

**PERFORMANCE AND INHERITANCE PATTERNS OF STORAGE ROOT YIELD
TRAITS IN THE NEW KAWOGO X BEAUREGARD SWEETPOTATO CROSS IN
UGANDA**

ORIBA ALICE

BSc. Agriculture (Hon)

Reg No. 2014/HD02/730U

Student No. 214021307

**A THESIS SUBMITTED TO THE DIRECTORATE OF RESEARCH AND GRADUATE
TRAINING IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE
AWARD OF MASTER OF SCIENCE DEGREE IN PLANT BREEDING AND SEED
SYSTEMS OF MAKERERE UNIVERSITY**

MAY, 2017

ABSTRACT

Performance and inheritance pattern of storage root yield related traits in the ‘New Kawogo’ x ‘Beauregard’ is crucial in genetic sweetpotato improvement in this population. This study was conducted to i) evaluate the performance of progenies of ‘New Kawogo’ x ‘Beauregard’ for dry matter content (DMC), Sweetpotato virus disease (SPVD) resistance; storage root yield (SRY), storage root shapes (SRS), harvest index (HI) and ii) determine broad sense heritability and correlation of dry matter content (DMC), Sweetpotato virus disease (SPVD) resistance, storage root yield (SRY), storage root shapes (SRS) and harvest index (HI) in the ‘New Kawogo’ x ‘Beauregard’ sweetpotato cross. A total of 288 genotypes including 286 progenies plus the 2 parents were evaluated at two sites for two seasons.

The 288 genotypes were planted using an alpha lattice design with two replications per site. The trials were planted at Abi Zonal Agricultural Research and Development Institute and Bulindi Zonal Agricultural Research and Development Institute during the first and second seasons of 2015. At harvest, data were collected on DMC, SPVD resistance, SRY, SRS and HI. SRY in tons per hectare (t/ha) was determined as $SRY (t/ha) = [(Marketable\ root\ weight\ (MRW) + non-marketable\ root\ weight\ (NMRW) / Net\ plot\ area\ in\ m^2) \times 10]$. Approximately 100 g of fresh storage root samples of each clone were sliced and weighed (DMF) and then dried in paper bags in an oven at 65°C for 72 hours to a constant weight. The samples were immediately weighed after drying (DMD). Storage root dry matter content was calculated as $DM = [(DMW2 / DMW1) \times 100]$. The SPVD resistance and SRS were scored using field descriptors of 1-9 where 1-means no virus symptoms and 9 severely stunted plants and 1- round shape and 9 - long irregular or curved shape, respectively. The trait overall means for SRY and HI were 19.2 (t/ha) and 44.2 (%), respectively.

The overall genotype means for DMC was 33.1 (%). The trait overall means was 3.0 for SPVD resistance

and 4.4 for SRS. The broad sense heritability (H^2) estimates for DMC (H^2) was 0.1, SPVD resistance ($H^2=$ 0.3), SRY ($H^2=$ 0.3), HI= ($H^2=$ 0.1) and SRS ($H^2=$ 0.4) were observed. We observed a high positive ($p\leq$ 0.001) genetic correlation between SRY and SRS and positive but non-significant correlations between SPVD resistance and HI. However, DMC was negatively correlated with HI, SRY and SRS. This suggests that the traits cannot be improved in the same direction.