Toward Food Security & Energy Sustainability: Genomic Resources for Breadfruit

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CONTEXT FOR STUDY
Approximately 90% of human food needs worldwide are met by only about 30 crops, many of which are annuals, require massive amounts of energy input (i.e. fertilizers, pesticides, irrigation, mechanization for planting and harvesting), and are shipped throughout the world to meet food needs. In 2010, agriculture (food production, transportation, and processing) accounted for 30% of worldwide energy consumption. Realizing the potential of locally grown, underutilized perennial crops (which require less energy input than annuals) can reduce energy use in the agriculture sector and increase food security in vulnerable areas, many of which lie in the tropics. Genomic resources are a vital part of the toolkit for improving and broadening our agricultural base worldwide, yet very few genomic resources exist for underutilized crops.

Breadfruit, Artocarpus altilis, is a staple starch crop that is a major component of many traditional agroforestry systems in the tropical South Pacific Islands. Unlike major annual crop monocultures, which must be replanted each year, agroforestry systems are more permanent ecosystems that sequester carbon over longer periods. Breadfruit is a multi-use, low-input tree crop that requires relatively little maintenance, fertilization, or pest control and can be produced and consumed locally on small and large scales. The tree bears fruit in three to five years of planting, and remains productive for generations, reducing the energy input of planting required by annuals, and serving as a carbon sink.
PROJECT GOALS

Develop a reference draft genome for breadfruit’s wild progenitor species (Artocarpus camansi). Because most breadfruit cultivars are triploid, a diploid wild species was targeted. This is an important step in further development of breadfruit genomic resources and research into breadfruit domestication.

Develop exon capture tools for targeted sequencing of coding genes in Artocarpus species (ca. 70 species). Once developed, these tools can be used in breadfruit and related species (many of which are also important underutilized crops) and can be used to provide a genus-wide picture of gene evolution and domestication.

Produce annotated transcriptomes of breadfruit cultivars and breadfruit’s wild progenitor species to provide insight into genes regulating important traits in breadfruit.

Identify putative SNPs (single nucleotide polymorphisms) which can enable genome-wide association studies and marker-assisted selection to improve breadfruit cultivars.

OUTCOMES

All of the above goals were accomplished and the products of this research will facilitate large-scale genotyping of breadfruit germplasm collections and massively-parallel exome genotyping of Artocarpus species. This should provide a genus-wide picture of gene evolution and crop domestication in a group of low energy input underutilized tropical crops. The results will also create tools for crop improvement and can help increase the local growing and consumption of breadfruit and possibly over a dozen other low energy input tropical fruit tree crops in the genus Artocarpus.