

Diverging cell wall strategies for drought adaptation in two maize inbreds with contrasting lodging resistance.

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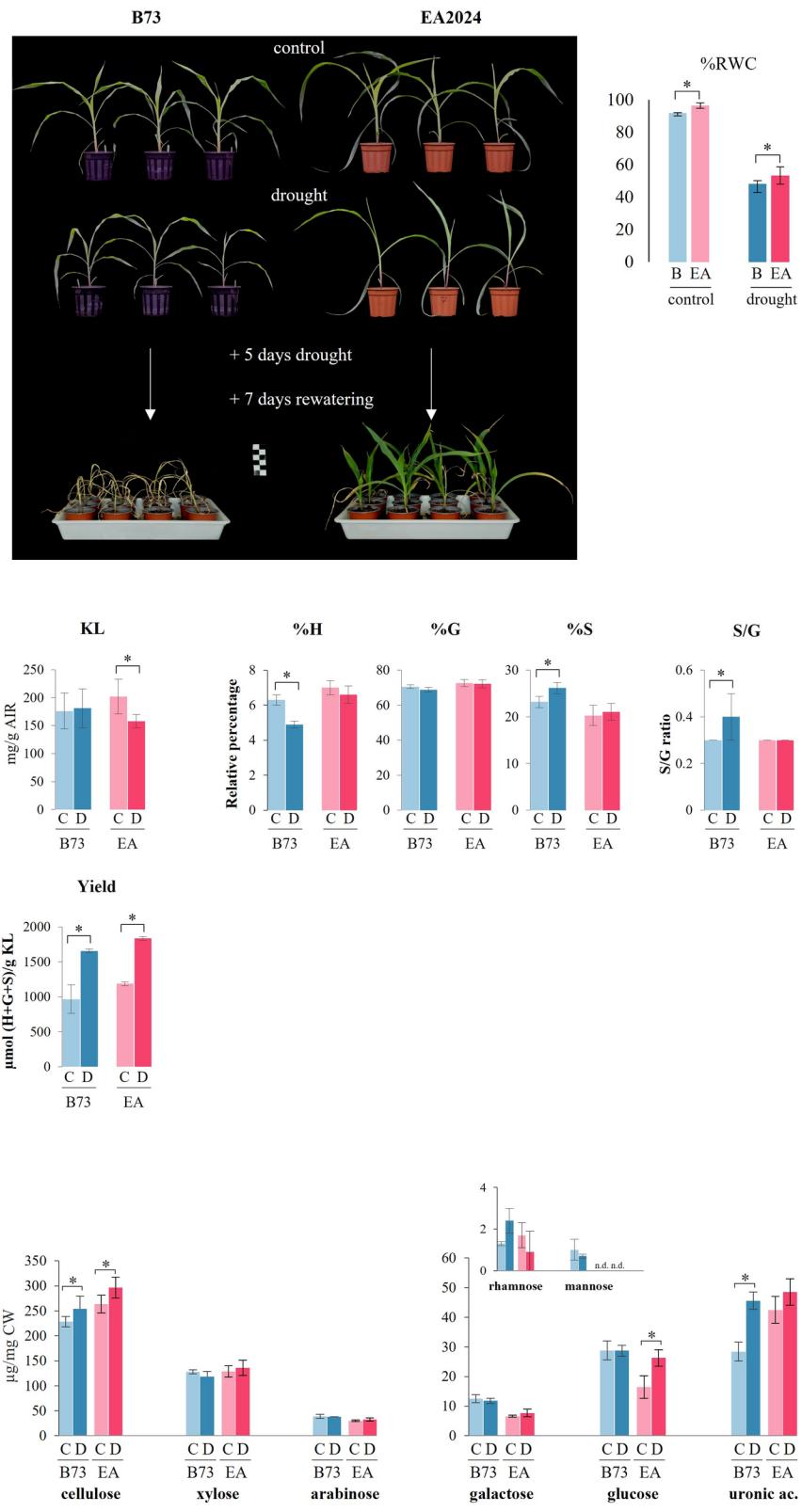
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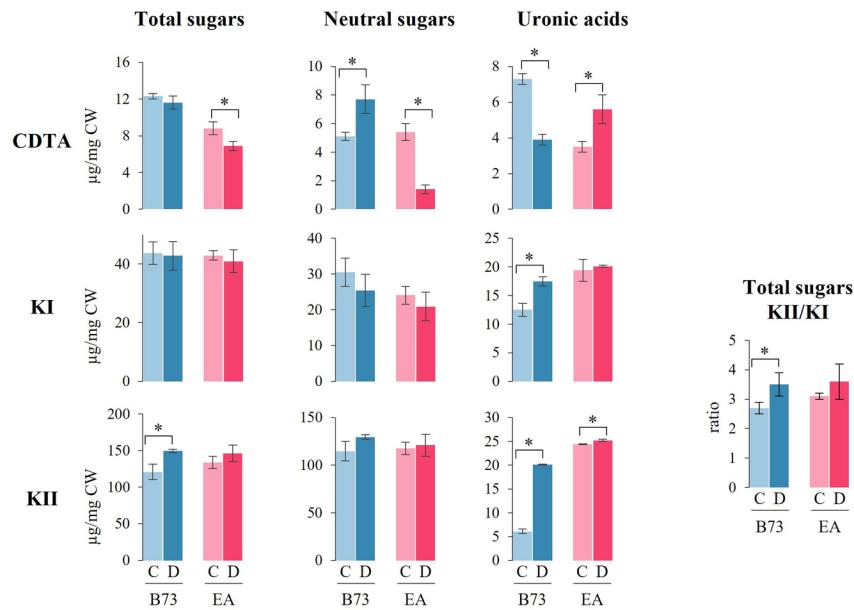
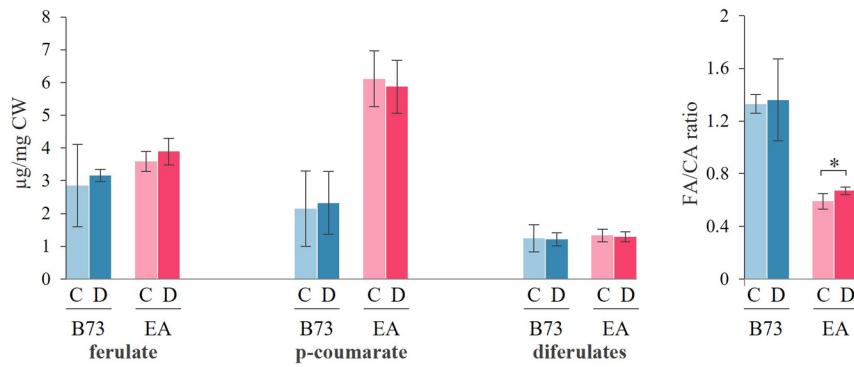
Abstract

