Using Genomics to Thwart Two Plant Viruses Decimating a Source of Dietary Carbohydrates

Illumina sequencing is enabling BecA-ILRI Hub researchers to better understand two viruses responsible for infecting cassava crops throughout Africa.

Recognizing that its technology could play a critical role in alleviating global hunger, malnutrition, and poverty, Illumina created the Agricultural Greater Good initiative. Each year, Illumina awards Greater Good grants to agricultural research organizations that are focused on identifying and breeding plants and animals that will increase the sustainability, productivity, and nutritional density of crop and livestock species. Under the grants, Illumina sequencing and genotyping reagents are provided free of charge.

biosciences eastern and central africa

BecA-ILRI Hub
2013 Illumina Greater Good Initiative Award Winner

Introduction

People living in sub-Saharan Africa have learned to make the most of plants that can survive the environmental extremes of the region. Cassava, a woody flowering shrub that grows well in poor soil and requires little water, is one such plant. Introduced to Africa from Brazil in the 16th century by Portuguese traders, every part of the plant has a use. The leaves are eaten as vegetables. The leaves and branches are processed into biofuel and animal feed. The tuberous roots are an excellent source of carbohydrates and can be eaten fresh, cooked, fried, or processed into syrup, flour, or powder, forming the basis of a variety of culinary dishes.

Cassava is a staple food in Africa, providing more than 200 million people with 50% of their daily carbohydrate intake. It's the third-largest source of food carbohydrates in the tropics, after rice and maize.

While it can withstand the withering heat and drought-like conditions of the region, cassava is susceptible to several viral infections that damage its tubers, making them inedible. The Biosciences Eastern and Central Africa (BecA) Hub is managed by the International Livestock Research Institute (ILRI) and possesses world-class research facilities where genomics tools, such as the Illumina MiSeq® sequencing system, are used to understand and combat these diseases.

BecA-ILRI Hub Supports Genomics Research and Innovation

"The BecA-ILRI Hub[1] is ten years old," said Appolinaire Djikeng, Ph.D., Director of the BecA-ILRI Hub. "We've refurbished and upgraded our laboratory infrastructure, established a world-class research program and revolutionary capacity-building activities, and now want to drive research innovation to support agricultural development in Africa."

All of the BecA-ILRI Hub's projects are in collaboration with national agricultural research institutions and universities in Africa. "The nature of that collaboration helps us to have a conduit for transferring the knowledge and data back to people who can use it," Dr. Djikeng said. "We created the Africa Bioscience Challenge Fund to identify

Appolinaire Djikeng, Ph.D., is Director of the BecA-ILRI Hub which is headquartered in Nairobi, Kenya.

Cassava is harvested not only for its roots, which resemble sweet potatoes, but also for its leaves, trunk, and branches.

scientists from universities and research institutions who are in need of integrating one aspect of the technology into their research programs. We host them at the BecA-ILRI Hub up to 9 months, during which they can learn genomic techniques and apply them to current projects."

Sequencing Ellucidates Cassava Virus Spread

High-throughput sequencing has enabled the BecA-ILRI Hub to better integrate genomics and support projects in the region. "We now offer a subset of genomic strategies, mainly SNP-based genotyping and sequencing," Dr. Djikeng said.

Receiving the Greater Good Initiative award provided support for Dr. Djikeng and his team to investigate the causes and transmission of cassava mosaic begomoviruses, the causal agents of cassava mosaic disease (CMD), and cassava brown streak viruses that cause cassava brown streak disease (CBSD). These diseases are transmitted by the white fly (*Bemisia tabaci*), which is responsible for their spread from plant to plant and field to field in Tanzania (the country of origin) and other parts of Africa.

"Statistics from 2005 indicate that CMD alone has spread to nine countries in eastern and central Africa, covering a region of about 2.6 million square kilometers," said Dr. Djikeng. "It's caused an estimated 47% loss in cassava production. Cassava isn't widely exported, so lower production rates negatively impact local populations that depend upon it as a food source."

Greater Good Award Supports Multiple Genomics Projects

According to Dr. Djikeng, the Greater Good Initiative award is funding three projects. "The first is in support of Dr. Joseph Ndunguru [Mikocheni Agricultural Research Institute (MARI)[2]] and focuses on disease diversity and using deep sequencing to assess viral diversity," Dr. Djikeng said. "The second project supports Dr. Morag Ferguson's research [International Institute for Tropical Agriculture (IITA)[3] and BecA-ILRI Hub] to resequence the genomes of different cassava varieties, looking for genome differences, and associating markers with phenotypic characteristics. Some of those phenotypic characteristics are for resistance or susceptibility to CMD and CBSD."

"We're in the early stages of a third project to interrogate cassava viruses in circulation in different agro-ecological zones," Dr. Djikeng added. "We're looking primarily at mixed crop systems. We want to see if there is any indication of CMD or CBSD host tropism—a mechanism that enables viruses to adapt and establish either an infection or the ability to live in a different host, causing the disease to spread even further."

The BecA-ILRI Hub team is also using the MiSeq system to look at the transcriptomes, as well as the microbial populations within these crops. "The MiSeq is a simple system to use and the running cost is low," said Dr. Djikeng. "It's the type of technology we need in this region to perform genomic analysis."

According to Dr. Djikeng, his team is also fortunate to be collaborating with Dow AgroBiosciences, and have access to their expertise and an Illumina HiSeq® system. "We're dividing the work between the two facilities, with any high-throughput sequencing jobs being performed at Dow AgroBiosciences," Dr. Djikeng said. "We hope to complete most of the sequencing by the end of this year, with analysis and data integration to follow."

References

1. http://hub.africabiosciences.org/
2. http://www.ari-mikocheni.org/home/mari-information/staff-profiles/
3. http://www.iita.org/

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