



DATA NOTE

Datasets on the variations of minerals in biofortified cassava (*Manihot esculenta Crantz*) as a function of storage root portion, maturity and environment [version 1; peer review: 2 approved]

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Abstract

Background: The accurate measurements of the mineral content of cassava roots are vital from a nutritional perspective. The research datasets were from the study assessing the influence of storage root portion, maturity, and environment on the variations of minerals in biofortified cassava roots.

Methods: Twenty-five biofortified clones with three varieties as checks were harvested 12 months after planting from five different environments. Also, a different thirty-nine (39) biofortified cassava clones from the unlimited yield trials (UYTs) that included five (5) white-fleshed varieties (as control) were harvested at the age of 9 and 12 months after planting. In addition, two different methods of sample preparations were employed, using a cork borer and without a cork borer. The samples' elemental (minerals) analysis was determined using a standard laboratory method.



Results and conclusion: The breeders could use the data in their biofortification cassava programs to know the distribution of minerals in the roots and identify the best promising pipelines. Also, the data could be used by food scientists and nutritionists to understand the parts of the roots with optimum minerals to design their processing protocols and to know those genotypes specific to different environments that could be used for various nutrition intervention programs.



Keywords

minerals, biofortified cassava roots, clones, environment, sample preparation method, maturity

Open Peer Review

Approval Status  

	1	2
version 1		
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2. **Peng Zhang** , Chinese Academy of Sciences, Shanghai, China

Any reports and responses or comments on the article can be found at the end of the article.



This article is included in the **Plant Science** gateway.

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Introduction

Biofortified cassava roots with yellow flesh colour could be a good source of essential minerals and micronutrients and potential functional food. The different values of minerals composition of cassava roots found in the literature have shown many discrepancies beyond those caused by genetic and environmental factors. However, this could be due to inaccurate laboratory measurements, especially errors due to the sample preparation method employed during the analysis. The documented data could help the analysts and processors choose the best sample preparation method to evaluate the mineral compositions of cassava roots. The accurate measurements of the mineral content of cassava roots are vital from a nutritional perspective, especially during the selection stages of the breeding program and for providing quality information on the mineral intake in sub-Saharan Africa. However, there is a shortage of data on the spatial distribution of biofortified cassava storage roots' mineral contents. The datasets presented the spatial distribution of minerals in biofortified cassava root genotypes and established the sampling method's effect and harvesting time on their mineral content.

The datasets provide information on the effect of clone and environment on the minerals in biofortified cassava root. Furthermore, they establish which of the two factors strongly influences the mineral contents. In addition, they provide information on the essential minerals in biofortified cassava roots and show any association between the mineral properties assessed. The information the datasets reveals is the distribution of the minerals and their concentrations within the cassava tuber (head, middle, and tail root portions) would primarily benefit cassava breeders, food scientists and nutritionists. Also, the datasets on the effect of clones and environment could help the cassava breeders and processors identify what cassava variety is suitable for growth in all the environments and contains optimum minerals.

Breeders could use the data in their biofortification cassava programs to investigate the distribution of minerals in the roots and identify the best promising pipelines. The data could also be used by food scientists, nutritionists, and processors to understand the parts of the roots with optimum minerals and understand those genotypes specific to different environments used for various nutrition intervention programs. The data could also contribute to Nigeria's food composition databases.