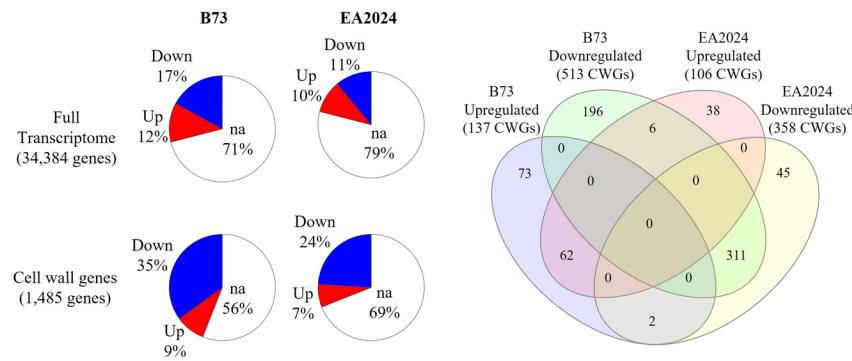
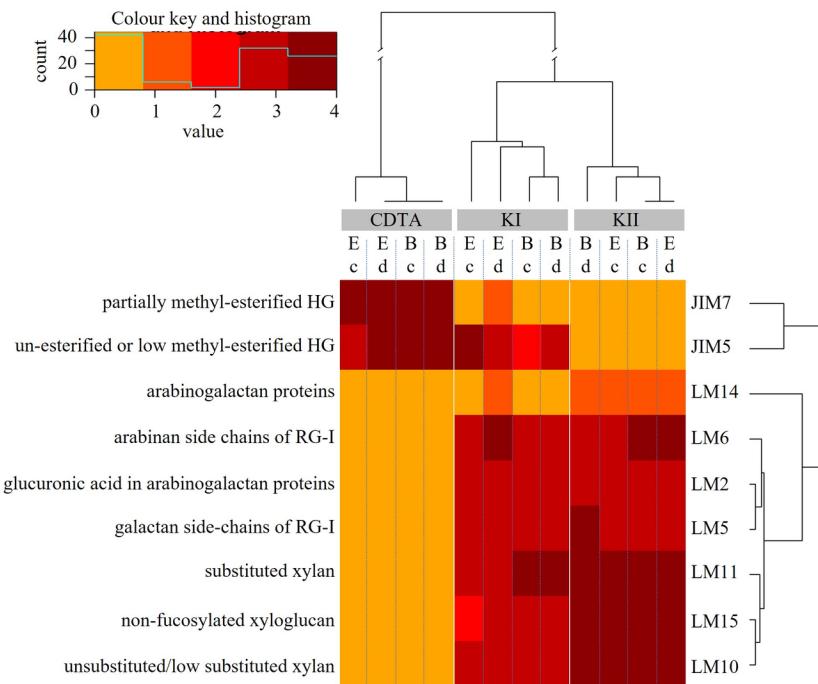
The plant cell wall is a plastic structure of variable composition that constitutes the first line of defense against environmental challenges. Lodging and drought are two stressful conditions that severely impact on maize yield. In a previous work, we characterized the cell walls of two maize inbreds susceptible (EA2024) or resistant (B73) to stalk-lodging. Here, we show that drought induces phenotypical, physiological, cell wall, and transcriptional changes with distinct dynamics in the two inbreds, and that B73 is less tolerant than EA2024 to this stress. While in control conditions, stalk of EA2024 had higher levels of cellulose, uronic acids and *p*-coumarate than B73, upon drought these displayed increased levels of arabinose-enriched polymers, such as pectin-arabinans and arabinogalactan proteins, and a decreased lignin content. By contrast, a deeper rearrangement of cell walls including the modification of lignin composition and an increase of uronic acids was observed in B73. Drought induced higher changes in gene expression in B73 compared to EA2024, particularly in cell wall-related genes, that were altered in an inbred-specific manner. Transcription factor enrichment assays unveiled inbred-specific regulatory networks coordinating cell wall genes expression. Altogether, these findings reveal that B73 and EA2024 inbreds, with opposite stalk-lodging phenotypes, undertake different cell wall modification strategies in response to drought. We propose that the specific cell wall composition that confers lodging resistance to B73 compromises its cell wall plasticity and renders this inbred more susceptible to drought.

