

## Novel Software package to democratize Epigenetic data in plant breeding

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A team of researchers at Sound Agriculture has released a new software package, called soundDMR, designed to reveal epigenetic variation in plant populations. The findings, published today in *Scientific Reports*, showcase the potential of soundDMR to enable high-resolution epigenetic profiling of plants without the need for expensive equipment or complex library preparations, fostering new opportunities in plant breeding.

Epigenetics is the study of heritable changes in gene expression that occur without changes to the underlying DNA sequence. DNA methylation is one of the key mechanisms through which epigenetic variation occurs. It plays an important role in regulating gene expression across all life forms, with a particular significance in plants. However, it is only recently that long and ultra-long read sequencing technologies have enabled the study of methylation patterns in complex genomic regions by accurately identifying 5mC methylation even in non-CG contexts. Using Oxford Nanopore technology, these methods can be applied to non-model organisms, such as crops, even in the absence of large sequencing facilities.

The research team, led by Travis Bayer, PhD and Jack Colicchio, PhD, used soundDMR to effectively replicate findings from the established gold-standard method for methylation sequencing called whole genome bisulfite sequencing (WGBS). In addition, the team was able to expand on these findings by using Oxford Nanopore's "adaptive sampling," which allowed for the targeted sequencing of approximately 400 specific genome regions. This data revealed that the known demethylating agent, zebularine, decreased methylation across the *Arabidopsis thaliana* genome and induced epigenetic variation, improving the understanding of its effects.

"There are epigenetic variations in all plant systems that haven't been considered in breeding because of the difficulty in identifying these nuances," said Travis Bayer, PhD, co-founder and CTO, Sound Agriculture. "With nanopore sequencing technology, we now have an added level of insight to support breeding decisions that can improve agriculture outcomes."

"Oxford Nanopore technology offers more comprehensive genomic insights, especially in DNA methylation. This is a great example of high-accuracy epigenetic insights in biological analyses being used to support new genomic discoveries for the benefit of agriculture" said Gordon Sanghera, CEO Oxford Nanopore Technologies.