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BSc in Horticulture

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## Home country

Ethiopia

## Supervisor:

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## Professional experience:

Expert of vegetables and fruits crop production in Oromia Irrigation Development Authority

## Scientific Publication:

2 published articles.

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## Crop of interest

Amaranth (*Amaranthus cruentus* L.) tolerates marginal cropping conditions and has the potential to alleviate malnutrition and address food insecurity. Both leaves and seeds are valued. The seeds can be used in numerous recipes ranging from popped amaranth snack, porridge, bread, creamy soup, pancakes, cakes, scones and pizza. Seeds contains nutritional compounds including crude protein 13.1 to 21.0% of which 90% is highly digestible, 5.6 to 10.9% of crude fat and 76 % of unsaturated fatty acids, 48 to 69% of starch mostly amilo-pectin (93.6 – 95.2%), 3.1 to 5.0% of dietary fiber and 2.5 to 4.4% of ash.



### **Summary of proposal:**

Amaranth (*Amaranthus cruentus* L.) originated in South America. It tolerates harsh environments, is fast-growing and early maturing. It is used for a dual purpose: both leaves and seeds are nutritious. Despite the wide distribution of amaranth in Africa, it remains a largely underutilized crop for both vegetable and grain purposes. In Africa and especially in Nigeria, there is little or no information on the extent of genetic variability present in amaranth germplasm collections to select superior genotypes for desirable traits. The objective of this research is therefore to determine the genetic variability and character association among amaranth (*Amaranthus cruentus* L.) genotypes for

yield components. The research will be carried out at Ebonyi State University in Nigeria and materials will be taken from IITA. The experiment will be laid out in 6x6 Simple Lattice Design with two replications. Data will be collected on Phenological, yield and yield component parameters and subjected to analysis of variance (ANOVA) using General Linear Model (GLM) procedure of SAS statistical software (9.3). Genotypic and phenotypic coefficient of variation and correlation, estimate of broad sense heritability ( $H^2$ ), estimate of expected genetic advance, path coefficient analysis, and cluster and genetic divergence will be analyzed.