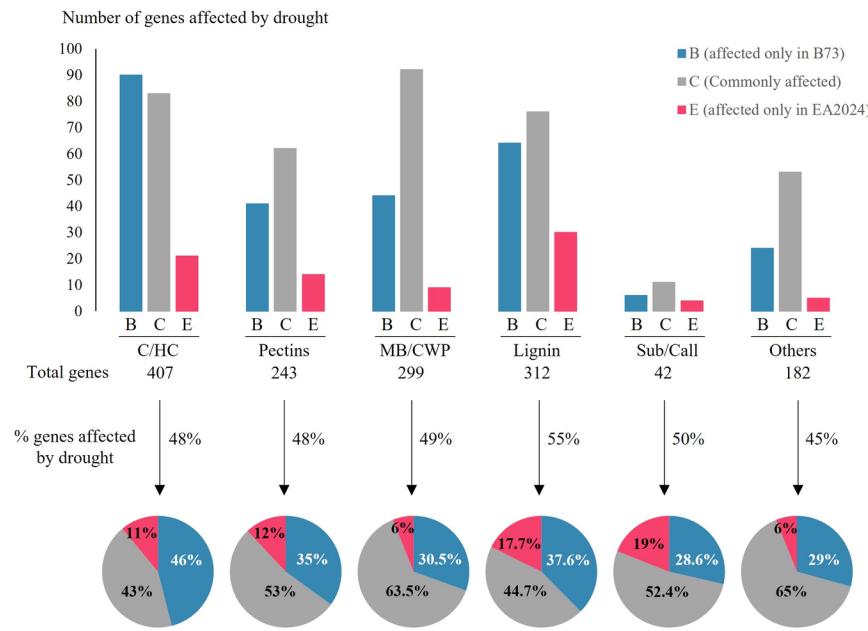
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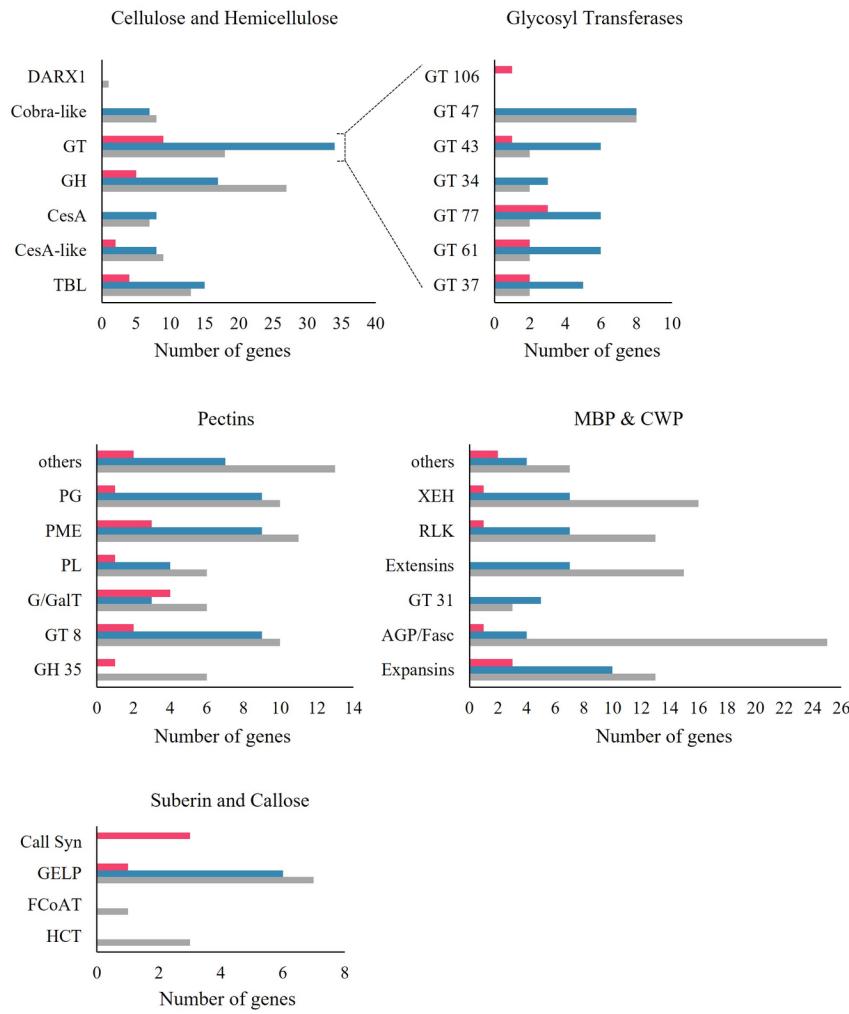
