

Annotation of transfer RNAs and microRNAs from *Coffea canephora* genome

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Abstract

Annotating plant genomes for non coding RNAs (ncRNAs) is helpful in the development of biotechnological products and plant breeding. Coffee is one of the most important commodities in agriculture and Brazil is the leading producer and second largest consumer market of coffee; however, research has mostly focused on identifying protein coding genes with few approaches addressing the non coding RNA component of coffee genome. We here used bioinformatic approaches to update the annotation of microRNAs and annotate transfer RNAs in the Robusta coffee (*C. canephora*) genome. Combining sequence similarity (BLASTN against ENSEMBL Plants database) and structural searches (Infernal/Rfam and tRNAscan - SE for transfer RNAs), we identified a set of 208 microRNA precursors and 663 transfer RNAs with their respective amino acids. A total of 144 microRNA precursors were identified for the first time in the present analysis: 122 using sequence similarity search and 22 using structural search. Sixty-four precursors were previously identified in a recent annotation; the majority, 63 were obtained in structural search. The proportion of transfer RNAs (tRNAs) was relatively similar to *Populus trichocarpa* and *Vitis vinifera*. The most common anti-codon is tRNA for methionine with 65 genes and the rarest is tRNA for tyrosine with only 14 copies. Our results represent an important improvement of the coffee ncRNA annotation, paving the way to further research on the contribution of post-transcriptional regulation to plant development and physiology. Future steps in this study include the annotation of other ncRNA classes and transcriptional support from small RNA sequencing data.

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