Materials and methods

Source of genetic materials

The genetic materials used to generate the presented datasets were from two trials. The first one comprised of the 39 biofortified cassava genotypes from the unlimited yield trial (UYT) stage of the breeding program and 5 white-fleshed varieties (as checks), totalling 44 genotypes. They were grown in two sets at the research farm of IITA, Ibadan, Nigeria. Set one had 22 biofortified genotypes with white roots varieties as checks, totalling 25 genotypes, while set two had 17 biofortified genotypes with two varieties with white roots as control (totalling 19 genotypes). The source (parent lines with different quality traits) used for the breeding crosses that could dictate the mineral properties of the genotypes was the main difference between the two sets.¹ The second one was a multi-environment field trial. It had 25 biofortified cassava genotypes and three varieties with white roots grown in five environments. The five growth locations were from six different agro-ecological zones of Nigeria, namely Ibadan, Ubiaja, Onne, Mokwa and Zaria. The latitude and longitude for the collected samples/data are as follows: Ibadan 7° 38' N, 3° 89' E; Onne 4° 41' N, 7° 09' E; Ubiaja 6° 65' N, 6° 38' E; Mokwa 9° 28' N, 5° 05' E; Zaria 11° 16' N, 7° 63' E.² The cassava clones in these trials were planted during the rainy season of July 2005 and 2006 and were grown without fertilizers or herbicides under rainfed conditions. The harvesting of the storage roots was done in April 2006 (9 months) and July 2006 (12 months) after planting (MAP), respectively, where the two middle rows were harvested per plot. Three plants per genotype were harvested and pooled. Six cassava roots of different sizes (two each of the large, medium, and small) were randomly selected and placed in a labelled polythene bag from the pooled roots per genotype. The sample bags were transferred to the laboratory and processed within 24 hours of harvest.

Preparation of cassava roots for analysis

Sampling Method 1

The method described by Maziya-Dixon *et al.*³ was employed for the first sample preparation method. The three non-damaged storage roots of different sizes of 900–2300 g (large), 500 to 899 g (medium), and 200 to 499 g (small) were selected at the laboratory level. The roots were washed thoroughly with potable water to remove dirt and sand particles and air-dried on a clean concrete floor for about 5–10 min under atmospheric conditions. After that, the cleaned roots were peeled using a stainless-steel knife and further washed with deionized water to ensure the samples were free of soil contaminants. Next, the peeled and cleaned storage roots were bored through using a cork borer, size 8. The bored depth ranged from 4.6 to 9.7 cm for the head, 3.8 to 7.1 cm for the middle and 3.6 to 6.4 cm for the tail parts of the roots, and each portion was pooled and homogenized.³ The procedures were repeated for each genotype.

Sampling Method 2

The second sample preparation method also followed the protocol described by Maziya-Dixon *et al.*³ It involved selecting a new set of the three non-damaged storage roots of different sizes (large, medium, and small) cleaned using potable water and air-dried on a clean concrete floor as indicated for Method 1. The storage roots were peeled manually using a stainless-steel knife and rinsed with deionized water. The peeled, cleaned roots were cut longitudinal into four equal parts from the proximal to distal ends. For each root, the two opposite sections were taken, chopped into small pieces, and mixed thoroughly before subsampling. The procedures were repeated for each genotype.

Determination of macro- and microelement content

The samples for mineral analysis were carefully sub-sampled from the batch samples from the two described sample preparation methods. After sub-sampling, the samples were placed in an already cleaned petri dish using deionized water and dried in an uncorroded conventional oven (Memmert UN 55, GmbH) at 40°C for three days. The dried samples were transferred into well-labelled mineral-free paper envelopes for analysis. The mineral contents were analyzed according to the validated method using inductively coupled optical emission spectrometry (ICP-OES).^{1,2,4} Specifically, a radial view Spectro Ciros CCD ICP-OES (Spectro Analytical Instruments, Kleve, Germany) model was used. Each of the dried samples were weighed (0.03 g) into 1 mg into 50 ml screw-cap polypropylene tubes, and initiation of sample digestion was achieved using 2 ml of HNO₃ and 0.5 ml of H₂O₂. The digestion was completed at 125°C for 120 min using 72-position DigiPrep digestion blocks (SCP Scientific, Baie D'Urf e, Quebec, Canada). An 18 MΩ.cm of water was used to make the final volume of 25 ml of the sample. The digested sample was injected at the flow rate was 2.0 ml/min, and the total analysis time per sample was approximately 2.5 min. The calibration curves for all elements were constructed using the mixtures of high-purity single-element standard solutions in a 4% (v/v) HNO₃ matrix. The software algorithms were used for the background correction of all wavelengths and spectral interferences, as described by Wheal *et al.*⁴

