

Genetics and the hidden story of wheat



An international research team, in the journal *Genome Research*, have uncovered the genetic secrets that give wheat its extraordinary ability for local adaptation – opening up a previously untapped resource for producing more resilient wheat.

The research team, led by the Earlham Institute in collaboration with HelmholtzZentrum München, University of Liverpool and the John Innes Centre, have revealed epigenetic variations that was previously unknown to current genotyping methods.

The new findings link crop evolution and phenotypic change to agricultural conditions - allowing us to protect future yields with a climate resistant armour through new breeding methods - contributing to the success of this global crop, as well as significant implications for the wheat community.

The research team found geographical patterns in epigenetic changes between the 100 landraces of wheat studied, which suggests that these changes have arisen due to environmental conditions in those local areas.

This is exciting, because it means that breeders have a hidden tool up their sleeves. Currently, it's all about SNPs - single changes in a DNA sequence that have an effect on disease or environmental resistance, for example. Now, even if the DNA sequence is the same, there might be subtle changes at the epigenetic level that we can use to improve how plants respond to local conditions.

Essentially, there are more tools to enable farmers to keep on growing the best possible crop for their local environment. Group Leader Professor Anthony Hall at the Earlham Institute says, “we are very proud of our ground-breaking piece of fundamental work indicating that DNA methylation offers a broad and stable source of variation for wheat breeders.

“Our next step is to translate this fundamental work on DNA methylation to a technology that is transformative, relevant and accessible to wheat breeders for the development of new cultivars.”

Dr Laura-Jayne Gardiner, Senior Postdoctoral Scientist, added, “what is really neat is, even though we are working with a hugely complex genome which is five times the size of the human genome, we're able to translate this discovery into a tool for breeders in likely to be just a few years. As a scientist, it's incredibly exciting that your research could have such an immediate impact.”