

# Characterization of *Vigna vexillata* (L.) Richard from Six African Countries

Jacob O. Popoola<sup>1</sup>, Bukola R. Aremu<sup>2</sup>, Fisayo Y. Daramola<sup>1</sup>, Alaba A. Adebambo<sup>3</sup> and Adegoke E. Adegbite<sup>3</sup>

<sup>1</sup>Department of Biological Sciences, School of Natural and Applied Sciences, College of Science and Technology, Covenant University, P.M.B. 1023, Canaanland Ota, Ogun State, Nigeria.

<sup>2</sup>Department of Biological Sciences, Fast North West University, Mafikeng Private Bag X2046, Mafikeng 2735, South Africa.

<sup>3</sup>Department of Biological Sciences, Ondo State University of Science and Technology, Okitipupa, Ondo State, Nigeria.

jacob.popoola@covenantuniversity.edu.ng

*Vigna vexillata* (L.) Richard is a wild relative of cowpea characterized by heavy pubescence of the leaves, stems and pods which could be utilized for genetic improvement of cowpea *V. unguiculata* (L.) Walp. Twenty-six (26) accessions collected from six African countries; Cameroun, Zaire, Ghana, Swaziland, Congo and Nigeria were obtained from International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria for morphological and cytological characterizations. Twenty-four morphological characters involving eighteen quantitative and six qualitative characters were used for intra-specific variabilities among the accessions. Young bud flowers were collected at the flowering stage for meiotic and mitotic chromosome behaviour of the accessions. The results showed significant differences among vegetative and floral characters ( $p \leq 0.000$ ) while pod and seed characters do not show much variability. The high significant correlation among characters such as calyx lobe length, standard petal length and width, peduncle length, days to 50% flowering, days to pod maturity, pod length and width, number of locules per pod, number of seeds per pod, and 100-seed weight indicates their suitability for breeding and genetic improvement purposes. The cluster analysis using the UPGMA method segregated the 26 accessions into three main clusters; cluster I (super group of 16 accessions), cluster II (9 accessions) and cluster III (1 isolated accession). All the accessions analysed for cytological relationship presented  $2n = 22$  chromosomes as previously reported for the genus *Vigna*. Chromosomes paired as bivalents and regular.