Unwinding the secrets of stress in plants could help feed the world during climate crisis

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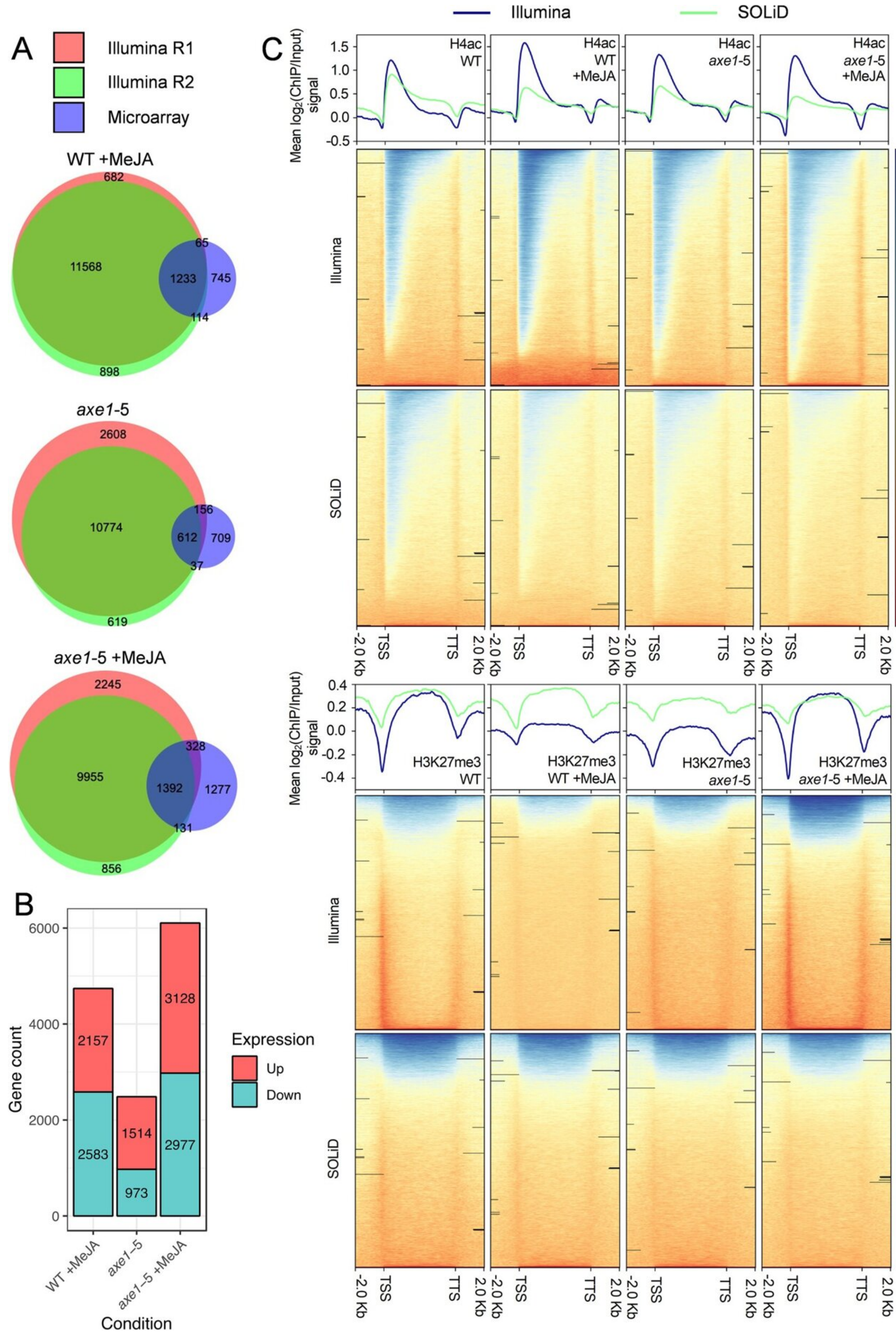
A
Illumina R1
Illumina R2
Microarray
WT +MeJA
682
11568
65
1233
745
114
898
axe1-5
2608
10774
156
612
709
37
619
axe1-5 +MeJA
2245
9955
328
1392
1277
131
856
B
Gene count
6000
4000
2000
0
2157
2583
1514
973
3128
2977
Expression
Up
Down
WT +MeJA
axe1–5
axe1–5 +MeJA
Condition
C
Illumina
SOLiD
Mean log2(ChIP/Input) signal
1.5
1.0
0.5
0.0
-0.5
H4ac WT
H4ac WT +MeJA
H4ac axe1-5
H4ac axe1-5 +MeJA
Illumina
SOLiD
3
2
1
0
-1
-2
-2.0 Kb
TSS
TTS
2.0 Kb
0.4
0.2
0.0
-0.2
-0.4
H3K27me3 WT
H3K27me3 WT +MeJA
H3K27me3 axe1-5
H3K27me3 axe1-5 +MeJA

