

Taking a shortcut to improving wheat

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In 2011 the world's farms produced a total of 681 million tonnes of wheat, but with an ever growing demand from a growing population, there is a real need for increasing yields yet further.

At the University of Liverpool, one PhD student has developed software which will allow farmers to identify [mutations](#) in wheat, such as [disease resistance](#) and early flowering, that can be bred into crops and increase production.

In 2010, the University of Liverpool successfully sequenced the [wheat genome](#), but at five times the size of the [human genome](#), sequencing new varieties remains prohibitively expensive. As a result, PhD student Laura Gardiner has been working on methods to cut the cost of identifying these mutations.

To find the right mutations, she takes advantage of the fact that 90% of the wheat genome is repetitive sequence and therefore not useful for the study, and picks out the remaining 10% that is gene sequence. By comparing the existing information on wheat with a simpler, but related plant, *Brachypodium distachyon*, Laura is able to 'stitch' together the active parts of the wheat gene and identify with confidence the areas which she is investigating.

"We have the complete sequence for brachypodium already," Laura explains. "This means that we know which areas of this plant's genome control flowering. We can then match them up to sections of the wheat genome and compare them with plants that we think are showing a mutation."

This means that a huge amount of computer power is saved. The whole genome of wheat is 17 gigabases – each gigabase is a billion pairs of the basic building blocks of DNA and RNA. Looking only at the 10% of wheat containing genes this is reduced to 110 megabases – a megabase is a more manageable million pairs.

Laura, who works within the Centre for Genomic Research at the University, runs this data through the software, implementing a unique algorithm to detect the region containing the mutation. This allows her to generate graphs with her software showing peaks where mutations cluster, and then identify their purpose.

This means that Laura has been able to investigate mutations in different

wheat samples sent to her from across Europe. So far she has mainly been focussing on plants which are resistant to stripe rust – a disease which can destroy whole fields of wheat. Using her software, Laura has successfully identified the location of resistant genes in wheat samples and her hope is that this will allow farmers to optimise their breeding programmes to create resistant crops.

She has also been examining mutations which cause some plants to flower earlier, raising the possibility of crops more suited to shorter growing seasons.

And there's another possibility opened up by Laura's research that goes back to the way wheat as we know it today evolved. Wheat is unusual in having three pairs of genomes, which were added during two separate events. The first was more than half a million years ago and gave wheat two pairs of genomes and then, about 8,000 years ago, humans interfered with wheat to cross-breed it with another plant and add a third pair.

As well as making [wheat](#) complex, this also causes methylation, where one genome can block the action of other genes. Laura's work has revealed that temperature can affect this process and that by changing this, various gene activity can be affected.

"It's vital that we can increase crop yields in the future," Laura said.

"Unfortunately, one of the most popular crops we have is also one of the most complex.

"Having a cheaper and quicker method which can identify the mutations to reduce disease and increase yield is a major advantage to farmers."

More information: "Using genic sequence capture in combination with a syntenic pseudo genome to map a deletion mutant in a wheat species." Laura-Jayne Gardiner, et al. *The Plant Journal*

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