



Potato genome set to revolutionise breeding and ensure food security

An international team of scientists – led here in the UK by researchers at The James Hutton Institute in Scotland – have succeeded in mapping the genome of the potato, the first major UK crop plant to be fully sequenced. UK partners included the University of Dundee and Imperial College London.

The research paper is to be published in this week's edition of *Nature*, the world's most cited interdisciplinary science journal.

The achievement holds great promise for speeding up the traditionally time-consuming process of developing new potato varieties. At the moment it can take 10-12 years to breed a new variety.

New types of potato could help to ensure future food security because of improved yield, quality, nutritional value, and resistance to pests and diseases.

The Chief Executive of The James Hutton Institute, Professor Iain Gordon, said: "This achievement is an exciting day for us and the result of many years of hard work by our team in Dundee.

"Potato is one of the top staple foods in the world and the most important non-grain crop for human consumption, particularly in developing countries, which now account for more than half of the global harvest. The potato's ease of cultivation and high energy content have made it a valuable cash crop for millions of farmers. With global population forecast 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 James Hutton Institute has many strengths including our proud history in crop research and plant breeding. We aim to build on this achievement for the benefit of Scottish farmers and consumers and the wider world. Our broad, inter-disciplinary science structure will allow us to continue to develop new crop varieties that meet future needs for food whilst safeguarding the environment."

The Scottish Government's Cabinet Secretary for Rural Affairs and the Environment, Richard Lochhead MSP said: "The publication of this research is a major achievement and represents the culmination of many years of dedicated work. The Scottish Government is a long-term and committed funder of scientific research which is hugely important to the rural economy and in supporting our drive to grow the food and drink sector and ensure our future food security. I'm delighted to see yet another example of how this investment has helped highlight the world-renowned expertise of Scottish based researchers and would like to offer my congratulations to all those involved."

The Scottish scientists were part of the Potato Genome Sequencing Consortium (PGSC). Funding for the UK-based research was provided by the Scottish Government, the Biotechnology and Biological Sciences Research Council (BBSRC), The Department for Environment Food and Rural Affairs and the Potato Council.

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."

The Chief Scientific Adviser for Scotland, Professor Anne Glover, said: "The pace of scientific advance continues to quicken and the significance of this achievement cannot be underestimated. Science generates new insights and delivers new tools that help address major challenges faced by the world, including food security. Global issues need global solutions and this groundbreaking work shows once again that the Scottish science base is strong and delivering impact at the highest level."

The Chairman of the Potato Council, one of the funding partners in the project, is an East Lothian farmer, businessman and a Director of The James Hutton Institute, Allan Stevenson. He commented: "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."

The Potato Council announced recently that the World Potato Congress will take place between 27-30 May 2012 in Edinburgh. The organisers are hoping for 600 delegates from more than 30 countries. News of the genome success is expected to boost interest.

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."

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NOTES TO EDITORS

The James Hutton Institute's Chief Executive, Professor Iain Gordon, will be available in Dundee to answer questions from journalists from 1500 to 1600 on Friday 8 July. This will be strictly on an embargo basis until Sunday 10 July at 1800. Professor Gordon will be joined by Professor Robbie Waugh from the Scottish genetics team.

To join, please call: 0844 4 73 73 73 and when prompted, enter the PIN: 054456. If you have filming requests, please call the Communications team on the numbers below.

JPEGS of the potato genotypes used are available on request.

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.

The humble tattie

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, commercially bred potatoes, 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 set of two from the father. This makes analysis rather complicated. Therefore we are working with a special research potato strain 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.

The Scottish Government

The Scottish Government provides around £70 million of funding per year towards a wide range of environmental, biological and agricultural research. This strategic research aims to ensure that all research funded is of high quality and relevant to the continuing challenges faced in agriculture and the environment. A large proportion of this research is carried out through the Scottish Government's Main Research Providers (MRPs) including The James Hutton Institute. For more information go to:

www.scotland.gov.uk/Topics/Research/About/EBAR/

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