

# Fighting Hunger in Africa with Geneious Prime

## The Cassava Virus Action Project

Cassava is a plant with starchy roots and protein-rich leaves that feeds nearly a billion people worldwide. In sub-Saharan Africa, 500 million people rely on cassava for their daily calories, and smallholder farmers grow cassava to feed their families and to sell at market for income.

This nutrient rich crop is under attack by pesticide-resistant whiteflies. Whiteflies destroy the leaves of cassava and transmit viruses to the plants, causing cassava brown streak disease and cassava mosaic disease which kill the plants.

When plants are infected with these viruses, an entire growing season can give no crop, devastating smallholder farmers and leading to more hunger and food insecurity.



**CASSAVA VIRUS  
ACTION PROJECT**

Farmers in Mbinga, Tanzania.

**"If there's no cassava, there's  
no food or income for millions  
of people."**

— Dr. Laura Boykin  
Computational Biologist and TED Fellow



“If the farmer knew what variety of cassava to plant in her fields that was resistant to these viruses and pathogens, they would have more food.”

— Dr. Laura Boykin  
Computational Biologist and TED Fellow



## The solution: understanding the virus at a genomic level

To fight these viruses and improve crop yields, farmers must learn more about the virus that is infecting their crop. Farmers can send off samples of their cassava plants and the whiteflies colonizing the plants for DNA sequencing. This information allows farmers to understand which virus is destroying their crop and make an informed choice regarding which cassava variant to replace their crop with.

However, DNA sequencing requires expensive equipment, and that equipment can only run if there is reliable power and internet. All of these things are in short supply in sub-Saharan Africa.

It can take 3-6 months for a farmer to get the sequencing results of their infected cassava crop. By the time the results are received, the growing season is almost over and there's no opportunity to start over with a new variant of cassava and salvage some of the crop for that year. In addition, if their crop is infected, the virus has had more time to spread, which can be devastating for eastern African societies during the hunger season.

## The Cassava Virus Action Project: A local solution for ending hunger

The Cassava Virus Action Project (CVAP) is a network of researchers, farmers and others that is working to develop local solutions for smallholder cassava farms.

CVAP is using portable genomics, like the Oxford Nanopore MinION and MinIT mobile sequencing devices to sequence the DNA of the infected cassava and the whiteflies in the field. Portable, external power sources can be used to run this equipment, so everything needed to obtain DNA sequencing results is brought directly to the farm.

The African cassava whitefly feeds on the underside of cassava leaves. The viruses that these whiteflies transmit destroy cassava plants and render their roots inedible.

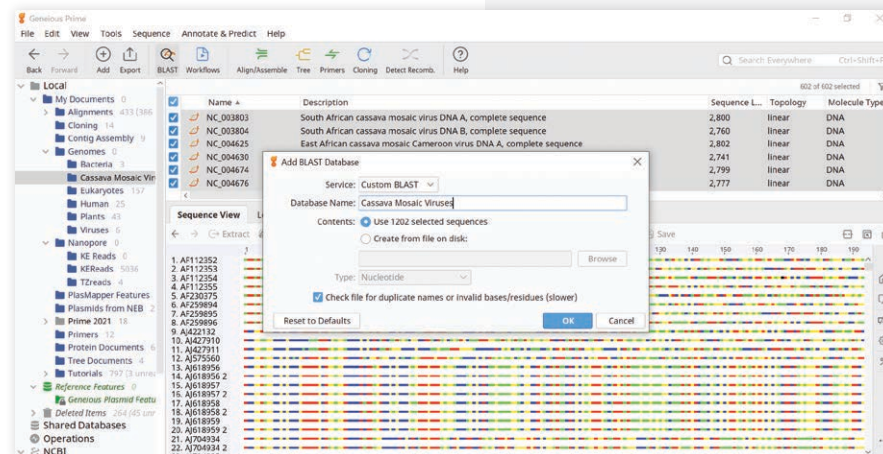
“I want to use the latest technology with the most diverse and inclusive teams on the planet to help farmers have more food.”

— Dr. Laura Boykin  
Computational Biologist and TED Fellow



Tree lab in Kenya.

## **Geneious Prime: portable, flexible, and fast analysis solutions for DNA sequencing data**



Create a local BLAST database within Geneious Prime.

Once the DNA sequence is obtained, the data must be analyzed to determine what virus is affecting the plant. Typically, this would require internet access to perform a BLAST search against various online databases at NCBI, and would be impossible to complete on a farm in sub-Saharan Africa.

Dr. Laura Boykin calls Geneious Prime a “game changer” in creating usable and visual sequencing results for CVAP.

Known cassava begomovirus whole genomes were downloaded from GenBank and used to create a customized, local database within Geneious Prime.

Geneious Prime’s user-friendly and flexible interface allows CVAP to also import Fastq files from the Nanopore sequencing results. Then, a local BLAST is performed on each sequence against the customized database of known cassava begomovirus whole genomes.

Geneious Prime’s custom multi-threaded BLAST implementation allows for offline searching of local databases. This ensures that the process CVAP is developing can be completed from start to finish in the field, even without access to reliable internet or a continuous power source.

The easy-to-read display of results in Geneious Prime gives the CVAP researchers and farmers a quick answer on which virus is infecting their crop.

Hit Table	Query Contig	Annotations	Distances	Info
Bit-Score	E-Value	% Identity	Hit start	Hit end
819.853	0	97.8%	2,053	2,547
819.853	0	97.8%	2,053	2,547
819.853	0	97.8%	2,053	2,547
819.853	0	97.8%	2,053	2,547
818.951	0	97.8%	2,053	2,545
818.951	0	97.8%	2,053	2,545
818.049	0	97.8%	2,053	2,545

Easy to read BLAST results from sequence reads.

**“I was able to create customized databases and we were able to give the farmers results in 3 hours vs. 6 months.”**

— Dr. Laura Boykin  
Computational Biologist and TED Fellow



"I want to do science that matters  
for people that matter."

— Dr. Laura Boykin  
Computational Biologist and TED Fellow



## Beyond CVAP: The impact of portable genomics

The Cassava Virus Action Project has shown that portable genomics is possible. Even on a remote farm in sub-Saharan Africa, the complete process of DNA sequencing, from extraction through analysis, can be performed on a blanket in the field.

In addition to saving cassava crops and preventing hunger for millions of Africans, CVAP has demonstrated what is possible with portable genomics. The process and technology that has been developed can be applied to any crop disease outbreak or pandemic in East Africa, or around the world.

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leading bioinformatics platform and start  
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