



Genome Sequencing to Unlock the Potential of African Indigenous Fruit Tree Species

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Sub-saharan Africa is endowed with several indigenous fruit tree species (IFTs) that were traditionally consumed in the region especially by children. Some of these fruits are rich in various vitamins and minerals (Stadlmayr *et al.*, 2012) important in fighting hidden hunger, a common problem in Sub-Saharan Africa (SSA) where there is over-reliance on staple food diets. Due to their nutritional qualities, some of these tree species e.g. *Tamarindus indica*, *Sclerocarya birrea*, *Adansonia digitata*, and *Dacryodes edulis* have attracted global markets (Rachel, 2015) and hence are potential income earners. However, this potential remains under-utilised. Unlike the tropical fruits from other regions that have undergone selection and improvement and are widely grown on farms, these IFTs continue being sourced from the wild. Being native of the land, IFTs also help in preserving local culture, cuisines, biodiversity and the societal heritage. With the continued forest and natural parklands degradation, the survival of these IFTs is threatened and much worse, the existing intra-species diversity is under peril. Due to social-cultural issues the introduced tropical fruit tree species such as mangoes, pineapple, bananas, avocados and pawpaw account for the largest amount of fruits grown and consumed in SSA; there are minimal attempts to grow and improve the African IFTs. Other factors that have limited the cultivation of African IFTs include the presumed trees' long reproductive cycle (some of the species are said to take about 10-20 years to the first fruiting); lack of suitable planting material, propagation techniques and poor productivity which is linked to lack of investment in African IFTs research. An IFT research geared towards global market development must respond to these issues. There is a need to develop African IFTs cultivars with improved reproductive cycles, propagation techniques, customer preferred fruit characteristics, improved productivity and tolerance to diseases and pests.

Employing Genomics to Accelerate IFTs Improvement

One of the keys to make the IFTs economically viable so that they can contribute to the economic resilience of the local communities is to make them yield high and better in nutrition and quality and also develop value chains and new markets. The new-age tools like genomics, phenomics, association mapping, etc. can immensely help to improve yield, quality and nutrition of the IFTs. These tools are already being applied to improve world's major food crops and some industrially important tree species such as eucalypts (Silva-Junior *et al.*, 2015; Muller *et al.*, 2015), *Populus trichocarpa* (Geraldes *et al.*, 2013) and oil palm (Singh *et al.*, 2013; Teh *et al.*, 2016).

With genome sequencing of the indigenous African tree species, the generated information can be used to accelerate the breeding of these species to overcome key limitations that have slowed their adoption in farming and utilisation. The African Orphan Crop Consortium (AOCC; <http://africanorphan crops.org/about/>) genome sequencing initiative is founded on such platform. Examples of Important traits for improvement in some of the African IFTs include:

1. *Adansonia digitata*: increased leaf production fruit traits (yield, pulp quality), fast growth
2. *Tamarindus indica*: fruit yield and pulp quality, fast growth, tree architecture
3. *Sclerocarya birrea* (dioecious species): fruit yield and pulp quality, sugar content in fruits, kernel oil, tree size and architecture
4. *Dacryodes edulis* (dioecious species): fruit yield and pulp quality, fast growth

For the dioecious species, genome sequencing can be employed to develop sex-specific markers which can

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be useful in early sex-screening so as ensure the correct female/male ratios and to avoid incurring expenses of raising male-only population.

Conclusion

Unravelling the genome sequences of the African IFTs lays a foundation to their future improvement and sustainable utilisation of important African fruit diversity before it is lost. Being the custodian of this diversity, African national governments need to play a bigger role in development of such initiatives as the AOCC as well as encouraging the use of the generated genome information in their country's IFT breeding programmes.

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