## Insights on the potential of RNA-Seq on improving pomological traits of African indigenous fruit trees: a mini review

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## Abstract

Fruit tree improvement has taken great strides by roping in improved and efficient biotechnological tools to increase fruit yield and quality to meet local and export demands. For the past decade, the RNA-Seq tool has successfully been used in fruit tree improvement programs to identify genes, dissect complex traits, and understand different molecular pathways and differential expression of genes. However, despite their growing importance in food and nutrition security, medicinal uses, and climate change mitigation strategies, very little has been done to improve the pomological traits of African indigenous fruits, especially at the molecular level. African indigenous fruit trees exhibit unexplained variation in flowering, fruit load, fruit size, fruit ripening, fruit taste, fruit nutritional composition and shelf-life. The booming local commercial companies and export markets are demanding consistent quality indigenous fruits. This has necessitated the need for fast and effective tools that will hasten the understanding and improvement of fruiting qualities. The improvement of fruiting and fruit qualities will go a long way in accelerating the domestication and commercialization of African indigenous fruit trees. This review paper gives molecular biology insights on how RNA-Seq has been successfully used in fruit improvement of exotic fruits through gene identification, comparative transcriptome analysis under different conditions, and understanding molecular pathways that influence important pomological traits. The review article also unearths opportunities where RNA-Seq can improve our knowledge and improvement of undesirable traits common in African indigenous fruits.

Keywords: RNA-Seq, indigenous fruit trees, Africa, pomological traits, fruit quality.