

## **Origin and diversity of an underutilized fruit tree crop, cempedak (*Artocarpus integer*, Moraceae)**

### **ABSTRACT**

#### **PREMISE OF THE STUDY:**

Underutilized crops and their wild relatives are important resources for crop improvement and food security. Cempedak [*Artocarpus integer* (Thunb). Merr.] is a significant crop in Malaysia but underutilized elsewhere. Here we performed molecular characterization of cempedak and its putative wild relative bangkong (*Artocarpus integer* (Thunb). Merr. var. *silvestris* Corner) to address questions regarding the origin and diversity of cempedak.

#### **METHODS:**

Using data from 12 microsatellite loci, we assessed the genetic diversity and genetic/geographic structure for 353 cempedak and 175 bangkong accessions from Malaysia and neighboring countries and employed clonal analysis to characterize cempedak cultivars. We conducted haplotype network analyses on the *trnH-psbA* region in a subset of these samples. We also analyzed key vegetative characters that reportedly differentiate cempedak and bangkong.

#### **KEY RESULTS:**

We show that cempedak and bangkong are sister taxa and distinct genetically and morphologically, but the directionality of domestication origin is unclear. Genetic diversity was generally higher in bangkong than in cempedak. We found a distinct genetic cluster for cempedak from Borneo as compared to cempedak from Peninsular Malaysia. Finally, cempedak cultivars with the same names did not always share the same genetic fingerprint.

#### **CONCLUSIONS:**

Cempedak origins are complex, with likely admixture and hybridization with bangkong, warranting further investigation. We provide a baseline of genetic diversity of cempedak

and bangkong in Malaysia and found that germplasm collections in Malaysia represent diverse coverage of the four cempedak genetic clusters detected.