Dataset description and validation

The samples from the two trials (44 + 28 biofortified clones and check varieties) were run in duplicate at the laboratory level. However, for quality data collection, there was an analysis of a mixture of all elements in 4% HNO₃ (drift correction solution) at every 25 samples. It helped to account for within-run variation in the flows. Furthermore, the blank subtraction, drift correction, and mass and volume adjustments were made offline. The study used six different reference materials (RMs) for the data quality establishment purchased from the US National Institute of Standards and Technology (NIST, Gaithersburg, MD, USA).⁴ The macro elements of focus in the data include calcium (Ca), magnesium (Mg), sodium (Na), potassium (K), phosphorus (P), and sulphur (S). At the same time, the microelements were Iron (Fe), Manganese (Mn), Boron (B), Copper (Cu), Molybdenum (Mo), Cobalt (Co), Nickel (Ni), Zinc (Zn) and Aluminium (Al), respectively. They were measured on an mg/kg dry weight basis. The storage portions included the proximal (A), middle (B), distal (C), the average ABC (AV) and longitudinal (L).

Data availability

Underlying data

Dryad: Quantitative Assessment of Trace and Macro Element Compositions of Cassava (*Manihot esculenta*) Storage Roots Enriched with B-Carotene as Influenced by Genotypes and Growing Locations,

<https://doi.org/10.5061/dryad.k3j9kd59r>.⁵

This project contains the following underlying data:

- Data_on_the_Variations_of_Macro_and_Microelements_as_influenced_by_sampling_method.xlsx
- Data_on_Trace_and_Macro_Element_in_cassava_roots_as_influenced_by_Genotype_and_environment.csv
- README.csv

Data are available under the terms of the [Creative Commons Zero “No rights reserved” data waiver](#) (CC0 1.0 Public domain dedication).

Acknowledgments

We acknowledged the CGIAR Research Program on Roots, Tubers and Bananas (RTB) and HarvestPlus for their support. Also, the support of the entire staff of Food and Nutrition Sciences Laboratory, IITA, Ibadan, Nigeria, and Cassava Breeding Unit, IITA, Ibadan, Nigeria, especially Drs Kulakow Peter and Parkes Elizabeth, was acknowledged. All authors have read and approved the manuscript and are aware of its submission.

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[Publisher Full Text](#)
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Peng Zhang 

Chinese Academy of Sciences, Shanghai, China

The manuscript reported the building of datasets on the variation of minerals from twenty-five biofortified cassava clones with cassava growth status and environment. Basically, the work is very meaningful and important for guiding cassava breeders and producers for cassava field management. The methods used are suitable and sufficient for the detection of the difference among the parameters. If the authors could provided the data related to the soil nutrient status, including macro and micro-nutrients, it would be more significant.

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Cassava genetic improvement and molecular breeding.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 06 April 2023

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Treenut Saithong 

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This dataset presented the variation of mineral contents in cassava roots from different genetic varieties and cultivated conditions. The data collection is basic information that could benefit various researches on cassava yield and quality improvement, and also food processing industry. While the data is interesting, I recommended revising the following issues before indexing:

1. The current version of the manuscript contained various confusing sentences, especially in the Introduction,

e.g. "In addition, they provide information on the essential minerals in bio-fortified cassava roots and show any association between the mineral properties assessed. The information the datasets reveals is the distribution of the minerals and their concentrations within the cassava tuber (head, middle, and tail root portions) would primarily benefit cassava breeders, food scientists and nutritionists."

and the first part of Materials and Methods

e.g. "The source (parent lines with different quality traits) used for the breeding crosses that could dictate the mineral properties of the genotypes was the main difference between the two sets".

2. It would be useful for later research work, if the source of the size category specified in this study (i.e. "The three non-damaged storage roots of different sizes of 900–2300 g (large), 500 to 899 g (medium), and 200 to 499 g (small) were selected at the laboratory level.") is described.
3. The data set in Excel file was presented in a user-friendly style. However, I found that it might increase the usefulness of the data if the author could also add information on genotype background of trait characteristics. Also, all measured number of mineral content should present with a clear unit.

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Partly

Competing Interests: No competing interests were disclosed.**Reviewer Expertise:** Plant metabolism, systems biology, plant computational modeling**I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

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