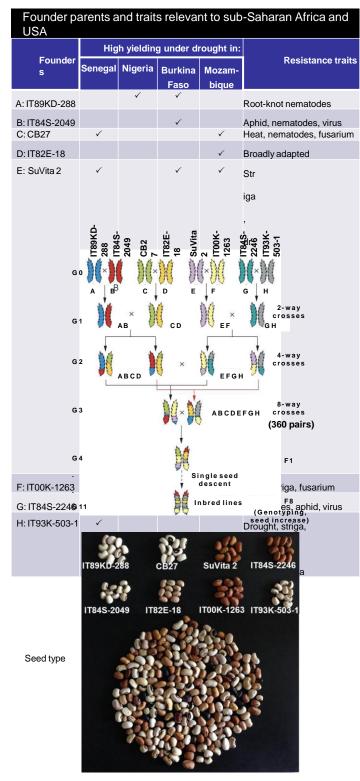
## A multi-parent advanced generation inter-cross (MAGIC) population for genetic analysis and improvement of cowpea (*Vigna unguiculata* L. Walp.)

Bao-Lam Huynh, Jeffrey D. Ehlers\*, Timothy J. Close, and Philip A. Roberts

University of California, Riverside, CA 92521; \*Current address: The Bill and Melinda Gates Foundation, Seattle, WA 98102



Cowpea (Vigna unguiculata L. Walp.) is an important proteinrich grain legume and fodder crop grown across the semiarid zones of the tropics below the Saharan desert and in similar agro-ecological zones of eastern and southern Africa and globally. Although cowpea is more tolerant of harsh environments than most other crops, pests, diseases, parasitic weeds, drought, heat and poor soil conditions render heavy yield losses in traditional cultivars. As part of projects funded by the Generation Challenge Programme of the Consultative Group for International Agricultural Research and the USAID Feed the Future Innovation Labs, developed a Multi-parent Advanced Generation we Inter-Cross (MAGIC) population for cowpea. The 8 founder parents are highly diverse and carry many abiotic and biotic stress resistance, seed quality and agronomic traits relevant to cowpea improvement in sub-Saharan Africa and the USA. Due to its broad genetic base, the cowpea MAGIC population promises breakthroughs in trait discovery and genetic gain.

**Morphological Variation** 



**Availability:** Seeds of the MAGIC core set including 305  $F_{8:9}$  recombinant inbred lines (RILs) and 8 founder parents have been deposited at the IITA germplasm repository, Ibadan, Nigeria, for propagation followed by worldwide distribution on request. In addition, seeds of the RILs and parents

have been deposited at the USDA-ARS National Center for Genetic Resources Preservation, Fort Collins, CO. Original seed stocks for every generation of the MAGIC development including the  $F_8$  RILs and parents are conserved at the UCR cowpea gene bank. Information on population development, marker genotyping, genetic map positions, genome-wide recombination rate within the MAGIC, and association mapping for basic agronomy traits can be obtained from Huynh *et al.* (Plant J 93:1129-1142; J Plant Reg. 13:281-286).

Emails: BL Huynh (baolam.huynh@ucr.edu), JD Ehlers (jeff.ehlers@gatesfoundation.org), TJ Close (timothy.close@ucr.edu), and PA Roberts (philip.roberts@ucr.edu)