

# Insights into plant adaptations to occupy a challenging Amazonian habitat

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## Abstract

Canga substrates are a well-known example of a harsh environment for plants. Canga is the name of Brazilian ferruginous field formations, and it refers to the ecosystems associated with superficial iron crusts typical of Minas Gerais and Pará. This ecosystem is marked by high temperature and UV radiation, acidic and nutrient-depleted soils (especially phosphorus, magnesium, and calcium), and high metal concentrations (such as iron and manganese), all challenging for the establishment of plants. In the present study, we generated the first transcriptome data from two native Fabaceae species widely distributed in the canga outcrops in the State of Pará, *Parkia platycephala* Benth. and *Stryphnodendron pulcherrimum* (Willd.) Hochr, to understand the adaptive genetic mechanisms behind the establishment of these plants in the canga environment. Transcriptomics were carried out from leaves of plants growing in canga and forest substrates collected at the Carajás Mineral Province, Pará, Brazil. A combination of methods was used to recover complete and accurate transcriptomes. We achieved over 95% of the complete single-copy genes of eudicotyledon orthologs with BUSCO evaluation. Both species had more down-regulated genes in plants growing under canga substrate compared to the forest substrate: 391 up-regulated and 723 down-regulated for *P. platycephala* and 264 up-regulated and 574 down-regulated for *S. pulcherrimum*. The gene ontology enrichment analysis showed that the enriched differentially expressed genes (DEGs) of *P. platycephala* are associated with response to abiotic stimulus with the up-regulation of thiazole and thiamine (vitamin B1) biosynthetic process. For *S. pulcherrimum*, the DEGs are mainly associated with the up-regulation of guard cell differentiation and stomatal complex development. However, the plants' shared 64 up-regulated and 163 down-regulated genes, mainly associated with the rhythmic process and polysaccharide catabolic process. The KEGG enrichment pathway analysis revealed also enriched DEGs involved in the plants' circadian rhythm regulation, biosynthesis of secondary metabolites, and starch and sucrose metabolism. The differences in gene expression between *P. platycephala* and *S. pulcherrimum* in canga substrates were lower than between plants in forest substrates, suggesting a more conservative strategy when they grow in canga. Cross-species differential expression analysis was conducted using single-copy orthologues shared between species. Samples clustered by species indicated the difference in the adaptive strategies of each species. Looking at the DEGs between canga and forest, 204 gene orthologs were found to be DE between substrates. Our results reveal some insights over the adaptive convergence in the canga environment and suggested different strategies between species.

Funding:

Link to Video: