



### Nitrogen-starvation responsive microRNAs in *Coffea arabica* roots: is this a 3-player game?

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Nitrogen (N) is an essential macronutrient for plant growth and development. In the case of *C. arabica*, fertilization practices are the second major cost in coffee production. MicroRNAs (miRNAs) play key roles in regulating nitrogen metabolism in plants, but the crosstalk between N and miRNAs was mostly studied in plant models and/or herbaceous species from temperate climates. In this study, we used deep sequencing of *C. arabica* root small RNAs to reveal miRNAs that were differentially expressed in response to N starvation. We obtained 55 million raw reads using Illumina HiSeq 2000. After cleaning, 5,5 million unique reads were obtained. Three miRNA families were differentially expressed between N-sufficient and N-deficient libraries. Two of them, miR858 and miR166, are predicted to target *Myb* and *HD-Zip* transcription factors, respectively. *MYBs* targeted by mir858 are involved in crosstalk between ABA, sugar, and nutrient signals which is remarkable from an developmental standpoint. *HD-ZIPs* regulated by mir166 are involved in the development of cambium and secondary vascular tissues. The third family do not have any homolog in miRBase and it targets TFs related to ethylene signal transduction. For miR858 and the new family we found target transcripts in roots mRNA-seq. These initial findings warrant further investigation of these miRNA families and targets. In summary, we report the *in silico* identification of three miRNA families never associated to N-deficiency in roots, shedding light on the identification of new miRNAs relevant to the crosstalk between hormones and nutrients in root development.

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