

# Spatial Multivariate Cluster Analysis for Defining Target Population of Environments in West Africa for Yam Breeding

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## ABSTRACT

Yam (*Dioscorea* spp.) is a major staple crop with high agricultural and cultural significance for over 300 million people in West Africa. Despite its importance, productivity is miserably low. A better understanding of the environmental context in the region is essential to unlock the crop's potential for food security and wealth creation. The article aims to characterize the production environments into homologous mega-environments, having operational significance for breeding research. Principal component analysis (PCA) was performed separately on environmental data related to climate, soil, topography, and vegetation. Significant PCA layers were used in spatial multivariate cluster analysis. Seven clusters were identified for West Africa; four were country-specific; the rest were region-wide in extent. Clustering results are valuable inputs to optimize yam varietal selection and testing within and across the countries in West Africa. The impact of breeding research on poverty reduction and problems of market accessibility in yam production zones were highlighted.

## KEYWORDS

*Dioscorea* SPP., Environmental Clusters, Mega-Environment, Target Set of Environment, Targeting, Varietal Testing, Yam Belt

## INTRODUCTION

The population of West Africa is among those in the world that are increasing most quickly and is projected to be over 500 million in 2030 (ECOWAS-SWAC/OECD, 2007). The predicted rise in the regional human population poses risks and challenges to food security. Yam (*Dioscorea* spp.) is one of the strategic crops for sustainable food production and supply in Africa and beyond as it possesses the potential to produce more food per unit of land and water than some other crops. It is a preferred staple food for over 300 million people in West Africa. It provides nutritional benefits in the form of starch, protein, vitamins, and micro-nutrients meeting the dietary demands of people in

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the region (Asiedu and Sartie, 2010). The crop features prominently in the social-cultural activities of the people in the region (Obidiegwu and Akpabio, 2017). Yam production in Africa, though 40% of the total for cassava, has a value which exceeds all other African staple crops and is equivalent to the total value of the top three cereal crops, maize, rice, and sorghum (FAO, 2014). Despite its high value, yam productivity in West Africa is miserably low and has remained stagnant over decades. The achieved tuber yield of less than 10 t/ha under current production practices is around 20% of its potential yield of 50 t/ha (FAO, 2014) and is further constrained by losses of about 30% in storage (Mignouna et al., 2014). The low productivity is attributed to a combination of biotic and abiotic factors mostly associated with the shortened fallow under current extensive cultivation practices.

International Institute of Tropical Agriculture (IITA) and its partners in West African countries have been implementing several research and development initiatives to unlock the potential of the yam crop for sustainable food security and wealth creation. Genetic improvement is among those initiatives that aim at translating current advances in genetics and plant breeding sciences into more resilient, productive, and end-user preferred varieties for West Africa. The genetic improvement focuses on two major yam species, white yam (*Dioscorea rotundata*) and water yam (*D. alata*). The yam genetic improvement effort in the region seeks to build the capacity for breeding to accelerate genetic gain and lead to a strong pipeline of products to meet the needs of farmers and the markets.

Better understanding of target environments is essential for a yam breeding effort that is committed to developing and identifying improved genotypes that are in some way superior with reference to plant production purposes in the region. The target environments composed of a set of farms and seasons are often highly variable and the cause of differential phenotypic expressions of plants in a crop under cultivation (Hyman et al., 2013). The connection of phenotypic expression of a crop plant (value) which depends on environment (effect) often referred as genotype  $\times$  environment interaction (GEI), is one of the major factors limiting the efficiency of plant breeding programs as it influences the nature, magnitude, and predictability of the selection response (Cooper, 1999; Ceccarelli and Grando, 2007). Although GEI poses a big challenge to breeding program efficiency it cannot be ignored but could instead be exploited. Characterizing and defining target sets of environments (TSE) for breeding and cultivar recommendation are among the strategies to exploit the space and time dimension of GEI. Environment profiling helps to strategically locate the experimental or selection sites with a greater power in predicting the breeding trials' performance in the TSE in a period extending into the future.

Several studies have shown the utility of agricultural zoning for research and development based on environmental or biophysical variables. Costantini et al., (2016) applied the approach of multivariate clustering for the study of environmental drivers for delineating wine growing zones in Italy. Garcia et al., (2014) used a combination of climate, soil, and terrain data to identify coffee growing zones with high potential in Colombia. Similarly, Muthoni et al., (2017) employed the method of cluster analysis to delineate sustainable recommendation domains for scaling maize technologies in Tanzania. Furthermore, other studies have delineated geographic space by climate and soil classification schemes as a basis for extrapolating and applying agricultural information and research to a broader spatial scale (Wood and Pardey, 1998; Padbury et al., 2002; van Waart et al., 2013). Such environmental clustering schemes have been used to detect yield variability and limiting factors for crop growth (Caldiz et al., 2002; Williams et al., 2008), to regionalize optimal crop management recommendations (Seppelt, 2000), to determine suitable locations for new crop production technologies (Geerts et al., 2006; Araya et al., 2010), and to analyze impacts of climate change on agriculture (Fischer et al., 2005).

Generally, the two approaches of matrix and cluster methodologies have been used in environmental classification studies. In a matrix classification system each variable used to delineate zones is divided into classes or class-ranges. Class cutoff values for each variable can be based on expert-opinion or frequency distributions of the variable's range of values. Zones are then formed by the matrix cells of intersecting classes (van Waart et al., 2013). This approach involves some expert

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