Research Application Summary

Diallel analysis of root dry matter content in sweetpotato

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Abstract

There has been much emphasis on breeding for increased sweetpotato storage root yields, but less on the dry matter yield, and its inheritance. High dry matter content (DMC) is associated with consumer preferences, and is important for processing industry. This study was conducted to determine the type of gene action controlling DMC and to assess GxE interaction effect on DMC in sweetpotato. Five parental clones varying in DMC have been hand-crossed in a half-diallel design to generate 10 families. After scarification, seeds were raised in seedboxes in a screenhouse at Namulonge, Uganda. Ten genotypes of each family were planted in a trial at Namulonge (swamp and upland environments) and Serere in a randomized complete block design, with two replications, during October 2009 and March 2010. To assess DMC, 200g from each genotype was oven-dried at 65^{0}C up to constant weight. Data were analyzed using GenStat program. General combining ability (GCA) and specific combining ability (SCA) were computed according to model II, Method 4 as described by Griffing (1956). Highly significant differences were found among genotypes for DMC for all sites. However, significant differences between families were found only for Namulonge upland and swamp environments. Families didn't differ significantly in DMC for Serere site. The cross with the highest mean in DMC was NKA x KYA, while the genotype belongs to JEW x HUA. Understanding the type of gene action and the effect of G x E interaction should help guide breeding strategies for DMC in sweetpotato. The study is on-going and efforts are currently focused on understanding the gene action controlling DMC.

Key words: Sweetpotato, dry matter content, general combining ability, *Ipomoea batatas*

Résumé

Il y a eu beaucoup d'insistance sur l'élevage pour augmenter les rendements de tubercules de patate douce, mais moins sur le rendement en matière sèche, et son héritage. Le contenu de la haute teneur en matière sèche (DMC) est associé à des préférences des consommateurs, et est important pour l'industrie de transformation. Cette étude a été menée afin de déterminer le type d'action des gènes qui contrôle le DMC et d'évaluer l'effet d'interaction GXE sur le DMC dans la patate douce. Cinq clones parentaux variant DMC ont été croisés à la main dans un design demi-diallèle pour générer 10 familles. Après la scarification, les graines ont été soulevées dans la boite de semence dans une moustiquaire à Namulonge, en Ouganda. Dix génotypes de chaque famille ont été plantés en essai à Namulonge (dans les marais et les environnements de montagne) et Sérère en blocs aléatoires complets, avec deux répétitions, en Octobre 2009 et en Mars 2010. Pour évaluer DMC, 200g de chaque génotype a été séché au four à 65ºC jusqu'à poids constant. Les données ont été analysées à l'aide du programme GenStat. L'habileté générale à la combinaison (GCA) et spécifique à la combinaison (SCA) ont été calculés selon le modèle II, Méthode 4 tel que décrit par Griffing (1956). Des différences très significatives ont été observées entre les génotypes pour DMC dans tous les sites. Toutefois, des différences significatives entre les familles ont été trouvées seulement dans les environnements de montagne de Namulonge et de marécages. Les familles n'ont pas changé significativement dans le DMC pour le site Sérère. Le croisement avec la moyenne la plus élevée dans DMC a été NKA x KYA, tandis que le génotype x appartient à JUIF HUA. La compréhension de type d'action des gènes et l'effet de l'interaction G x E devraient contribuer à orienter les stratégies de sélection pour DMC dans la patate douce. L'étude est en cours et des efforts sont actuellement axés sur la compréhension de l'action de gène contrôlant la DMC.

Mots clés: Patate douce, la teneur en matière sèche, l'aptitude générale à la combinaison, *Ipomoea batatas*

Background

Sweetpotato *(Ipomoea batatas)* is an important world food crop ranking seventh in the world. In sub-Saharan Africa, it is the third most important crop with nearly 90% of the total output coming from Eastern and Southern Africa (Ewell and Mutuura, 1994). Uganda and Rwanda are the biggest sweetpotato producing countries in sub-Saharan Africa (1,861 and 773 thousand tons, repectively).

