

## Mitochondrial genome of *Garcinia mangostana* L. variety Mesta

### ABSTRACT

Fruits of *Garcinia mangostana* L. (mangosteen) are rich in nutrients with xanthenes found in the pericarp having great pharmaceutical potential. Mangosteen variety Mesta is only found in Malaysia, which tastes sweeter than the common Manggis variety in Southeast Asia. In this study, we report the complete mitogenome of *G. mangostana* L. variety Mesta with a total sequence length of 371,235 bp of which 1.7% could be of plastid origin. The overall GC content of the mitogenome is 43.8%, comprising 29 protein-coding genes, 3 rRNA genes, and 21 tRNA genes. Repeat and tandem repeat sequences accounted for 5.8% and 0.15% of the Mesta mitogenome, respectively. There are 333 predicted RNA-editing sites in Mesta mitogenome. These include the RNA-editing events that generated the start codon of *nad1* gene and the stop codon of *ccmFC* gene. Phylogenomic analysis using both maximum likelihood and Bayesian analysis methods showed that the mitogenome of mangosteen variety Mesta was grouped under Malpighiales order. This is the first complete mitogenome from the *Garcinia* genus for future evolutionary studies.