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Population epigenomics of plant DNA methylation: perspectives for molecular breeding

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Background

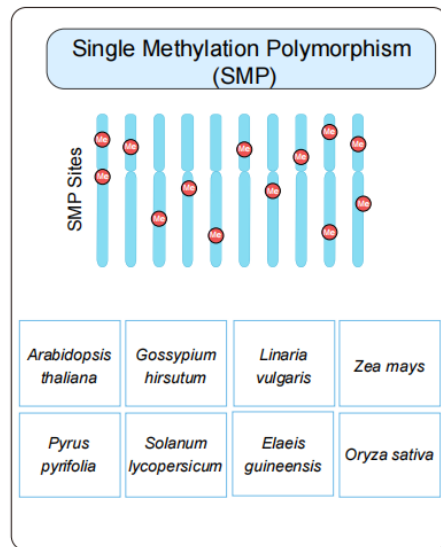
1. DNA methylation is a key plant epigenetic modification occurring in **CG, CHG and CHH** contexts.
2. It contributes to **transposon silencing, gene expression regulation, development, stress responses and agronomic traits**.
3. Population-scale methylome studies reveal extensive natural methylation variation across wild accessions, landraces and breeding germplasm.
4. Methylation variation can arise from **spontaneous epimutations, genetic variation and environmental induction**.
5. Integrating methylomes with genomics, transcriptomics and phenotypes enables the discovery of **functional epialleles and epigenetic markers** for molecular breeding.

Population epigenomics links methylation variation to regulatory diversity, adaptation and molecular breeding.

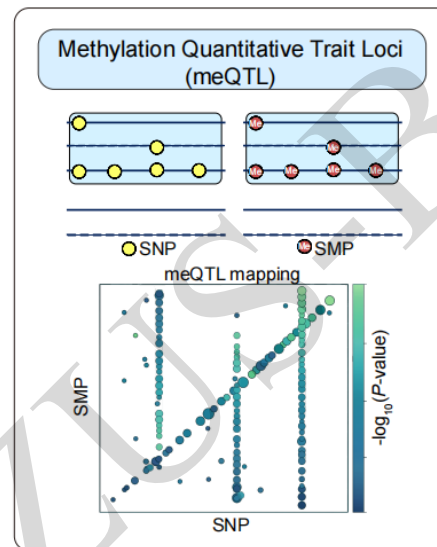


Main conclusion

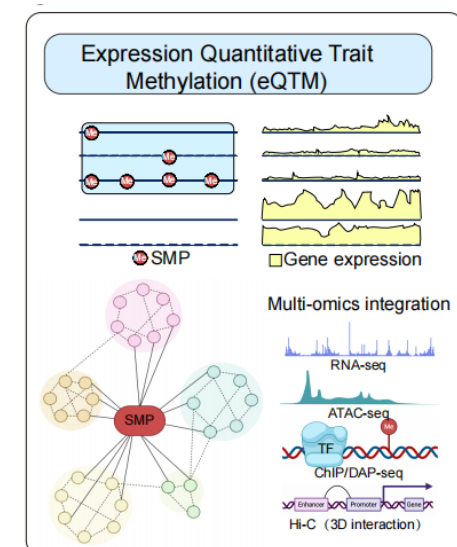
Integrated Genetic–Epigenetic–Transcriptomic Analysis



SMPs capture single-site methylation variation across populations.



meQTL mapping reveals genetic variants that shape methylation landscapes.

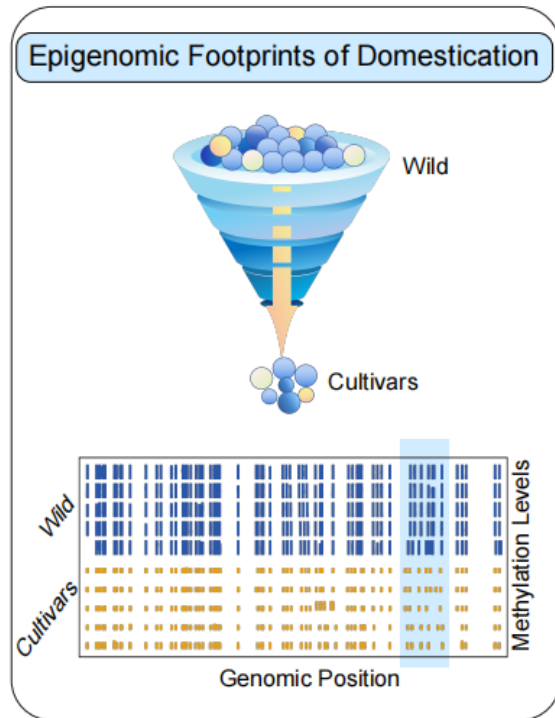


eQTM analysis connects methylation polymorphisms to transcriptional outputs.

