

A new genome assembly for the 'Fielder' wheat cultivar

July 30 2021



Credit: CC0 Public Domain

Wheat is a staple in the diets of numerous cultures. Increasing wheat production efficiency would help feed more people and reduce associated agricultural costs. Genetic engineering has the potential to

generate better wheat cultivars with characteristics we desire, but unfortunately, wheat is also one of the hardest crops to genetically modify. This is because wheat is resistant to "transformation," the process of introducing new genes into cells so that they are incorporated into the genome and passed down to the next generation, even with the development of a successful plant transformation system that uses *Agrobacterium tumefaciens*.

The [wheat](#) cultivar that is easiest to transform is 'Fielder', developed in the 1970s by the University of Idaho, but scientists do not know why this particular [cultivar](#) is so amenable to transformation when others are not. Additionally, difficulties in transforming other wheat cultivars limit the genetic enhancements that can be performed on this key crop. Not ones to back away from a challenge, a group of scientists, led by Dr. Kazuhiro Sato of Okayama University's Institute of Plant Science and Resources, has assembled the 'Fielder' [genome](#), and spatially arrange them into chromosomes.

A better understanding of wheat genomes is one step to addressing this problem, and scientists are hard at work uncovering the genetic sequence of wheat. In fact, in a massive project published in 2020, scientists sequenced as much as they could of entire genomes from 10 wheat cultivars. However, sequencing technology is constantly advancing, and a study published this year found that a process called circular consensus sequencing (CCS) can quickly and accurately read long sections of the barley genome, capturing the full sequence of most genes.

"The CCS technique can fill in any sequencing gaps from earlier sequencing efforts, while also being simpler and reasonably cost-effective. So, we figured that CCS would work for wheat as well as barley and went ahead to use it successfully. Our work here represents the next standard in wheat genome sequencing analysis," Dr. Sato explained. Their findings in their entirety are published in *DNA*

Research.

After sequencing the 'Fielder' genome using CCS, the researchers used another technique called high-throughput chromosome conformation capture to organize the sequences into individual chromosomes. The team was compared their results to previously published genomes and drew several important conclusions. First, their CCS-generated genome matched previous genomes in structure and quality but is less complex to perform. Second, 'Fielder' does not have an unusual gene set compared with the 10 wheat cultivars of the 2020 study. Third, comparisons with sequences from a previously created mutant wheat plant indicated that the CCS-generated genome is useful for verifying the success of earlier genome-editing efforts. For example, the team was able to confirm four regions of transgene insertion into the mutant wheat. They were also able to find regions that are candidates for off-target mutations, which are instances where [genetic modification](#) occurs in unintended locations of the genome. This discovery clearly benefits future efforts to reduce off-target effects during genome editing.

When asked to discuss the implications of their research, Dr. Sato commented, "Many countries, including the United States and Japan, are looking seriously into breeding genetically modified wheat to improve crop productivity. We demonstrated here that the CCS technique is effective on the highly complex wheat genome, and we hope this will encourage more researchers to analyze wheat haplotypes that they are targeting for [genetic engineering](#). Also, the high-quality genome sequence we generated is necessary for improving the efficiency of genome editing in 'Fielder' and to demonstrate that any new modifications are safe for human consumption—without any undesired mutations somewhere we didn't expect."

More information: Kazuhiro Sato et al, Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar

'Fielder', *DNA Research* (2021). [DOI: 10.1093/dnares/dsab008](https://doi.org/10.1093/dnares/dsab008)

Provided by Okayama University

Citation: A new genome assembly for the 'Fielder' wheat cultivar (2021, July 30) retrieved 24 May 2024 from <https://phys.org/news/2021-07-genome-fielder-wheat-cultivar.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.