

Tomato genes are valuable

The tomato genome has now been mapped. Plant breeders can use that gene map as a guide in their search for genes that will make tomatoes tastier, more attractive and less susceptible to disease.

TEXT NIENKE BEINTEMA PHOTOGRAPHY AGE





Three hundred researchers in fourteen different countries have been working on it for nine years – but now they have it: a detailed description of the tomato's DNA. Last May, the tomato genome was published in the scientific journal *Nature*.

Tomatoes are not the first vegetable to be sequenced, as scientists had already mapped the sequence of genes for Chinese cabbage, cucumbers and soya. But René Klein Lankhorst of Plant Research International, part of Wageningen UR, says the sequencing of the tomato genome is the most important result so far. 'Tomatoes are one of the major vegetable crops around the world: they constitute a key source of vitamin C in people's diet. Tomatoes also constitute the biggest vegetable export in the Netherlands. The export of tomatoes and tomato

seed is worth hundreds of millions of euros every year.' There is another reason why the tomato genome is so special, continues Klein Lankhorst. 'I am prepared to claim that this is one of the three best plant genome descriptions so far in terms of quality. Many sequenced genomes still have gaps but the tomato has far fewer of these than the average genome.' Several Dutch partners worked on this endeavour, including biotech company Keygene, Plant Research International and two groups at Wageningen University (part of Wageningen UR) – the Genetics Laboratory and the Plant Breeding group. Klein Lankhorst says that Wageningen UR as a whole played a relatively major role. 'We provided the information technology required to fit the genome pieces together', he explains. 'The tomato genome consists >

of about 35,000 genes and a total of more than 800 million base pairs. Sequencing produces fragments, each of which contains 50 to 2000 base pairs. These fragments may be repeated a thousand times. Putting the fragments in the right order is like trying to do a jigsaw puzzle with billions of pieces.'

So how do you fit the pieces of the puzzle together? Klein Lankhorst explains that the fragments overlap to a certain extent. The Wageningen bioinformatics scientists developed software that lets you identify the overlapping bits and then slot the fragments together like roof tiles. That is no easy task, says the researcher. 'This is highly sophisticated information technology. And you need pretty heavy-duty computers for this with enormous computational power.'

MASS OF LETTERS FOR GENETICISTS

Once you have the sequence of base pairs, the geneticists can get down to work. They want to know which genes are behind the mass of letters. But how do you know where one gene ends and the next begins? 'We have known for a while more or less what genes look like', explains Klein Lankhorst. 'They all have the same setup, broadly speaking. For example, they all start with exactly the same three-letter code. If you use a computer to search for that, then you know which genes are in the genome.' But of course you still don't know what the genes mean, or in other words what characteristics they encode. 'Fortunately we didn't have to start from scratch', says the Wageningen researcher. 'We could build on existing knowledge about the genes of plants, animals and micro-organisms. They often have very similar or identical genes for a lot of processes. That knowledge has been collected in databases that are easy to search.'

This enabled the consortium find out the function of no less than 70 percent of the tomato's genes – roughly speaking, that is. In many cases, the researchers still have to check that gene X does indeed have the same function in tomatoes as in other organisms with the

same gene. And of course they also want to find out what purpose is served by the remaining 30 percent of tomato genes (which is still about 10 thousand genes). Both tasks involve them donning their lab coats.

'Finding out what function genes have requires a large amount of meticulous work', says Klein Lankhorst. 'You have to remove genes, or add them, or introduce them into another plant, and see what effect that has.'

Fortunately the researchers often know where to start, thanks the gene databases. 'For example, genes in different plants relating to resistance to diseases have a lot in common. If you come across one of those resistance genes, it is simply a question of figuring out which disease the gene protects the plant from.'

Plant breeding companies can also work in the reverse direction, taking the deciphered tomato genome and looking specifically for genes that code for resistance to a certain disease, or indeed a wide range of other properties such as colour, aroma, flavour and size. Because that is ultimately what this project is about, says Klein Lankhorst. 'Of course, as geneticists and biologists we are very curious to see how the genome is composed but the idea in the end is obviously to put that knowledge to practical use. It is up to the plant breeders now. They can decide which properties they want to start working on. They understand how markets are changing and what consumers want.'

LARGE AND SWEET

The average tomato on display in supermarkets is the result of years of sophisticated breeding programmes, but there is still plenty of room for improvement. 'Plant breeders are particularly interested in the relationship between size and taste', says Klein Lankhorst. 'Larger tomatoes are generally not so sweet. Companies want to develop tomatoes that are large but still as sweet as a cherry tomato, preferably in a variety of colours such as bright red and bright yellow. Because that is what consumers want.' Another priority for consumers is to have tomatoes that are as healthy as possible. That is why plant breeders are also experimenting with properties such as the amount of vitamin C and anti-oxidants.

There are also properties that are interesting for the market gardeners who grow the tomatoes; they want



'Finding out what functions genes have, is meticulous work'

varieties that need less water and energy and can cope with hot weather and disease. Finally, there are the properties retailers focus on, such as how tomatoes behave during transportation. Do they stay nice and smooth or do they end up bruised and wrinkled in the supermarket? And how long does it take before they go mouldy? All in all, plant breeding is a question of looking for the best compromise between all those competing requirements.

The breeding process is essentially the same today as it was centuries ago. You cross promising varieties in countless different combinations, then select the offspring that have the best results in terms of the desired properties. You then selectively cross the offspring until you are satisfied with the outcome. That sounds easier than it is: each cross also produces unwanted properties that you need to eliminate by means of more crosses. All in all, it takes generations of plants before you have a tomato variety that really is that little bit better.

Having the gene map will make this work a lot easier.

From now on, plant breeding companies will be able to zoom in on the genes they want to keep – or eliminate – much more quickly. It will be simpler for them to determine which bit of DNA was passed on in a particular cross and to select specific parts of the genome where several desirable properties are encoded close together. Klein Lankhorst: 'I am expecting the development of new tomato varieties to take just a few years now instead of decades. If you compare the DNA with Europe's road

network, it's as if plant breeders now have a sophisticated satnav that knows every single street, whereas they used to have to work from a map left over from the Roman Empire.'

OLD VARIETIES

According to Klein Lankhorst, plant breeding companies will now also be able to work further on vegetables closely related to the tomato such as potatoes, bell peppers and aubergines. The Wageningen scientists have plans too. The Plant Breeding science group and the Bioinformatics cluster at Plant Research International will be playing a leading part in the follow-up project over the next few years, together with partners in China. The institutes will be collaborating on mapping the genome of 150 other tomato varieties, including a number of old varieties. They may well have useful properties that have been lost in the breeding process over the past few centuries. 'If you know what genes these are and what properties they represent', says Klein Lankhorst, 'then it is a relatively simple task to cross those useful properties back into modern tomato varieties.' Unravelling the first tomato genome took nearly a decade, so is it not rather overambitious to try and sequence 150 tomato varieties? 'No', says Klein Lankhorst firmly. 'Most of the work has been done now that we have sequenced the first tomato; we just have to focus on relatively minor differences in certain gene areas. Besides, there have been spectacular improvements in the technology over the past few years. What used to take a couple of years can now be done in a month.' ■



PHOTO BART DE GOUW

RENÉ KLEIN LANKHORST, Plant Research International

'The ball is in the breeders' court now. They can decide which characteristics they want to work on.'