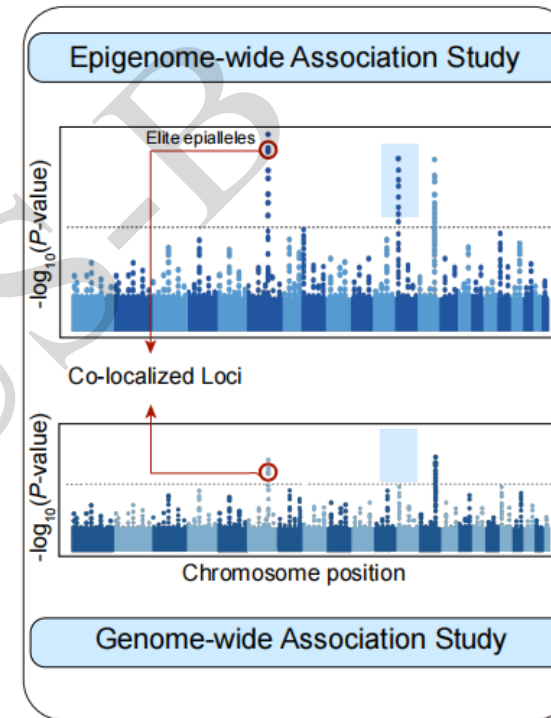
These analyses provide a framework to identify **functional epialleles** and regulatory variants underlying complex traits



EWAS and Domestication Analysis Link Methylation Variation to Crop Traits



Domestication-associated DMRs, selected epialleles



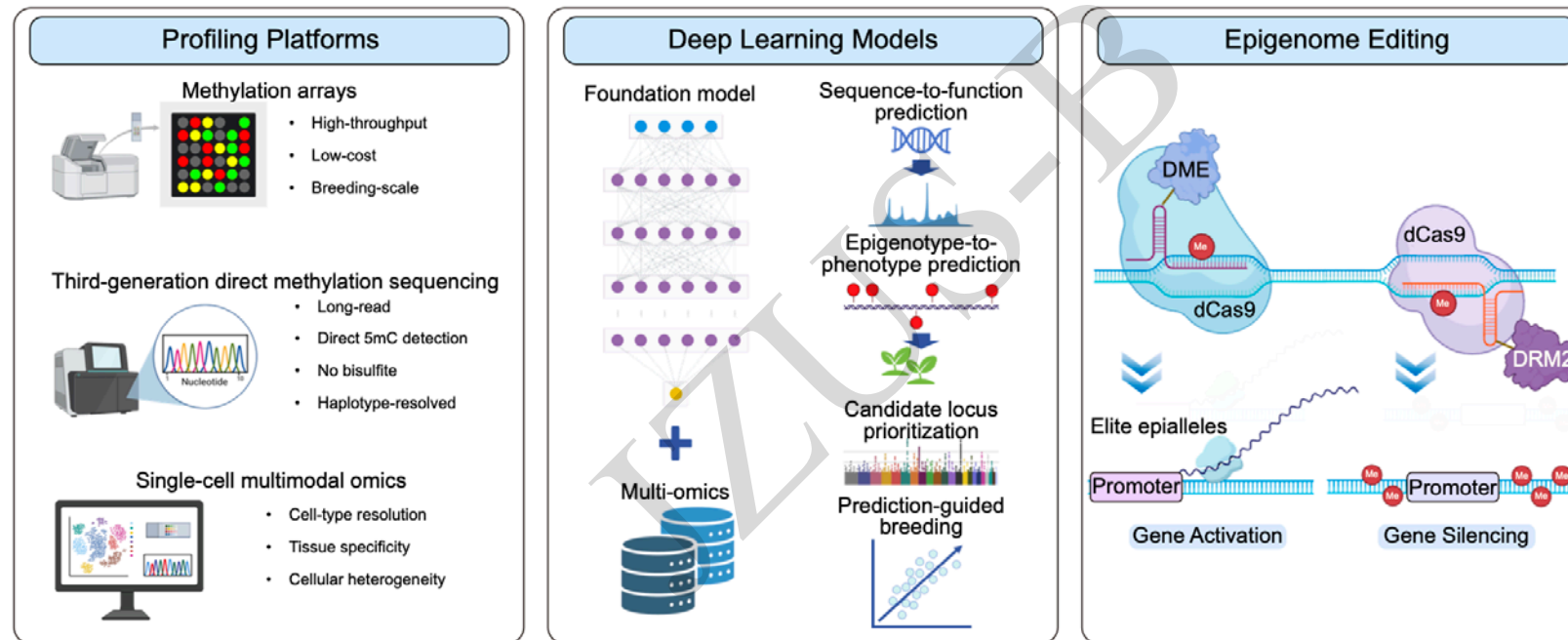
Candidate epigenetic markers for agronomic traits

EWAS identifies methylation variants associated with traits, while domestication analysis reveals whether these variants were shaped by artificial selection.



Main conclusion

From Epigenome Profiling to Prediction and Editing



A closed-loop framework for epigenome-guided crop improvement