Histone markers enrichment across different platforms and loci. A Venn diagrams showing comparison between Illumina and microarray data for H4ac-associated genes. Comparison of H4ac-associated loci identified in three conditions of interest on different platforms: Illumina HiSeq replicates of ChIP-Seq data, and comparison of this data on the transcriptome level with microarray analysis. For Illumina, genes were considered to be significant in that condition if the peak summit generated by MACS was situated within identified loci. In the microarray data, genes with at least a 2-fold difference in their expression levels were evaluated with Student's t test, and genes with p-values BMC Biology (2022). DOI: 10.1186/s12915-022-01273-8

New research from Royal Holloway has discovered how natural responses to stress in plants modify the way DNA is wrapped up in the cell to help it withstand the adverse effects that climate change has on its growth.

The novel research published in *BMC Biology*, by Professor Alessandra Devoto, Department of Biological Sciences, Royal Holloway, and her team, in collaboration with Dr. Motoaki Seki, RIKEN, Centre for Sustainable Resource Science, Yokohama, Japan and Dr. Jong-Myong Kim, from Ac-Planta Inc and the University of Tokyo, Japan, used the model plant Arabidopsis thaliana (Thale cress) treated with the plant hormone Jasmonate to stress out the plant's internal mechanism.

By doing this, the team analyzed how stress can alter the way DNA is coiled in cells to switch genes on and off. The understanding of such mechanisms could lead to improved plant survival to adverse environmental conditions, such as drought, resulting in a stronger plant capable of withstanding climate changes.

Professor Alessandra Devoto, from the Department of Biological Science at Royal Holloway, said: "Our research has shown that changes in the natural modifications of the proteins binding the plant DNA (namely 'histone modifications such as acetylation or methylation'), could lead to durable, inherited traits to make future plant generations more robust against other stresses like cold or pathogen attacks.

"This is very important data in light of the climate change crisis, as growing crops to feed the world will become increasingly difficult."

Stacey Vincent, Ph.D. student from Royal Holloway, added: "Being able to generate plants which can resist adverse environments would be a real game-changer. We're very excited to have discovered these finely-tuned stress responses in plants."

Dr. Jong-Myong Kim, from Ac-Planta Inc and the University of Tokyo, added: "This investigation shows how the effect of stress has repercussions across the whole plant genome and it is universally conserved between plants and animals."

Dr. Seki, from RIKEN, Centre for Sustainable Resource Science, Yokohama said: "These findings are an important milestone in understanding the mechanisms through which plants, that are of fundamental importance to guarantee animal life on the planet, can become more resilient to the challenges they face in the future.

"We are extremely proud to be able to lend a helping hand to plant life."

More information: Stacey A. Vincent et al, Jasmonates and Histone deacetylase 6 activate Arabidopsis genome-wide histone acetylation and methylation during the early acute stress response, *BMC Biology* (2022). DOI: 10.1186/s12915-022-01273-8

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