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## Sequencing completed for wild wheat, mutant rice genomes

Monday, 10 July, 2017





The world of genomics just got a whole lot richer, with scientists completing sequencing for not one but two crop genomes over the past week.

### **Wild wheat**

On Thursday, it was announced that a global team of researchers has published the first-ever wild emmer wheat genome sequence. Wild emmer is the original form of nearly all the domesticated wheat in the world, including durum (pasta) and bread wheat. Wild emmer is too low-yielding to be of use to farmers today, but it contains many characteristics that are being used by plant breeders to improve wheat.

The study was published in the journal [\*Science\*](#) and led by Dr Assaf Distelfeld of Tel Aviv University, Israel, in collaboration with international scientists and Israel-based company NRGene. According to Dr Distelfeld, NRGene’s bioinformatics technology enabled the researchers to create a “time tunnel” that they could use to examine wheat from before the origins of agriculture.

“Our comparison to modern wheat has enabled us to identify the genes involved in domestication — the transition from wheat grown in the wild to modern-day varieties,” Dr Distelfeld explained. “While the seeds of wild wheat readily fall off the plant and scatter, a change in two genes meant that in domesticated wheat, the seeds remained attached to the stalk; it is this trait that enabled humans to harvest wheat.”

“This new resource allowed us to identify a number of other genes controlling main traits that were selected by early humans during wheat domestication and that served as foundation for developing modern wheat cultivars,” added Dr Eduard Akhunov of Kansas State University, a co-author on the study. “These genes provide an invaluable resource for empowering future breeding efforts. Wild emmer is known as a source of novel variation that can help to improve the nutritional quality of grain as well as tolerance to diseases and water-limiting conditions.”

“New genomic tools are already being implemented to identify novel genes for wheat production improvement under changing environment,” added co-author Dr Zvi Peleg of the Hebrew University of Jerusalem. “While many modern wheat cultivars are susceptible to water stress, wild emmer has undergone a long evolutionary history under the drought-prone Mediterranean climate. Thus, utilisation of the wild genes in wheat breeding programs promotes producing more yield for less water.”

For the first time, the sequences of the 14 chromosomes of wild emmer wheat have been collapsed into a refined order, thanks to additional technology that utilises DNA and protein links. As noted by co-author Dr Nils Stein, from the Leibniz Institute of Plant Genetics and Crop Plant Research, “It was originally tested in humans and recently demonstrated in barley, both of which have smaller genomes than wild emmer wheat.”

“This sequencing approach used for wild emmer wheat is unprecedented and has paved the way to sequence durum wheat (the domesticated form of wild emmer),” said co-author Dr Luigi Cattivelli, head of the CREA Research Centre for Genomics and Bioinformatics and coordinator of the International Durum Wheat Genome Sequencing Consortium. “Now we can better understand how humanity transformed this wild plant into a modern, high-yielding and high-quality crop.”

## **Mutant rice**

News of the wheat sequencing came just one day after US scientists reported the first whole-genome sequenced fast-neutron induced mutant population of Kitaake, a model rice variety that completes its life cycle in just nine weeks and is not sensitive to photoperiod changes. Scientists are investigating this variety as part of their work to optimise crops for biofuel production, seeking to identify genes that control key traits such as yield, resistance to disease and water use efficiency.

