Transcriptomics to unravel regulation of nutrient uptake rates upon synthetic CEP1 peptide application in plant roots

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Abstract

Plant roots are responsible for essential functions like nutrient uptake, anchorage, and storage. Study of root uptake mechanisms for macro nutrients like nitrogen, phosphorus, potassium, and sulphur is vital to our understanding of their role in plant growth and development. Small signaling peptides (SSPs), are hormones which regulate diverse plant developmental processes including root growth. However, their involvement in regulation of nutrient uptake by roots is poorly understood. We recently developed a hydroponics- based plant growth system which combines ion chromatography with synthetic peptide application, to analyze the depletion rates of nutrients by Medicago truncatula roots. Application of the synthetic SSP MtCEP1 and AtCEP1 led to enhanced uptake of nitrates, sulphates, and phosphates. To further elucidate the molecular mechanism of nutrient uptake mediated by these peptides, we conducted an RNAseq of M. truncatula roots treated with the peptides. A differential gene expression analysis revealed thousands of peptide responsive genes. Several known nitrate transporters and a sulphate transporter AtSULTR3:5-like gene showed enhanced expression under both, MtCEP1 and AtCEP1 peptide application. Multiple, as of yet uncharacterized, CEP peptide responsive pathway regulatory genes such as kinases and transcription factors were also identified through this transcriptomic analysis. This study highlights the potential of phenomics enabled biology to uncover target genes for improving agriculturally important traits such as nutrient uptake.

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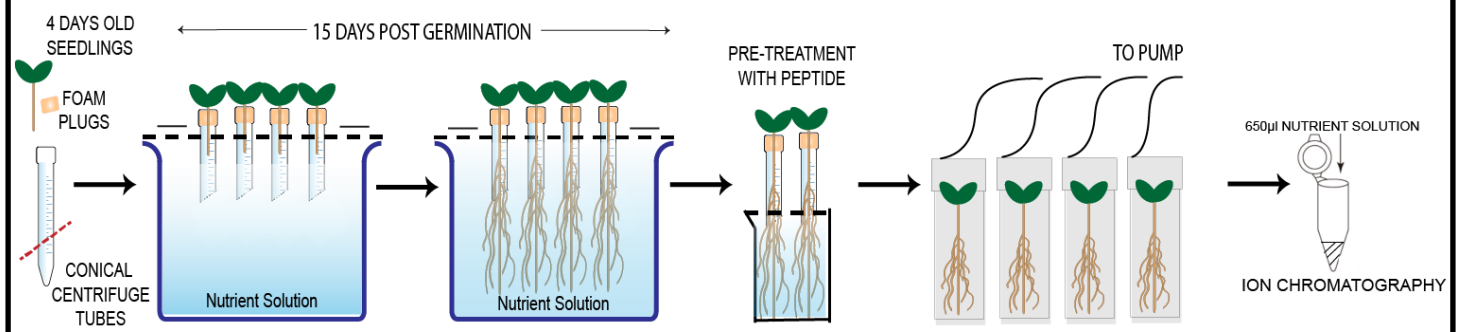
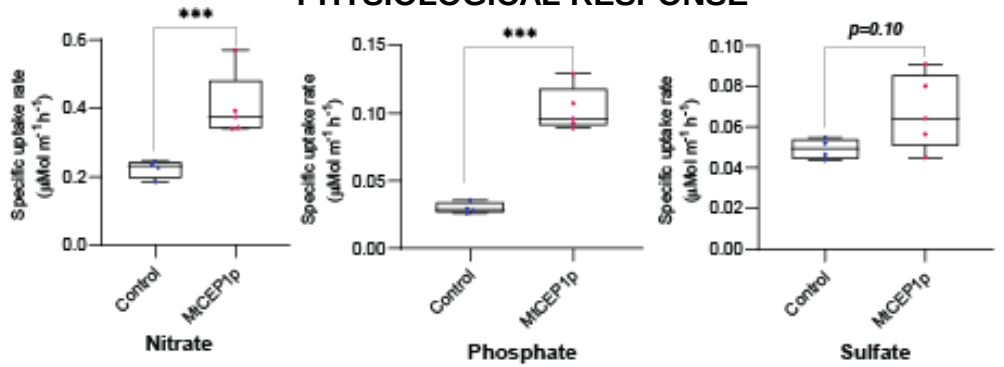
Understanding CEP1 mediated nutrient uptake regulation through Phenomics and Transcriptomics

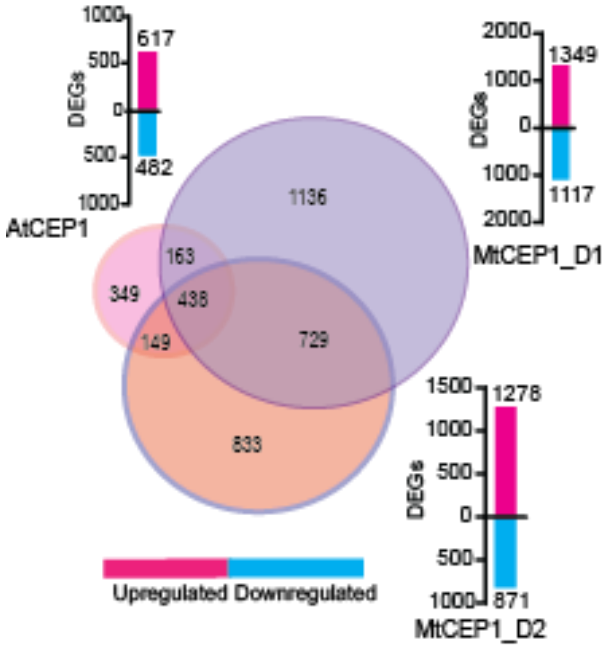
NUTRIENT UPTAKE PLATFORM



PHYSIOLOGICAL RESPONSE



MOLECULAR MECHANISM



Venn Diagram showing number of differentially regulated genes shared by application of three synthetic peptide variants

Top10 GO Categories

Cell division and proliferation

Auxin response genes were repressed by MtCEPs

Upregulation of phosphatase activity and ABA response

Transporters and Regulators

Seven NRTs were induced by MtCEP1D1

AtSULTR3;5 ortholog was highly induced by all CEP peptide domains

CEP1 peptide induced Cyclin dependent Kinase, Serine/Threonine Kinase and an LRR receptor like kinase.

Myb and MADS-box transcription factors were also induced by all three peptides