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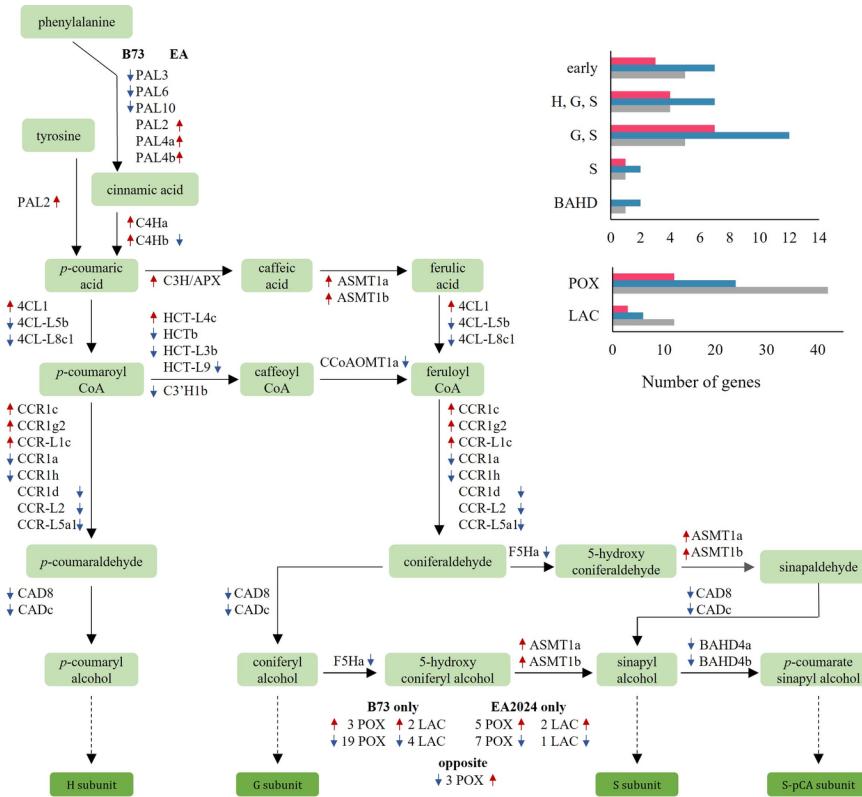




