



## Conclusions

- Cassava is a major staple food crop worldwide.
- The high cyanogenic glucosides content in some cassava varieties prevents herbivory but can be toxic for human consumption.
- Associated loci explained 30 and 7% variance.
- Identification of an intracellular transporter gene and its allelic variation allow to point out cultivars with up to 30 percent decrease in cassava root cyanogenic glucosides content.

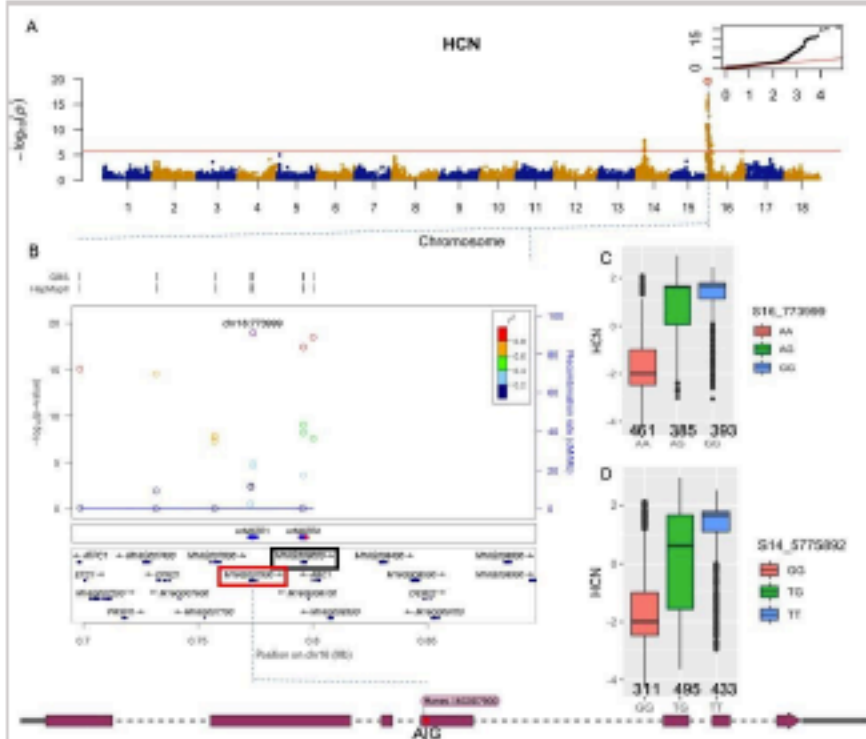


Fig. 1 GWAS of HCN for Brazilian germplasm.

A. Manhattan plot from a mixed linear model.

B. Shows the HCN associated region (lower figure: gene model).

C-D. Boxplot showing candidate SNP effect for HCN. The red and black rectangle indicate Manes.16G007900 and Manes.16G008000 gene [Pearson correlation of 0.96 ( $r^2$ )].

## Introduction

- Cassava has developed defense mechanisms against herbivores and pathogens, including the biosynthesis of cyanogenic glucosides (CG) (Tattersall 2001).
- However, one of the major challenge in cassava is high content of CG (Jørgensen et al. 2005).
- CG is a major component of root quality.
- Incomplete processing could result in acute to chronic exposure to cyanide (Leavesley et al. 2008).
- cassavabase.org is an open source global data repository.

## Our aim

- To understand the genetic architecture of CG trait.
- Map gene(s) associated to CG variation in cassava root.
- Develop fast and cost effective molecular diagnostic toolkit for breeding purposes.

## Our strategy

- Independent and combined GWAS was carried out on South American and African germplasm.
- We genotyped 3,354 landraces and modern breeding lines from Brazil using GBS and 1,389 individuals were phenotypically characterized across multi-year trials.
- Heritability and epistasis interactions were modelled.

