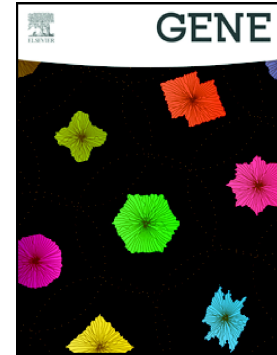


Accepted Manuscript

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PII: S0378-1119(18)30554-7
DOI: doi:[10.1016/j.gene.2018.05.064](https://doi.org/10.1016/j.gene.2018.05.064)
Reference: GENE 42875
To appear in: *Gene*
Received date: 5 April 2018
Revised date: 4 May 2018
Accepted date: 16 May 2018

Please cite this article as: Jinhua Zuo, Yunxiang Wang, Benzhong Zhu, Yunbo Luo, Qing Wang, Lipu Gao , sRNAome and transcriptome analysis provide insight into chilling response of cowpea pods. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. *Gene*(2017), doi:[10.1016/j.gene.2018.05.064](https://doi.org/10.1016/j.gene.2018.05.064)

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sRNAome and transcriptome analysis provide insight into chilling response of cowpea pods

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Abstract:

Cowpea is an important horticultural crop in tropical and subtropical areas of Asia, Africa, and Latin America, as well as parts of southern Europe and Central and South America. Chilling injury is a common physiological hazard of cowpea in cold chain logistics which reduce the cowpea pod's nutritional quality and product value. However, the molecular mechanism involved in chilling injury remains unclear in cowpea pods. RNA-Seq and sRNA-Seq technologies were employed to decipher the miRNAs and mRNAs expression profiles and their regulatory networks in cowpea pods involved in chilling stress. Differentially expressed miRNAs and mRNA profiles were obtained based on cluster analysis, miRNAs and target genes were found to show coherent relationships in the regulatory networks of chilling injury. Furthermore, we found that numerous miRNAs and nat-siRNAs' targets were predicted to be key enzymes involved in the redox reactions such as POD, CAT, AO and LOX, energy metabolism such as ATPase, FAD and NAD related enzymes and different transcription factors such as WRKY, bHLH, MYB, ERF and NAC which play important roles in chilling injury.

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