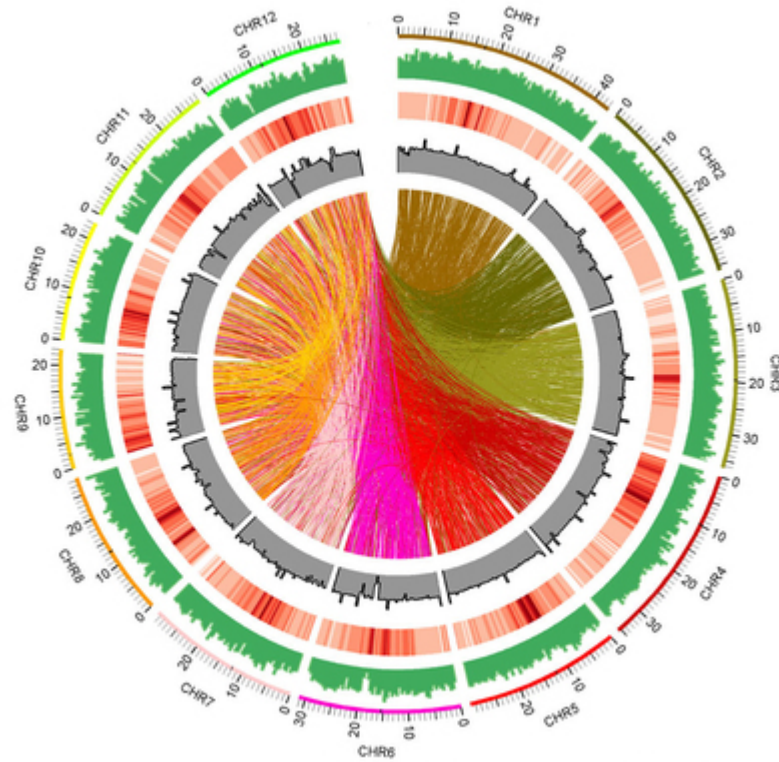
Populations of mutant plants, each one having one or more genes altered, are an important tool for elucidating gene function. With whole-genome sequencing at the single nucleotide level, researchers can infer the functions of the genes by observing the gain or loss of particular traits. But the utility of existing rice mutant collections has been limited by several factors, including the cultivars’ lengthy six-month life cycle and the lack of sequence information for most of the mutant lines.

Researchers led by Pamela Ronald, a professor at UC Davis and director of Grass Genetics at the Department of Energy’s Joint BioEnergy Institute, have now published their work sequencing a mutant population of Kitaake in [The Plant Cell](#). Their research is expected to accelerate functional genetic research in rice and other monocots, a type of flowering plant species that includes grasses.

“Some of the most popular rice varieties people use right now only have two generations per year,” noted co-author Guotian Li, deputy director of Grass Genetics at JBEI. “Kitaake has up to four, which really speeds up functional genomics work.”

In a previously published [study](#), Li and fellow co-authors Mawsheng Chern and Rashmi Jain demonstrated that fast-neutron irradiation produced abundant and diverse mutations in Kitaake, including single base substitutions, deletions, insertions, inversions, translocations and duplications. Li explained, “Fast-neutron irradiation causes different types of mutations and gives different alleles of genes so we really can get something that’s not achievable from other collections.”

Whole-genome sequencing of this mutant population — 1504 lines in total with 45-fold coverage — allowed the researchers to pinpoint each mutation at a single-nucleotide resolution. They identified 91,513 mutations affecting 32,307 genes, 58% of all genes in the roughly 389-megabase rice genome. A high proportion of these were loss-of-function mutations.



*Genome-wide distribution of fast-neutron-induced mutations in the Kitaake rice mutant population (green). Even distribution of mutations is important to achieve saturation of the genome. Coloured lines (centre) represent translocations of DNA fragments from one chromosome to another. Image credit: Guotian Li and Rashmi Jain/Berkeley Lab.*

Using this mutant collection, the Grass Genetics group identified an inversion affecting a single gene as the causative mutation for the short-grain phenotype in one mutant line with a population containing just 50 plants. In contrast, researchers needed more than 16,000 plants to identify the same gene using the conventional approach.

“This comparison clearly demonstrates the power of the sequenced mutant population for rapid genetic analysis,” said Ronald.

This high-density, high-resolution catalogue of mutations provides researchers with opportunities to discover novel genes and functional elements controlling diverse biological pathways. The Grass Genetics group has now established an open-access web portal called KitBase which allows users to find information related to the mutant collection, including sequence, mutation and phenotypic data for each rice line. To access the portal, visit <http://kitbase.ucdavis.edu>.

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