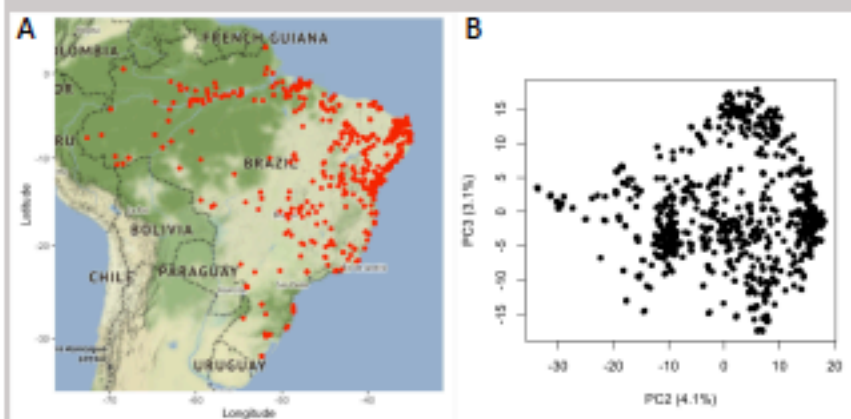


Fig. 2 (A) Accessions geographic locations and (B) principal component analysis (PCA). The red dot shows the specific site in Brazil where the accession was sampled.

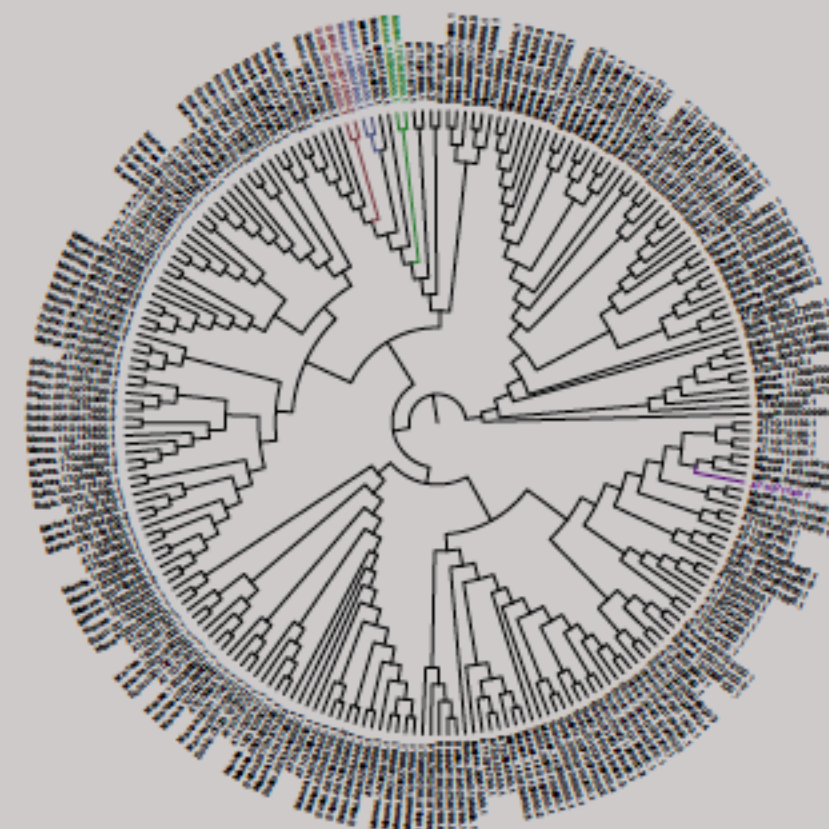


Fig. 3 Protein Alignment and comparative phylogeny show a close sequence homology between the GWAS candidate gene and SbMATE2 (Sobic.001G012600), a characterized vacuolar membrane MATE transporter in Sorghum, functions in the accumulation of plant specialized metabolites such as flavonoids and alkaloids.

## On-going

- Functional characterization of the putative CG transporters in cassava root are on-going.
- For details, scan barcode for link to article.



Alex Ogonna is a PhD student at Cornell University working in the lab of Dr. Lukas Mueller. His current research is focused on the impact of modern breeding on key traits architecture evolution through domestication and its implication for cassava breeding approach.