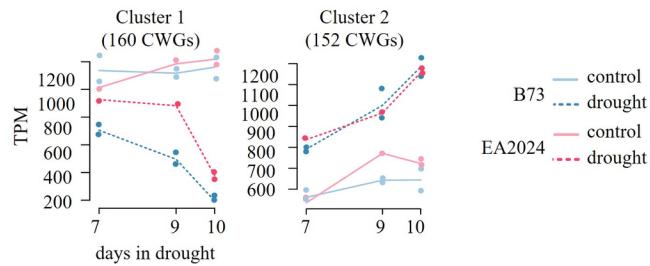




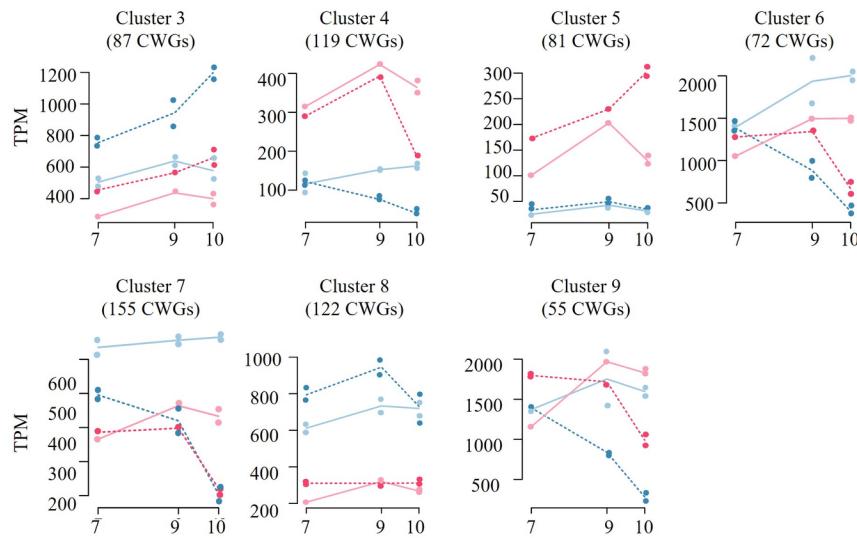




Inbred-independent CWGs expression pattern



Inbred-dependent CWGs expression pattern



Clusters 1 and 2

18.5%	81.5%	Lignin (200 genes)
27%	73%	Suberin & callose (26 genes)
30%	70%	C/HC (281 genes)
34.5%	65.5%	Pectins (171 genes)
40.5%	59.6%	MB/CWPs (200 genes)

Expression pattern

Inbred independent

Inbred dependent

