 years time.

“We must use modern research strategies as well as investigating technologies such as marker assisted breeding and genetic modification so that we can know what is required to ensure sustainable increases in crop yields.

“Genome sequencing is one of most important strategies we have at our disposal and with recent progress in data storage and accessibility it will be possible for plant breeders to identify the best genetic sequences to target and so accelerate breeding programmes.”

Allan Stevenson is Chairman of the Potato Council, which provided some of the funding for this research; he is also an East Lothian farmer, businessman and Board member of the James Hutton Institute. Mr Stevenson said “This research is valuable for the GB potato industry. It takes us much closer to understanding how the potato builds its own resistance to pest and diseases, as well as how the plant responds to lack of vital elements such as water. The industry needs to be in a position where we can utilise this understanding to continue to develop varieties of potatoes that meet the needs of consumers in a sustainable way.”

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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 PGSC released the draft version of the full potato genome towards the end of 2009, and since then it has been refining the 'assembly' and performing various types of analysis for publication.

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 tonnes 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, commercial varieties of potato, unlike man, have four, each slightly different, copies of the genome (they are polyploid). They get two copies of their genome sequence from the mother plant, and a separate set of two from the father. This makes analysis rather complicated. Therefore we are working with a research type of 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 raised the funding needed to contribute to the project independently, mostly through grants from government research agencies and industry bodies.

The potato genome assembly and other resources are now available in the public domain at www.potatogenome.net where a complete listing and contact details for all PGSC members can be found.

About BBSRC

BBSRC is the UK funding agency for research in the life sciences and the largest single public funder of agriculture and food-related research.

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