One of the most limiting factors to the deployment of high yielding, pest resistant varieties in the region is the low tuber dry matter. High dry matter is an important attribute of acceptable sweetpotato varieties with consumers preferring dry matter content above 25%. Besides, sweetpotato is becoming an important industrial crop, for which purpose it must have dry matter of about 35% (Tumwegamire *et al.*, 2004).

There has been much emphasis on breeding for increased sweetpotato storage root yields, but less on the dry matter yield. In particular, no studies have been conducted on the inheritance of dry matter content (DMC) of SP populations from which currently released SP varieties were selected in Uganda. A lower DMC has resulted in some released varieties being unpopular. Breeding for high DMC requires information on how this trait is inherited. For wide-scale deployment of varieties, it is also important to establish whether DMC in sweetpotato interacts with environment. This study was conducted to determine the type of gene action controlling DMC and to assess G x E interaction effect on DMC in sweetpotato.

Literature Summary

Most sweetpotato varieties have a dry matter (DM) content that is too low for industrial use and consumer preference. There has been less emphasis on heritability of dry matter yield in sweetpotato, yet this is the basis of selecting parents that have high likelihood of generating high dry matter progenies. Heritability estimates help to predict the performance of the offspring based on the performance of their parents using a particular combination of breeding materials and techniques of evaluation (Simmonds, 1981). Narrow- sense heritability of dry matter content of 0.65 and 0.92 has been reported (Jones, 1986; Courtney, 2007). These values show that there is a possibility for us to develop high dry matter sweetpotato from the available germplasm. G x E studies have shown that sweetpotato is sensitive to environmental variation (Manrique and Hermann, 2000). However, working with nutritional traits that included root dry matter, Wolfgang *et al.* (2005) found small G X E interactions.

Study Description

Five parental clones varying in DMC were hand-crossed in a half-diallel design to generate 10 families. After scarification, seeds were sown and raised in seedboxes with sterilized soil in a screenhouse at Namulonge, Uganda. Families with a high germination percentage were New Kawogo x Huameyano (89%) and New Kawogo x Kyabafuruki (80%). Ten genotypes of each family were planted at Namulonge in 2 environments (swamp and upland) and Serere in a randomized complete block design, with two replications, during October 2009 and March 2010. To assess DMC, 300 g from each genotype were oven-dried at 65^{0}C up to constant weight. DMC has been analyzed for Serere using GenStat 12th Edition program. General combining ability (GCA) and specific combining ability (SCA) will be computed according to model II, Method 4 as described by Griffing (1956). The gene action controlling dry matter content in these crosses will then be inferred from the relative magnitudes of GCA and SCA.

The establishment percentage was very good for eight families (>80%), but very low (<20%) for two genotypes of families SPK x Jewel and Jewel x Kyabafuruki. Virus incidence was very low, although *Alternaria* was very high at Serere. The cross with the highest mean in DMC was NKA x KYA (Table 1).

Table 1. DMC (%) for representatives crosses (Serere).

Cross	Parental DM	Mean	SD genotypes	Min	Max
JEW x HUA	L x L	34.9	4.8	27.5	42.0
SPK x HUA	H x L	36.6	3.0	29.7	41.0
SPK x KYA	H x H	36.5	3.0	30.7	40.5
NKA x KYA	H x H	37.6	2.3	33.7	41.1

L x L: Low x Low; H x L: High x Low; H x H: High x High.

Research Application

Highly significant differences were found among genotypes for DMC for all sites. However, significant differences between families were found only for Namulonge upland and swamp environments. Families didn't differ significantly in DMC for Serere site. Understanding the type of gene action and the effect of G x E interaction should help guide breeding strategies for DMC in sweetpotato. The study is on-going and efforts are currently focused on understanding the gene action controlling DMC.

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