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## Cis-regulatory code for predicting plant cell-type transcriptional response to high salinity

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摘要	Multicellular organisms have diverse cell-types with distinct roles in development and responses to the environment. At the transcriptional level, the differences in the environmental response between cell-types are due to differences in regulatory programs. In plants, although cell-type environmental responses have been examined, it is unclear how these responses are regulated. Here, we identify a set of putative cis-regulatory elements (pCREs) enriched in the promoters of genes responsive to high salinity stress in six Arabidopsis ( <i>Arabidopsis thaliana</i> ) root cell-types. We then use these pCREs to establish cis-regulatory codes, i.e., models predicting whether a gene is responsive to high salinity for each cell-type with machine learning. These pCRE-based models outperform models using in vitro binding data of 758 Arabidopsis transcription factors. Surprisingly, organ pCREs identified based on the whole root high salinity response can predict cell-type responses as well as pCREs derived from cell-type data, because organ and cell-type pCREs predict complementary subsets of high salinity response genes. Our findings not only advance our understanding of the regulatory mechanisms of the plant spatial transcriptional response through cis-regulatory codes, but also suggest broad applicability of the approach to any species, particularly those with little or no trans regulatory data.
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