ABSTRACT

Oil palm (*Elaeis guineensis*) is the world's major perennial monocot crop and contributes highly to the economies of South East Asia. As the oil palm fruit is the source of the main economic output for this crop, floral development is a critical process related to oil palm productivity. miR172 has been shown to be an important regulator of the AP2 family transcription factors involved in floral timing in a number of plants and belongs to a group of highly conserved miRNA that can be identified based on sequence homology.

Six oil palm miR172 paralogs, representing two distinct mature miR172 sequences, and an AP2-like target were identified based on sequence identity and predicted hairpin structures, using a combination of RT-PCR cloning and bioinformatic analysis of oil palm EST data. Expression of mature miR172a sequences was higher in floral organs than vegetative tissues, confirming the role of this miRNA in floral organ identity and flowering time. Some variation in the expression of the six paralogs egu-miR172 precursors in different oil palm tissues was observed with each of the two isoforms showing different expression patterns during floral development.

miR172 and the AP2-like gene showed an inverse expression pattern to that of the predicted AP2-like target in some tissues while they also showed overlapping expression patterns and did not show an obvious negative correlation in some other tissues. These data are consistent with previous reports that although in some tissues the cleavage of the potential target was observed, miR172 may also act via translational repression.