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Research Application Summary

Genetic effects of inbreeding on harvest index and root dry matter content in cassava

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Abstract

Inbreeding of predominantly cross-pollinating crops is expected to result in progeny with reduced fitness and or improved phenotypes. The effects of inbreeding in cassava are not well quantified. Accordingly, in this exploratory study, S_1 progeny from six cassava genotypes were examined for two agronomic traits harvest index (HI) and root dry matter content (DMC). With introduction of inbreeding, an average HI reduction of 36% was recorded when six non-inbred parents were compared to the S_1 progeny. Similarly, an average DMC reduction of 13.2% was observed with cassava inbreeding. Thus, with inbreeding, highest reduction was observed in HI as compared to DMC.

Key words: Inbreeding depression, *Manihot esculenta*, S_1 progenies

Résumé

L'endogamie des cultures principalement à pollinisation croisée est attendue pour avoir pour résultat la descendance avec la forme physique réduite et / ou des phénotypes améliorés. Les effets de l'endogamie dans le manioc ne sont pas bien quantifiées. Par conséquent, dans cette étude exploratoire, les descendances S1 de six génotypes de manioc ont été examinées pour l''indice de récolte (HI) de deux traits agronomiques et teneur en matière sèche (DMC) de la racine. Avec l'introduction de l'endogamie, une réduction moyenne de 36% de HI a été enregistrée alors que six parents non consanguins ont été comparés à la descendance S1. De même, une réduction moyenne de 13,2% de DMC a été observée avec la consanguinité du manioc. Ainsi, avec l'endogamie, la plus forte baisse a été observée dans l'indice de récolte HI par rapport à la teneur en matière sèche.

Mots clés: Dépression de consanguinité, *Manihot esculenta*, S_1 descendances

Background

Inbreeding, defined as the mating between individuals related by a shared ancestry, is a major component of most successful breeding programmes involved cultivar development. Once inbreeding occurs in cross-pollinated species, it can lead to varying levels of inbreeding depression (ID), loss in fitness, that has been observed in nearly all cross-pollinated species (Wricke and Weber, 1986), including cassava (*Manihot esculenta* Crantz) (Rojas *et al.*, 2009). This decline in fitness is well illustrated by experiments in maize that were conducted since the early 1900s (Begg, 1959). On the other hand, inbreeding also presents enormous benefits when strategically employed in cross-pollinating species like cassava.

Walsh (2005) observed that inbreeding provides an opportunity to exploit both additive and non-additive genetic effects. It is envisaged that inbreeding in cassava will provide several advantages including: 1) reduction of genetic load, that limits attainment of sustainable genetic progress, 2) increased probability of attaining useful recessive traits, and 3) facilitation of the implementation of mutation breeding (Ceballos *et al.*, 2004). These benefits were a major motivation for this study.

Research Approach

Six cassava genotypes (I92/00067, TMS 30572, 95/SE-00036, NASE 4, MH95/0469 and Bamunanika) were used as progenitors (S_0) to generate S_1 progeny. For each genotype 20 stem cuttings were planted in isolation plots at a spacing of 1 m x 0.9 m. For each selfed genotype, mature fruits were carefully harvested and left to shatter naturally. Harvested S_1 botanical seeds were not treated, but allowed a two month dormancy breakdown period before being established in nurseries. After two months in the nursery, S_1 seedlings were transplanted to a well-prepared field where they were grown until 10 months, after which they were cloned to generate at least 6-10 cuttings (middle section) per seedling.

Each S_1 seedling (genotype) was represented by six plants, which were established in the field for evaluation at National Crops Resources Research Institute (NaCRRI) in 2008. At harvest, which coincided with 11 months after planting, four innermost plants per clone were uprooted and used for phenotypic assessments. Harvest index (HI) was computed for each clone following the procedure outlined by Kawano (1990). Estimation of DMC in the root samples was based on the oven dry method that involves drying samples to constant weight at 72°C. Summary statistics (range, mean, variance and skewness) for

DMC and HI were computed for each family. Inbreeding depression (ID) was estimated for both HI and DMC as a percentage of the S_0 average. ID = [(s_0 mean – s_1 mean)/s_0 mean] x 100.

