

Concurrent drought stress and vascular pathogen infection induces secondary cell wall biosynthesis specific genes for the defense response in chickpea

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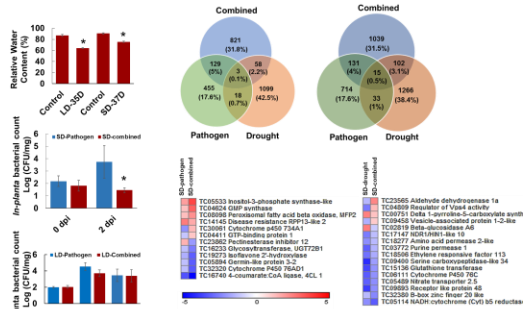
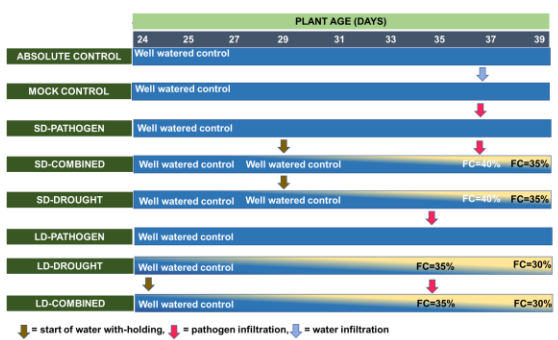
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Introduction

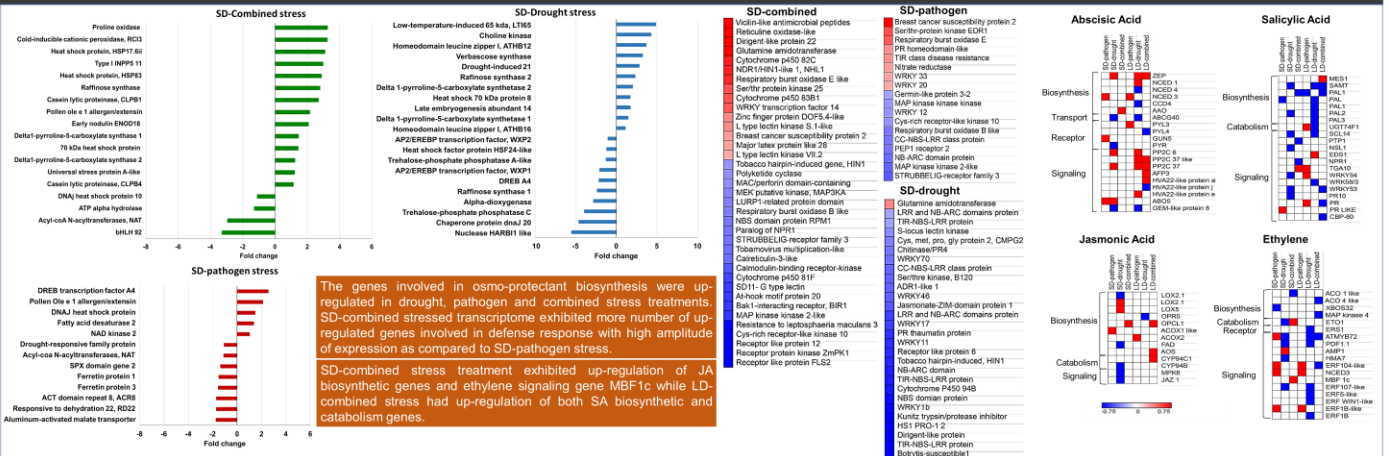
Chickpea (*Cicer arietinum*) is an important legume grown worldwide. However, it is susceptible to drought and various pathogen infections. In field, drought often co-occur with pathogen infection which could impose a severe threat. We studied the effect of drought stress on interaction of chickpea with xylem inhabiting wilt causing pathogen *Ralstonia solanacearum* (Rs), and net-impact of combined drought and pathogen stress on the plants. We observed decreased Rs multiplication with the progression of drought stress imposition. Further, we studied the plant transcriptomic changes in response to combined stress at short duration (SD, drought stress with 2 days of Rs infection) and long duration (LD, drought stress with 4 days of Rs infection) stress and compared it with individual stress transcriptome. Microarray results showed 821 and 1039 differentially expressed genes (DEGs) to be unique to SD-combined stress and LD-combined stress respectively. Combined stress induced the expression of genes involved in secondary cell wall modifications, alkaloid biosynthesis, hormone signaling and various defense responsive genes. In this study, we provide the evidence that drought stress decreases the Rs multiplication and chickpea plants induces genes involved in secondary cell wall deposition and alkaloid production as defense strategy under combined stress. Hereby, the present study implicates these unique genes as potential candidates for in-depth characterization of the molecular response of the plant to concurrent drought-pathogen stress.

Methodology

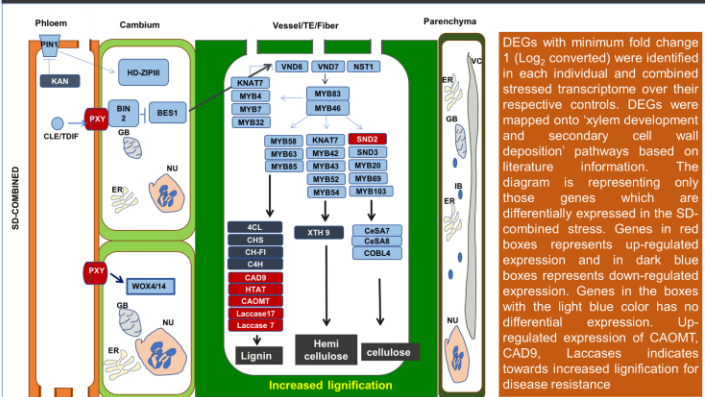


Notable reduction in *R. solanacearum* was observed under SD-combined stress compared to SD-pathogen stress. However, in *R. solanacearum* bacterial count was unchanged under LD-combined stress compared to LD-pathogen stress treatments. * in graphs indicates significant at $p < 0.05$, significance was tested using Student's t-test. The DEGs (Log₂ FC ≥ 1) under drought stress compared to absolute control, and under combined and pathogen stresses compared to mock control were screened using unpaired t-test ($p \leq 0.05$).

Differential expression of genes involved in disease resistance, drought stress tolerance and hormone metabolism-signaling



Differential expression of genes involved SCW synthesis



Conclusion

- Combined stress impact depends on the timing and mode of stress imposition.
- Slow drought stress imposition or drought acclimation does not impact the Rs multiplication in chickpea however, rapid imposition of drought stress in combined drought and *Ralstonia solanacearum* (Rs) stress decreases the Rs multiplication.
- Combined stress invokes some of the unique transcriptome changes however, some of the shared responses are also tailored.
- SD-combined stress in chickpea causes up-regulation of genes involved in JA biosynthesis and SA and ET signaling.
- SD-combined stress exhibited up-regulation of various genes involved in xylem biosynthesis and secondary cell-wall biosynthesis and phytoalexin biosynthesis.
- Increased lignification and phytoalexin accumulation might be responsible for the decreased bacterial multiplication in chickpea under combined stress.

Acknowledgment

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References: Sinha R, Gupta A, Senthil-Kumar M (2017) Concurrent Drought Stress and Vascular Pathogen Infection Induce Common and Distinct Transcriptomic Responses in Chickpea. *Frontiers in Plant Science*. Vol 8, PP 333.

Website: http://www.nipgr.res.in/research/dr_skmuthappa.php