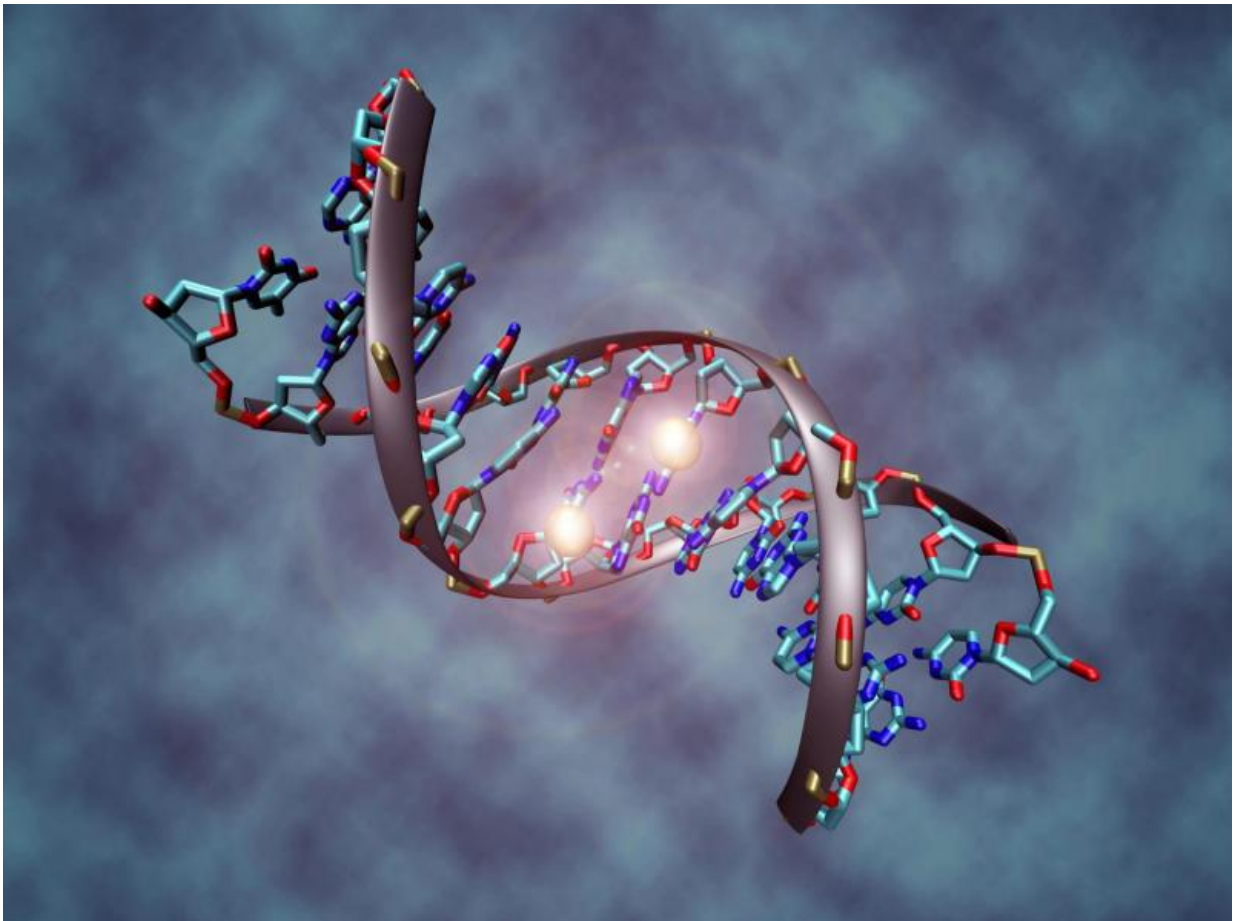


Scientists create first map of the wheat epigenome

December 10 2015



DNA methylation is pictured. Credit: Wikimedia Commons

Scientists at the University of Liverpool have carried out the first ever

genome-wide survey of heritable molecular changes that regulate gene activity in wheat, in what could become a new tool to improve crop breeding technologies.

Epigenetic marks are chemical tags which physically attach themselves to DNA, and modify its function without changing the genetic code. DNA methylation is one such mechanism of epigenetic gene expression control that can be passed down to future generations.

Now, developing technology has allowed scientists to study DNA methylation across the complex and challenging [wheat genome](#).

Dr Laura Gardiner, from the University's Centre for Genomic Research, said: "Due to the sheer size of the wheat genome, undertaking a survey like this has been technically unworkable until now, but understanding how and when genes are activated is a key part of understanding its complexity.

"This work opens up a whole new level of genetic variation which can be exploited by wheat breeders. In the future we see [epigenetic marks](#) becoming an important new tool in this area."

Using a combination of sodium bisulphate treatment and targeted gene enrichment, the team observed that methylation is highly conserved across all three genomes of hexaploid wheat, but found evidence of sub-genome specific methylation.

Methylation changes were also found to be associated with changes in gene-expression and, although not demonstrated, these changes are likely to affect the phenotype. The stability of methylation in the wheat genome was also shown, with some [methylation patterns](#) conserved for over 0.5 million years.



Wheat fields. Credit: Professor Anthony Hall

Liverpool scientists created the first draft of the wheat genome in 2012, enabling new levels of precision breeding for this globally important food source which provides 20% of daily calories and protein for the world's population.

Professor Anthony Hall, who led the study, added: "With the ability to characterise genome-wide patterns of methylation we can now address fundamental questions in wheat, such as the role of epigenetics in the

domestication of crops and the stability and long-term function of methylation.

"We can also seek to understand how methylation changes important traits for farmers like disease resistance and yield variability. These are all key topics for future research at Liverpool and will impact on world agriculture."

More information: Laura-Jayne Gardiner et al. A genome-wide survey of DNA methylation in hexaploid wheat, *Genome Biology* (2015). DOI: [10.1186/s13059-015-0838-3](https://doi.org/10.1186/s13059-015-0838-3)

Provided by University of Liverpool

Citation: Scientists create first map of the wheat epigenome (2015, December 10) retrieved 24 March 2023 from <https://phys.org/news/2015-12-scientists-wheat-epigenome.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.