Research Application

Data on HI was highly variable between and within the families, with lowest (0.08) observed in progeny derived from the parental genotype Bamunanika and the highest (0.42) in progeny derived from the parental genotype MH95/0469 (Table 1). For HI, inbreeding depression varied among the different families ranging from 15.7-83.3%. Highest ID was observed in progeny derived from Bamunanika (83.3%). Only progeny derived from parental genotypes 95/SE-00036, NASE 4 and MH95/0469 showed ID of less than 20% (Table 1). Harvest index reflects the efficiency of dry matter distribution and thus higher HI values are desirable. With inbreeding an average reduction of 36% in HI was recorded. This indicated that on average S_1 progeny yielded only 64% of the non-inbreds. Inbreeding depression could therefore explain the low HI observed in the S_1 inbreds. However, some individual S_1 inbreds from parental genotypes MH95/0469, NASE 4, 95/SE-00036 and I92/00067 had higher HI values than their respective non-inbred parents suggesting that they did not succumb to ID and/or tolerated inbreeding and hence justifying the need to further inbreeding in cassava.

Table 1. Variation in harvest index in S_1 cassava progeny generated from six genotypes.

Family	Parent[a]	S_1 progeny[b]	Min[d]	Max[e]	Mean	Variance	Skewness	ID[f]
MH95/0469	0.52	16 (5)[c]	0.14	0.66	0.42	0.017	-0.57	19.23
NASE 4	0.48	16 (5)	0	0.62	0.39	0.024	-1.11	18.75
TMS 30572	0.57	23 (0)	0.07	0.5	0.28	0.009	0.03	50.87
I92/00067	0.48	18 (2)	0.15	0.57	0.34	0.014	0.33	29.16
Bamunanika	0.48	28 (0)	0	0.35	0.08	0.016	0.96	83.33
95/SE-00036	0.38	30 (1)	0	0.69	0.32	0.027	-0.49	15.78

[a]Parent represents harvest index values for respective non-inbreds; [b]S_1 progeny represents individuals evaluated; [c]numbers in parentheses indicate number of progeny with harvest index values > 0.5; [d]Min and [e]Max indicate minimum and maximum harvest index, respectively. [f]Inbreeding depression estimated as [(s_0 mean – s_1 mean)/ s_0 mean] x 100. The confidence interval associated with the data at 95% ranged from 0.042 to 0.082.

Root DMC varied both between and within the families, with the lowest (28.5%) recorded for progeny derived from parental genotype Bamunanika, and the highest (35.1%) recorded for progeny derived from TMS 30572 (Table 2). Inbreeding depression for DMC varied between 2-23.8%, with the highest (23.8%) observed in progeny from I92/00067. Higher root DMC is a major breeding objective of many breeding programmes.

Table 2. Variation in root dry matter content in S_1 cassava progeny generated from six parental genotypes.

Family	Parent[a]	S_1 progeny[b]	Min[d]	Max[e]	Mean	Variance	Skewness	ID[f]
MH95/0469	32	13 (4)[c]	24	38	31.3	20.2	0.2	2.1
NASE 4	35	8 (0)	26	33	30.1	5.26	-0.39	14
TMS 30572	41	22 (11)	20	43	35.1	32.9	-0.89	14.3
I92/00067	39	17 (2)	15	40	29.7	41	-0.96	23.8
Bamunanika	37	9 (1)	18	38	28.5	32.5	-0.23	22.9
95/SE-00036	34	27 (11)	11	42	33.3	42.8	-1.67	2

[a]Parent represents DMC values for respective non-inbreds; [b]S_1 progeny represents individuals evaluated; [c]numbers in parentheses indicate number of progeny with DMC > 35%; [d]Min and [e]Max indicate minimum and maximum DMC respectively. Inbreeding depression estimated as $[(s_0 \text{ mean} - s_1 \text{ mean})/s_0 \text{ mean}] \times 100$. The confidence interval associated with the data at 95% ranged from 1.918 to 4.383.

Average DMC in the six non-inbred cassava genotypes was 36.3%, while in S_1 progeny it was 31.3%. Hence, with introduction of inbreeding, an average reduction of 13.2% in DMC was observed, a finding that could point to ID as already indicated above for HI. However, some inbred lines within the families of I92/00067, TMS30572, 95/SE-00036, MH95/0469 and Bamunanika, had DMC values well above those of their respective non-inbred parents indicating that they did not succumb to ID and/or tolerated inbreeding hence justifying the need to further inbreeding in cassava.

Recommendation

This study presented the first Ugandan report on effects of inbreeding in cassava, information of which will be important for the general cassava breeding community. The obtained results provided general trends on the effect of inbreeding on DMC and HI. Inbreeding depression was evident in some of the inbreds as demonstrated by the relatively lower values for HI and DMC. In parallel, inbreeding resulted in the generation of some vigorous S_1 progeny (with high DMC and HI), which appeared to have benefited from either additive or non-additive genetic effects or a combination of the two. These finding justify the need to further inbreeding in cassava as a responsive measure towards attainment of specific breeding objectives.

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